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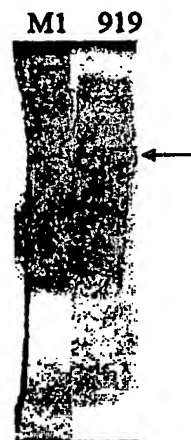
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(54) Title: NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

(57) Abstract

The invention provides proteins from *Neisseria meningitidis*, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.

919 (46 kDa)**A) PURIFICATION**

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NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

BACKGROUND

Neisseria meningitidis is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

N. meningitidis causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (eg. Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (e.g. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least n consecutive amino acids from the sequences and, depending on the particular sequence, n is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (eg. native, fusions *etc.*). They are preferably prepared in substantially pure or isolated form (ie. substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins)

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least n consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence, n is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (i) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Methodology - Summary of standard procedures and techniques.

General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

All publications, patents, and patent applications cited herein are incorporated in full by reference.

Expression systems

The *Neisseria* menB nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, *Gibberellins*: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilkink and Dons, 1993, *Plant Mol. Biol. Repr.*, 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet.*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl. Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to

those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO

Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human (α) α -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghrayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with CaCl_2 or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by

electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Eur. Cong. Biotechnology* 1:412.

v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.

Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCI/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guillermondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

Bacteriol. 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; *Pichia*]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular *Neisseria* protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular *Neisseria* protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisseria* sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria* menB proteins.

Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and

are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ^{125}I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ^{125}I , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance

or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hypodermic sprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection)....

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) RibiTM adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DetoxTM); (3) saponin adjuvants, such as StimulonTM (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ

described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human

immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No. 08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu &

Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A. Polypeptides

One example are polypeptides which include, without limitation: asialoglycoprotein (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of *Plasmodium falciparum* known as RII.

B. Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C. Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D. Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, eg. Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See eg. Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E.Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (*supra*); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin[®], and lipofectAMINE[®] are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are

assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

Nucleic Acid Hybridisation

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T_m of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy

yeast gene can be detected with an exposure time of only 1 hour starting with 1 μg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/ μg . For a single-copy mammalian gene a conservative approach would start with 10 μg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/ μg , resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (T_m) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4[\%(G + C)] - 0.6(\%\text{formamide}) - 600/n - 1.5(\%\text{mismatch}).$$

where C_i is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [eg. see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (e.g. to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

Chromosomal DNA Preparation

N.meningitidis strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl₃/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	(<i>Bam</i> HI- <i>Nde</i> I)
	<u>CGCGGATCCGCTAGC</u>	(<i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	(<i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	(<i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	(<i>Xho</i> I)
	<u>CCCGCTCGAG</u>	(<i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) <u>AAAGAATTC</u>	(<i>Eco</i> RI)
	(AAA) <u>AAAGGTACC</u>	(<i>Kpn</i> I)
3'-end primer tail:	(AAA) <u>AAACTGCAG</u>	(<i>Pst</i> I)
	(AAA) <u>AAATCTAGA</u>	(<i>Xba</i> I)

5' or 3'-end primer tail:

	<u>AAAGCATGC</u>		(<i>SphI</i>)
		AAAAAAGTCGAC	(<i>SalI</i>)

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridized to the sequence to be amplified. The melting temperature depended on the number and type of hybridising nucleotides in the whole primer, and was determined for each primer using the formulae:

$$T_m = 4 (G+C) + 2 (A+T) \quad (\text{tail excluded})$$

$$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N \quad (\text{whole primer})$$

The melting temperatures of the selected oligonucleotides were usually 65-70°C for the whole oligo and 50-55°C for the hybridising region alone.

Table 1 shows the forward and reverse primers used for each amplification. In certain cases, the sequence of the primer does not exactly match the sequence of the predicted ORF. This is because when initial amplifications were performed, the complete 5' and/or 3' sequences for some meningococcal B ORFs were not known. However the corresponding sequences had been identified in *Gonococcus* or in *Meningococcus A*. Hence, when the *Meningococcus B* sequence was incomplete or uncertain, *Gonococcal* or *Meningococcal A* sequences were used as the basis for primer design. These sequences were altered to take account of codon preference. It can be appreciated that, once the complete sequence is identified, this approach will no longer be necessary.

Oligonucleotides were synthesized using a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2.0ml NH_4OH , and deprotected by 5 hours incubation at 56°C . The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were centrifuged and the pellets resuspended in either 100 μl or 1.0ml of water. The OD_{260} was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration adjusted to 2-10pmol/ μl .

Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a template in the presence of 20-40 μ M of each oligonucleotide primer, 400-800 μ M dNTPs solution, 1x PCR buffer (including 1.5mM MgCl₂), 2.5 units *TaqI* DNA polymerase (using

Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H₂O or 10mM Tris, pH 8.5.

Digestion of PCR fragments

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-

terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30µl or 50µl with either H₂O or 10mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD₂₆₀ of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50µl of 10mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD_{260nm} and the concentration adjusted to 50µg/µl. 1µl of plasmid was used for each cloning procedure.

Cloning

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

ratio of 3:1 fragment/vector was ligated using 0.5 μ l of NEB T4 DNA ligase (400 units/ μ l), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100 μ l *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800 μ l LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200 μ l of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100 μ g/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30 μ l. 5 μ l of each individual miniprep (approximately 1g) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20 μ l, that included 0.5 μ l T4 DNA ligase (400 units/ μ l, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100 μ l of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800 μ l LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200 μ l of the supernatant and plated onto LB ampicillin (100mg/ml) agar.

Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD₆₀₀ ranged between 0.1 and 0.15. The flasks were incubated at 30°C into gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

GST-fusion proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD₂₈₀ of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer 10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M') (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD_{280nm} of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD_{280nm} of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

His-fusion soluble proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

His-fusion insoluble proteins large-scale purification.

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD₂₈₀ of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

Purification of His-fusion proteins.

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni²⁺-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD_{280nm} of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD_{280nm} of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions

collected until the $O.D_{280nm}$ indicated all the recombinant protein was obtained. 20 μ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

His-fusion proteins renaturation

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 μ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 μ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

Purification of proteins

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 μ l buffer M1 (PBS pH 7.2). 25 μ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] overnight at 4°C. The

supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

Mice immunisations

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)₃ as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

ELISA assay (sera analysis)

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H₂O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA was considered positive when OD₄₉₀ was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

phenildiamine and 10 μ l of H₂O₂) were added to each well and the plates were left at room temperature for 20 minutes. 100 μ l of 12.5% H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD₄₉₀ value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD₄₉₀ of 0.4 was higher than 1:400.

FACScan bacteria Binding Assay procedure.

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN₃) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD₆₂₀ of 0.07. 100 μ l bacterial cells were added to each well of a Costar 96 well plate. 100 μ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 μ l/well of blocking buffer in each well. 100 μ l of R-Phicoerytrin conjugated F(ab)₂ goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 μ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 μ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

OMV preparations

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice (50% duty cycle, 50% output). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

Whole Extracts preparation

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

Western blotting

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

Bactericidal assay

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD₆₂₀ was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD₆₂₀ of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward) CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse) GGCAGGGAATGGCGGATTAAAG
919.1	(forward) AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCT
919.6	(reverse) CAAATAAGAAAGGAATTTTG or GGTATCGCAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° (in according to T _m of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTGATCCAACC

- 919.1 (forward) AAAATGCCTCTCCACGGCTG or
CTGCGCCCTGTGTTAAAATCCCCT
- 919.2 (forward) ATCCTTCCGCCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAACCTC
- 919.5 (forward) GCGCGTGGATTATTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or
GGTATCGCAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAGTGCCG
- 919.8 (reverse) TAAAAAAAGTTCGACAGGG
- 919.9 (reverse) CCGTCCGCCTGTCGTCGCC
- 919.10 (reverse) TCGTTCCGGCGGGGTCGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 1: Oligonucleotides used for PCR for Examples 2-10

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCTGCAATCACGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTGTCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
206	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA <SEQ ID 3032>	XhoI
	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
287	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
406	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC <SEQ ID 3036>	XhoI
	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the

279 gnm4.seq

1	ATAACGCGGA	TTTGCGGCTG	CTTGATTTC	ACGTTTTC	GGCTTCGGC
51	AAGTTTGTG	GCGGCGGGT	TCATCAGGCT	GCAATGGGAA	GGTACGGACA
101	CGGCGACGG	CAGGCGCGT	TTGGCCTCG	CTTCTTTGGC	GGCAGCCATG
151	GCGCGTCCGA	GCGGCGCGC	TTGGCTCGCA	ATCACGATT	GTCCGGGTGA
201	GTGAAAGTTG	ACGGCTTCGA	CCACTTCGCT	TTGGCGGCT	TCGGGACAAA
251	TGGCTTTAAC	CTGCTCATCT	TCCAAGCCGA	GAAATCGCCG	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	GGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	TCAATGCGCC	GGCGGCAACG	AGTGCAGTGT
401	ATTCGCCGAG	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCGCGT
451	TCTAAATAG				

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1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTSLWAA SAQMALTCS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPA
151 SK*

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1   atgacgcgga tttgcggctg ctgatttca acggttttga gtgtttcggc
51  aagtttgtcg gcggcggggt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgcgct ttggctcgcg cttctttggc ggcagccatg
151 gtgcgtccga cggcgggcgc gttgctcgca atcacgactt gtccggggcga
201 gttgaagtta acggtcttga ccacttcgcc ctgtgcggat tcgggacaaa
251 tctgcctgac ctgttcattc tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatacgt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcggcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451 tccaaataq

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1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAFASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCS SSKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPP
151 SK*

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      10          20          30          40          50          60
m279-pep  ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAMARPTAAALPA
           :|:|||||:|:|||||||:|||||||:|||||||:|||||||:|||||||
g279       MTRICGCLISTVLVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAMVRPTAAALPA
           10          20          30          40          50          60

```


	70	80	90	100	110	120
m279 . pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
	: :					
g279	ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRTSLTA					
	70	80	90	100	110	120

	130	140	150
m279 . pep	SAKFNAPAATSAVYSPRLCPATAAGVLPASKX		
	:		
g279	SAKSNASAATSAVYSPRLCPATAAGVLPPTSKX		
	130	140	150

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3043>:

```

a279 . seq
1  ATGACNCNGA TTTGCGGCTG CTTGATTCA ACGGTTTNA GGGCTTCGGC
51  GAGTTTGTG GCGGCGGGT TCATGAGGCT GCAATGGGA GTACNGACA
101 CNGGCAGCG CAGGCGCGT TTGGCGCCG CTTCTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGG ATTGCCTGCA ATCACGACT GTCCGGGCGA
201 GTTGAAGTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTTAC CTGTTTCATC TCCAAGCCGA GAATCGCCG CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCGCT
451 TCCGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 3044; ORF 279.a>:

```

a279 . pep
1  MTXICGCLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAT SAVYSPXLCP ATAAGVLPPA
151 SE*

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m279/a279 ORFs 279 and 279.a showed a 88.2% identity in 152 aa overlap

	10	20	30	40	50	60
m279 . pep	ITRICGCLISTVFRASASLSAAGFIRLOWEGTDTGSGRARLAPASLAAAMAREPTAAALPA					
	: : :					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWE TDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60

	70	80	90	100	110	120
m279 . pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
	: :					
a279	ITTCPGELKLTASTTSSCADSAQICFTCS SKPRIAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120

	130	140	150
m279 . pep	SAKFNAPAATSAVYSPRLCPATAAGVLPASKX		
	:		
a279	SAKSNAPAATSAVYSPXLCPATAAGVLPASEX		
	130	140	150

519 and 519-1 gnm7.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3045>:

```

m519 . seq (partial)
1  ..TCCGTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCA

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251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTCG CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCCGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
551 TGATTTCTGC CCGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3046; ORF 519>:

```

m519.pep (partial)
  1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
  51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGGQREAE IQQSEGEAQA
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLSISAGMK IIDSSKTAK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3047>:

```

g519.seq
  1 atggaatttt tcattatctt gttggcagcc gtcgcccgtt tcggcttcaa
  51 atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
 101 ggcgtttcca tcgcgccctg acggccggtt tgaatatctt gattcccttt
 151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
 201 acccagccag gtctgcatca cgccgcgataa tacgcaattg actggtgacg
 251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
 301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
 351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
 401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcggg ggcttggggt
 451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
 501 ccttcgcgca atgcagggac aaattaccgc cgaacgcgaa aaacgcgccc
 551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
 601 ggtcagcggtg aagccgaaat ccaacaatcc gaaggcgagg ctgaggtgc
 651 ggtcaatgctg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
 701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
 751 cgtcaaattg ccgcccgcct tcaaacccaa agcggggcgg atgcggtcaa
 801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
 851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaccct
 901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaaata
 951 a

```

This corresponds to the amino acid sequence <SEQ ID 3048; ORF 519.ng>:

```

g519.pep
  1 MEFFIILLAA VAVFGFKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
  51 IDRVAIRHSL KBIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAAN
 251 RQIAAALQTO SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
 301 NFRRHEKFSP EAKTAK*

```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519/g519
m519.pep
          10      20      30
          SVIGRMELDKTFEERDEINSTVVAALDEAA
g519      YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
          90      100     110     120     130     140
m519.pep
          40      50      60      70      80      90
          GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGGQREAE

```



```

          |||
g519      GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRIEQINLASGQREAE
          150      160      170      180      190      200

          100      110      120      130      140      150
m519.pep  IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQGGADAV
          |||
g519      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAEANRQIAAALQTQSGADAV
          210      220      230      240      250      260

          160      170      180      190      200
m519.pep  NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK
          |||
g519      NLKIAEQYVTAFLAKEDNTRIKPAKVAEIGNPNFRHEKFSPEAKTAK
          270      280      290      300      310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3049>:

```

a519.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGC AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATG CCGCCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3050; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGEKSFV VIPQVEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQOS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 ORFs 519 and 519.a showed a 99.5% identity in 199 aa overlap

```

          10      20      30
m519.pep  SVIGRMELDKTFEERDEINSTVVAALDEAA
          |||
a519      YFQVTDPKLASYGSSNYIMAITQLAQTTLSVIGRMELDKTFEERDEINSTVVSALDEAA
          90      100      110      120      130      140

          40      50      60      70      80      90
m519.pep  GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRIEQINLASGQREAE
          |||
a519      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRIEQINLASGQREAE
          150      160      170      180      190      200

          100      110      120      130      140      150

```



```

m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
a519          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                210      220      230      240      250      260

m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
a519          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51  ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GCGGTTTCCA TCGCGCCTG ACGGcCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCA AACTCGCTC ATACGGTTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCCAA GCGGGTGGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEFFIILLVA VAVFGFKSFV VIPOQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCA AACTCGCTC ATACGGTTG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCGGTTACGA AATCAAGGAT TTGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCCAA GCGGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCG GTTCAACAAT CTTGCCAAAG

```


851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAATAAA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep

1 MEFFFIILLAA VAVFGFKSFV VIPQOEHVHV ERLGRFHRAL TAGLNILIPF
51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAELI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

g519-1.pep	10	20	30	40	50	60
	MEFFFIILLAAVAVFGFKSFVVIPQOEHVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFFIILLVAVAVFGFKSFVVIPQOEHVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	70	80	90	100	110	120
	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	130	140	150	160	170	180
	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	190	200	210	220	230	240
	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	250	260	270	280	290	300
	LVAEANAELIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAELIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
g519-1.pep	310					
	ISAGMKIIDS SKTAKX					
m519-1	ISAGMKIIDS SKTAKX					
	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq

1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT
201 ACCAGCCAGT GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTGAAGAA CGCGACGAAA


```

401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCATTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVFGRKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GOREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAELI
251 RQIAAALQTQ GGADAVNLKI AEQYVAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

a519-1.pep	10	20	30	40	50	60
	MEFFIILLAAVVVFGRKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
a519-1.pep	70	80	90	100	110	120
	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
a519-1.pep	130	140	150	160	170	180
	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
	130	140	150	160	170	180
a519-1.pep	190	200	210	220	230	240
	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
a519-1.pep	250	260	270	280	290	300
	LVAEANAELIRQIAAALQTQGGADAVNLKIAEQYVAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAELIRQIAAALQTQGGADAVNLKIAEQYVAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
a519-1.pep	310					
	ISAGMKIIDS SKTAKX					
m519-1	ISAGMKIIDS SKTAKX					
	310					

m576.seq.. (partial)

1	..	ATGCAGCAGG	CAAGCTATGC	GATGGCGCTG	GACATCGGAC	GCTCCCTGAA
51		GCAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGAAG
101		CCATCGAGGC	AGTGTATGC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
151		CTCTAGGAAG	TCATGATGAA	ATTCTTTCAG	GAACAACAGG	CTAAAGCCGT
201		AGAAAAACAC	AAGCGGGACG	ACGAGGCCAA	TAAAGAAAAA	GGCGAAGCGT
251		TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGC
301		CTGCATATCA	AAATCACCAA	ACAGGGCGAA	GGCAAACAGC	CGACCAAAGA
351		CGACATCGTT	ACCGTGGAAAT	AGCAAGGCCG	CCTGATTGAC	GGTACGGTAT
401		TCGACAGCAG	CAAGGCCAAC	CGCGCCCGCG	TCACCTTTCC	TTTGAGCCAA
451		GTGATTCCGG	GTTGGACCGA	AGCGTATCAG	CTCTGTAAG	AAGGCGCGCA
501		AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG
551		GCGACAAAAT	CGGTCCGAA	GCCACTTTGG	TATTTGATGT	GAAACTGGTC
601		AAAATCGGCG	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	CTCAAGTCGA
651		CATCAAAAAA	GTAATTAA			

m576.pep.. (partial)

```

1  ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMKFKLQ  EQQAKAVEKH KADAKANKEK GEAFLENAA  KDGVKTTASG
101 LQYKITKQGE  GKQPTKDDIV  TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVE  LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFVDKLV
201 KIGAPENAPA  KQPAQVDIKK  VN*

```

q576.seq.. (partial)

1	..atgggcgtgg	acatcggacg	ctccctgaaa	caaatgaagg	aacagggcgc
51	ggaatcgcg	ttgaaagtct	ttaccgatgc	catgcaggca	gtgtagtacg
101	gcaaaagaa	caaaatgacc	gaagagcagg	cccaggaa	gatgatgaaa
151	ttctcgagg	agcagcagg	taaagccgta	gaaaaacaca	agggcgatgc
201	gaaggccaac	aaagaaaaag	cgcgaagcct	cctgaaggaa	aatccgcgcg
251	aagacggcgt	gaagaccact	gcttcgggtc	tgcagtacaa	aatcaccaaa
301	cagggctgaag	gcaaacagcc	gacaaaagac	gacatcgtta	ccgtggaata
351	cgaaaggccg	ctgattgacg	gtaccgtatt	cgacagcagc	aaagccaacg
401	gcggcccgcc	caccttcctt	ttgagccaag	tgattccggg	ttggaccgaa
451	ggcgtaccgc	ttctgaaaga	aggcggcgaa	gccacgttct	acatcccgtc
501	caacctttgcc	taccgcgaac	agggtcgggg	cgaaaaaatc	ggtccggaacg
551	ccacttttgg	atttgacgtg	aaactgggtc	aaatcgggcg	accgaaaaac
601	gcgcccgcga	agcagccgga	tcaagtcgac	atcaaaaaag	taataata

g576.pep.. (partial)

```

1  ..MGVDIGRSLK QMKEQGAeid LKVETDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGAEFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFdSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKOPDOVD IKKVN*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

m576.pep 10 20 30 40 50 60
MQQASYAMGVDIGRSLKQMKEQGAEIDLKFVTEAMQAVYDGGKEIKMTEEQAQEVMMKFLO
||| ||| ||| ||| ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| |||


```

g576          MGVDIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQ
                10      20      30      40      50

                70      80      90      100     110     120
m576.pep      EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGEKQPTKDDIV
                |||
g576          EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGEKQPTKDDIV
                60      70      80      90      100     110

                130     140     150     160     170     180
m576.pep      TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
                |||
g576          TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE
                120     130     140     150     160     170

                190     200     210     220
m576.pep      QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN*
                |||
g576          QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN*
                180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTCCG CCGCTTTGGC
51  ACTTTCGCC  TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCGCG TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGATATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAA CCGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1   MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVEDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

m576.pep          10      20      30
                  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                  |||
a576              30      40      50      60      70      80
CGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV DIGRSLKQMK EQGAEIDLKV

                40      50      60      70      80      90
m576.pep      FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                |||
a576          FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                90      100     110     120     130     140

```


	100	110	120	130	140	150
m576.pep	K D G V K T T A S G L Q Y K I T K Q E G K Q P T K D D I V T V E Y E G R L I D G T V F D S S K A N G G P V T F P L S Q					
a576	K D G V K T T A S G L Q Y K I T K Q E G K Q P T K D D I V T V E Y E G R L I D G T V F D S S K A N G G P V T F P L S Q					
	150	160	170	180	190	200
m576.pep	V I P G W T E G V Q L L K E G G E A T F Y I P S N L A Y R E Q G A G D K I G P N A T L V F D V K L V K I G A P E N A P A					
a576	V I L G W T E G V Q L L K E G G E A T F Y I P S N L A Y R E Q G A G D K I G P N A T L V F D V K L V K I G A P E N A P A					
	210	220	230	240	250	260
m576.pep	K Q P A Q V D I K K V N X					
a576	K Q P A Q V D I K K V N X					
	270					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

m576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCCCGCG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGCTGCGG
701 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQOMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVEDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

g576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TECTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCCCGCG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGCTGCGG

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701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

g576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LOYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPDQVDIKK VN*

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TL	SAALALSA	CGKKEAAPAS	ASEPAASAA	QGDTSSIGSTM
m576-1	MNTIFKISAL	TL	SAALALSA	CGKKEAAPAS	ASEPAASAA	QGDTSSIGSTM
	10	20	30	40	50	60
	70	80	90	100	110	120
g576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
	130	140	150	160	170	180
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LOYKITKQGE	GKQPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LOYKITKQGE	GKQPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
	190	200	210	220	230	240
g576-1.pep	GT	VF	DSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF
m576-1	GT	VF	DSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF
	190	200	210	220	230	240
	250	260	270			
g576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

a576-1.seq

1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
 101 CTGCCGCGC TTCTTCCGCG CAGGCGGACA CCTCTTCGAT CGGCAGCAGC
 151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
 201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
 251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG
 301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
 351 AGAAAAACAC AAGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
 451 CTGCAATACA AAATACCAA ACAGGGCGAA GGCAACAGC CGACCAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGCCCG CCTGATTGAC GGTACGGTAT
 551 TCGACAGCAG CAAAGCCAAC GGCGGCCCG TCACCTTCCC TTGAGCCAA
 601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGCTGCGG

701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGATGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep

1 MNTIFKISAL TLSAALALS CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

a576-1/m576-1 ORFs 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISAL	TLSAALALS	SACGKKEAAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV
m576-1	MNTIFKISAL	TLSAALALS	SACGKKEAAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTeamQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTeamQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITQGE	GKOPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITQGE	GKOPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKAN	GGPVTFPLSQ	VILGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN
m576-1	GTVFDSSKAN	GGPVTFPLSQ	VILGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VN		
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq

1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT
 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
 101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
 151 GGAACGACGG TCGGCGGCGG CGGGGCCGTC TATACCGTTG TACCGCACCT
 201 GTCCCTGCCG CACTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
 251 TCCGCCTCGG CTGCGCCAAT TTGAAAACC GCCAAGGCTG GCAGGATGTG
 301 TCGGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCTTTCAGG CAAAACAGTT
 351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
 401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG


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451 CGGACGGCAC AAGCCCGCTT CCGATTTCAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCTGCGCG GTTTCGCGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCGG ACCTCTCCCG ATTCCCACAT ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTACGCC
751 GAAGACCCTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGTATA TGGCGGATA GGGCTACCTC
901 AAATCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGGCGCAAAA
951 TCCGCAACGC CTCGCGAAG TTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAG AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

m919.pep

```

1 MKKYLFRAL YGIAAAILAA CQSKSIQTFP QPDSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAPQTPVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGGDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYL
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMQRNPQR LAEVLGQNPS YIFFRELAGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

g919.seq

```

1 ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51 CctcgCGGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCC GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCTCCG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTCACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGCAGG
451 CGGACGGAAC GGGCCCGCTT CCGATTTCAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGAc ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCGG ACCTCTCCCG ATTCCCACAT ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCcg tccggcaaat acatCCGCAt cggaTaccgc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGTCCG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGATACGT CTGGCAGCTC CTGCCCCAAG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```


This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

g919.pep
 1 MKKHLRSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
 51 GTTVAGGGAV YTVVPHLSMP HWAADFQAKS LQSFRLGCAN LKNRQGWQDV
 101 CAQAFQTPVH SFOAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
 151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
 201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
 251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
 301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVGALG
 351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
 401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

m919/g919

m919.pep	10	20	30	40	50	60
	MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
g919	MKKHLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
m919.pep	70	80	90	100	110	120
	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFOAKQFFER					
g919	YTVVPHLSMPHWAADFQAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFOAKRFFER					
	70	80	90	100	110	120
m919.pep	130	140	150	160	170	180
	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGIIPDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGTHADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
	190	200	210	220	230	240
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
	250	260	270	280	290	300
m919.pep	310	320	330	340	350	360
	KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAYSNDGPVGALGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAYS GNEGPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420


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          430      440
m919.pep  QKTTGYVWQLLPNGMKPEYRPX
          |||||
g919      QKTTGYVWQLLPNGMKPEYRPX
          430      440

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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCGG CGCCGCCCTG TGCGGCATCG CCGCCGCCAT
51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGCCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCGTTCAGG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCGCTT CCCGATTAC GGTATTCGG ACGATTTTAT
501 CTCCGTCCCC CTGCGTCCG GTTTGCAGG CGGAAAAGCC CTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCGCG ACCTCTCCCA ATTCCCATC ACTGCGGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTACGCC
751 GAAGACCCCG TCGAATTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGCAAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGCGATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCAAG TTTTGGGGCA AAACCCAGC TATATCTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCGCTGA TGGCGGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCGTATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGCAGCAAG CCGGCGAAGT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCACCG
1301 GTATGAAGCC CGAATACCG CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```

a919.pep
1  MKKYLFRAL CGIAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQAARFPIY GIPDDFISVP LPAGLRSGKA LVRIQRTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQONPOR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

```

          10      20      30      40      50      60
m919.pep  MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          10      20      30      40      50      60

          70      80      90      100     110     120
m919.pep  YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
          |||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
          70      80      90      100     110     120

```


m919.pep	130	140	150	160	170	180
	YFTPWQVAGNSLAGT	VTGYE	PVLKGD	DRRTAQAR	FPIYGIP	DDFISVPLPAGLRSGKA
a919	YFTPWQVAGNSLAGT	VTGYE	PVLKGD	DRRTAQAR	FPIYGIP	DDFISVPLPAGLRSGKA
	130	140	150	160	170	180
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
a919	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMH	IQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL				
a919	DGKAPILGYAEDPVELFFMH	IQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL				
	250	260	270	280	290	300
m919.pep	310	320	330	340	350	360
	KLQOTSMQGIKSYMRQNPORLA	EVLGONPSYIFFREL	AGSSNDGPVGALGTPLMGEYAGA			
a919	KLQOTSMQGIKAYMQONPORLA	EVLGONPSYIFFREL	TGSSNDGPVGALGTPLMGEYAGA			
	310	320	330	340	350	360
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
a919	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420
m919.pep	430	440				
	QKTTGYVWQLLPNGMKPEYRPX					
a919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTG
201 GCAAGAACTC AGCCGCCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxCAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCC TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```


m121.ppt

```

1 METQLYIGIM SGTSMGDGADA VLIRMDGGKW LGAEGHAFTP YPGLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCQNLAAPS DITALGCHGQ
101 TVRHAPHEGY S IQLADLPLL AXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
151 XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLRSF TAQTVCDAVS HAAADARQMY ICDGGIRNPV
301 LMDALACEFG TRVSLHSTAD LNLDPQWVEA AXFAWLAAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

g121.seq

1	ATGGAACAC	AGCTTTACAT	CGGCATTATG	TCGGAACCA	GTATGGACGG
51	GCGGATGCC	GTGCTGTATC	GGATGGACGG	CGGCAAATGG	CTGGGCGCGG
101	AAGGGCAGC	CTTTACCCC	TACCGTAAC	GGTTGCGCCG	CAAATTGCTG
151	GATTTCAGG	ACACAGGCAC	AGACCAACTG	CACCGCAGCA	GGATGTTGTC
201	GCAAGAACTC	AGCGCGCTGT	ACGCGCAAAAC	CGCCGCGGAA	CTGCTGTGCA
251	GTCAAACCT	CGCTCCGTGC	GACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTtac	AGCATACAGC	TTGCCGATTT
351	GCCGCTGCTG	GCGGAACtGa	cgcggatttT	TACCGTCggc	gacttcCGCA
401	GCCGCGACCT	TGCTCCGCGC	GgacaAGGTG	CGCCGCTCGT	CCCCCGCTTT
451	CACGAAGCCC	TGTTCCGCGA	TGACAGGGAA	ACACGCGTGG	TACTGAACAT
501	CGGCGGGATT	GCCAACATCA	GCGTACTCCC	CCCCGGCGCA	CCCGCCTTCG
551	GCTTCGACAC	AGGGCCGGGC	AATATGCTGT	TGGAcgcgtg	gacgcaggca
601	cacTGGcagc	TGCTTTACGA	CAAAAacggt	gcAAAGgcg	cacAAGGCAA
651	catatTGCcg	CAACTGCTCG	cgagcgtGCT	CGCCaccCG	TATTTCTCAC
701	AACCCcacc	aaAAAGCACG	GGgcGCCgaac	TgtttgccccT	AAattggctc
751	gaaacctAcc	ttgacgycgg	cgaaaaccga	tacgacgtat	tgcggaacgct
801	ttcccgattc	accgcgcaaa	ccgTttggga	cgccgtctca	CACGACCGGG
851	CAGATGCCCC	TCAAATGTAC	ATTTGCGGCG	CGCGCATCCG	CAATCCTGTT
901	TTAATGGCGG	ATTTGCGAGA	ATGTTTTCGGC	ACACGCGTTT	CCCTGCACAG
951	CACCGCGGAA	CTGAACCTCG	ATCCTCAATG	GGTGGAGGCG	gccgCATTtg
1001	cgtggttggC	GGCGTGTGG	ATTAACCGCA	TTCCCGTAG	TCCGCACAAA
1051	GCGACCGGCG	CATCCAAACC	GTGTATTCTG	GGCGCGGGAT	ATTATTATTG
1101	A				

g121.pap

```

1 METQLYIGIM SGTSMGDGADA VLVRMDGGKW LGAEGHAFTP YPDLRLRRKLL
51 DLQDTQSDDEL HRSRMSLQSEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPAP
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGEDTGBG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRLTSRF TAQTQWDAYS HAAADARQMY ICGGGIRNPV
301 LMDLAEFCFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYT*

```

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRQLLDLQDTGADEL					
	: : : :					
g121	METQLYIGIMSGTSMGDGADAVLVLRMDGGKWLGAEGHAFTPYDRLRRKLDDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLPASDITALGCHGQTVRHAPHEHGYSIQLADPLLL					
	:					


```

g121      HRSRMLSQELSRLYAQTA AELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
           70      80      90      100      110      120
           130      140      150      160      170      180
m121.pep  AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : : : : :
g121      AELTRIFTVGDFRSRDLAAGGQGAPLVPAPFHEALFRDDRETRVVLNIGGIANISVLPPGA
           130      140      150      160      170      180
           190      200      210      220      230      240
m121.pep  XXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : : ||||| : ||||| ||||| : |||||
g121      PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLRLLAHPYFSQPHPKST
           190      200      210      220      230      240
           250      260      270      280      290      300
m121.pep  GRELFAINWLETYLDGGENRYDVLRTLRSRFTAQTVCDAVSHAAADARQMYICDGGIRNPV
           ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g121      GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVDVSHAAADARQMYICGGGIRNPV
           250      260      270      280      290      300
           310      320      330      340      350      360
m121.pep  LMADLAECFGTRVSLHSTADLNLDPOWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
g121      LMADLAECFGTRVSLHSTAELNLDPOWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           310      320      330      340      350      360

m121.pep  XAGYYYY
           |||||
g121      GAGYYYY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TGCGGCCGGC GGACAAGGCG CGCCGCTCGT CCCC GCCTTT
451 CACGAAGCCC TGTTCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCC GACGCA CCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCACACCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTG ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCGCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRRLRKL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAP
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMOA
201 HWQLPYDKNG AKAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRSR TAQTVFDDAVS HAAADARQMY ICGGGIRNPV

```


		10	20	30	40	50	60
m121.pep		METQLYIGIMSGTSM	DGADAVLIRM	DGGKWLGAEGHAFT	PYPGRLRRQL	LDLQDTGADEL	
a121		METQLYIGIMSGTSM	DGADAVLIRM	DGGKWLGAEGHAFT	PYPGRLRRKL	LDLQDTGADEL	
		10	20	30	40	50	60
		70	80	90	100	110	120
m121.pep		HRSRILSQELSR	LYAQTAELLCS	QNLAPSDITAL	GC	HGQTVRHA	PEHGYSIQ
a121		HRSRILSQELSR	LYAQTAELLCS	QNLAPSDITAL	GC	HGQTVRHA	PEHSYSVQ
		70	80	90	100	110	120
		130	140	150	160	170	180
m121.pep		XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX
		:	:		:		
a121		AERTQIFTVGDF	RSRDLAAGGQ	GAPLVPAF	HEALFRDDRE	TRAVLNIGG	IANISVLP
		130	140	150	160	170	180
		190	200	210	220	230	240
m121.pep		XXXXXXXXXXXXXXXX	XXXXXQLPYD	KNGAKSAQ	GNILPQLL	DRLLAHPY	FAQRHPKST
		:					
a121		PAFGFDTGPGN	MLMDAWMQAH	WQLPYDKNGA	KAQAQGNIL	PQLLDRLLA	HPYFAQPHKST
		190	200	210	220	230	240
		250	260	270	280	290	300
m121.pep		GRELFAINWLE	TYLDGGENRY	DVLR	TLRSRTAQ	TVCDAVSHAA	ADARQMYIC
a121		GRELFALNWLE	TYLDGGENRY	DVLR	TLRSRTAQ	TVCDAVSHAA	ADARQMYIC
		250	260	270	280	290	300
		310	320	330	340	350	360
m121.pep		LMADLAECFG	TRVSLHSTAD	LNLDPOQW	VEAAXFAW	LAACWINR	IPGSPHKAT
a121		LMADLAECFG	TRVSLHSTAE	LNLDPOQW	VEAAAFAW	MAACVWNR	IPGSPHKAT
		310	320	330	340	350	360
m121.pep		XAGYYYY					
a121		GAGYYYY					

m121-1.seq

1	ATGGAACAC	AGCTTTACAT	CGGCATCATG	TCGGAACCA	GCATGGACGG
51	GGCGGATGCC	GTACTGATAC	GGATGGACGG	CGGCAAATGG	CTGGGCGCGG
101	AAGGGCACCG	CTTTTACCGT	TACCCCGGCA	GGTTACGCGG	CCAATTGCTG
151	GATTTCGAGG	ACACAGCCGC	AGACGAACTG	CACCCGACGA	GGATTTTGTC
201	GCAAGAACTC	AGCGGCTTAT	ATCGGCAAC	CGCCGCCGAA	CTGCTGTGCA
251	GTCAAAACCT	CGCACCCTCC	GACATTACCG	CCCTCGGTG	CACGGCGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTTAC	AGCATACAGC	TTGCCGATTT
351	GCCGCTGCTG	GCGGAACCGA	CGCGGATTTT	TACCGTCGGC	GACTTCCGCA
401	GCCGCGACCT	TGCGGCCGGC	GGACAAGGGC	CGCCACTCGT	CCCCGCTTTT
451	CACGAAGCCC	TGTTCCGCGA	CACAGGGGAA	ACACGCGCGG	TCTGAACAT
501	CGGCGGGATT	GCCAACATCA	CGGTACTCCC	CCCCGACGCA	CACGCCTTCG
551	GCTTCGACAC	AGGGCCGGGC	AATATGCTGA	TGGACGCGTG	GACGACGGCA
601	CACTGGCAGC	TTCTTACGA	CAAAAACGGT	GCAAAGGCGG	CACAAGGCAA
651	CATATTGCCG	CAACTGCTCG	ACAGGCTGCT	CGCCACCCG	TATTTGCGAC
701	AACCCCAACC	TAAAGCACG	GGGCGCGAAC	TGTTTGCCCT	AAATTGGCTC
751	GAAACCTACC	TTGACGGCGG	CGAAAACCGA	TACGACGTAT	TGCGGACGCT
801	TTCCCGTTTT	ACCGCGCAA	CCGTTTGCGA	CGCCGTCTCA	CACGACGCGG


```

851 CAGATGCCCC TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GGCGTGTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

m121-1.pep

```

1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDGTGP NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
	: : : : :					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	: : : : :					
g121	HRSRILSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
	: : : : :					
g121	AELTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDGTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	: : : : :					
g121	PAFGFDGTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDAYS HAAADARQMYICGGGIRNPV					
	: : : : :					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAYS HAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	: : : : :					
g121	LMADLAECFGTRVSLHSTAE LNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121-1.pep	XAGYYYYX					
g121	GAGYYYYX					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

a121-1.seq

```

1 ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

```



```

51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TGCGGCCGGC GGACAAGGCG CGCCGCTCGT CCCCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCACGCA CCCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGATTG ACCGCGCAAA CCGTTTCGA CGCCGTCTCA CACGACGGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGCGAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGADAVLIRMDGGKW	LGAEGHAFTPYPGRLLRRQLLDLQDTGADEL				
a121-1	METQLYIGIMSGTSMGADAVLIRMDGGKW	LGAEGHAFTPYPGRLLRRKLLDLQDTGADEL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPHEHGYISQLADLPLL					
a121-1	HRSRMLSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPESYSVQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDNRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGPNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300


```

          310      320      330      340      350      360
m121-1.pep  LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
          |||||:|||||:|||||:|||||:|||||:|||||
a121        LMADLAECFGTRVSLHSTAELNLDPOWVEAAAFAWMAACWVNRIPGSPHKATGASKPCIL
          310      320      330      340      350      360

m121-1.pep  XAGYYYYX
          |||||
a121        GAGYYYYX

```

128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

```

m128.seq (partial)
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAACTC AACCAC
1  TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51  wGTCAAAAAA TAYTTCCCYG TCGGCAAwGT ATTAACCGA CTGTTCCGCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAC yGTCCCGTC
151 TGGCACAAG ACGTGCCTA TTKTGAATTG CAACAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGAAGGCC CGCyTGAGCC ACGACGAAAT CCTCATCTC TTCCACGAAA
401 CCGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGAAAAAT TTCGTTTGGG AATACAATGT CTTGGCACA mTGTACAGCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAsG CGGCATGTTT yTsGTCCGGC AAwTGGAGTT
651 CGCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCGCCCCG AATACAACCG CTTGCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGCGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGgAT CGCGCAGCGG
951 nGCAGAATCC TTCAAAGCCT TCCGCGCGG CGAACCgAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3086; ORF 128>:

```

m128.pep (partial)
1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

//

1  YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTPV
51  WHKDVRYXEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFS DGT
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQOVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT
301 GKRFWQEBILA VGXSRSGAES FKAFRGREPS IDALLRHS GF DNAV*

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

```

g128.seq
1  atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTtaatca
51  aatccaaacc gaagACAtca AACCGCGCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCGGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCTG AGCGTCTGAC CGGCATCACC GAACGCGTCTG GCAGGATTTG
201 GGGCGTCTGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCGCC
351 CGAATTGCA ACGCTTTCCC CCGCACAAA AACCAGCTC GATCACGACC
401 TGCGCGATTT CGTATTGAGC GCGCGGAAC TGCCGCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGT CCGCATTAC TTTGACGATG
551 CCGCACGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTGCCGCC
601 GCCGCGCAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGCG
751 AAATCGACA ACACCGCAA CATCGACGCG ACCTCGAAA ACGCATTGAA
801 AACCgcaaaa cTGCTCGGCT TAAAAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCGCGCGG CCAAACCTTA CGCCGAAAA GACCTCGCGG AAGTCAAAGC
951 CTTGCGCCGC GAACACCTCG GTCTCGCCGA CCCGACGCG TGGGACTTGA
1001 GCTACGCGCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGCAAAA GTTCTGGCAG GCCTGTTGCG
1101 CCAAATCAA AAACCTACG GCATCGGATT CGCCGAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGCGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGActaca AAGGCGCGG CCGCTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTGGC
1351 GGCAAGAAG CGCGTTAAG CCACGACGAA ATCCTCACC TCCTCCACGA
1401 AacCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAacggcgtA GAATGGGACG CGGTGGAAC GCCCAGCCAG
1501 TTTATGGAAC ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgCGGAGC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TcgCGCCAA AAACCTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCCGAGG CTATTACAGC TACGATGGG CCGAAGTCct
1851 cAGCACCGAT GCCTACGCCG CTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAACG CTTCTGGCAA GAAAtccttg ccgtcggcgg ctCCCGCAGC
1951 gcgCGGGAAT CCTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTGCTGCGC CAaagcggT TCGACAACGC gGcttga

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

```

g128.pep
1  MIDNALLHLG EEPFRNQIQT EDIKPAVQTA IEARQGIQA VKAQTHTGWA
51  NTVERLTGIT ERVGRWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDV R YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKRRRFA DGTQLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLPHETGH GLHLLTQVD ELGVSGINGV EWDVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QVLDsvrKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRFWQ EILAVGGSRs

```


651 AAESFKAFRG REPSIDALLR QSGFDNAA*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)
from *N. gonorrhoeae*:

m128/g128

g128.pep	10	20	30	40	50	60
	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
g128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
g128.pep	130	140	150	160	170	180
	TLSPAQKTKLDHDLRDFVLGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
g128.pep	340	350	360			
	YAGEKLREAKYAFSETEVKKYFPVGVKVLG					
m128	YASEKLREAKYAFSETXVKKYFPVGXVLNG					
	10	20	30			
g128.pep	370	380	390	400	410	420
	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
g128.pep	430	440	450	460	470	480
	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHLHLLTQVDELGV					
m128	GRRRPSDGTQLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVDELGV					
	100	110	120	130	140	150
g128.pep	490	500	510	520	530	540
	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQRCGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQXGMF					
	160	170	180	190	200	210
g128.pep	550	560	570	580	590	600
	LVRQMEFALFDMMIYSESDCRLKNWQQVLDSVRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQKEFALFDMMIYSEDDEGRKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
g128.pep	610	620	630	640	650	660
	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSAGAESFKAFRGREPS					
	280	290	300	310	320	330


```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTGGTG TCGCACCTCA ACTCCGTAC CGACACGCCC GAACTGCGCG
251 CCGCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACACGATC
401 TCGCGGATTT CGTCTCAGC GCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAC CGAAGGCGCG CAACTTTCCG CCAAATCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGCGATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCGC CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GTACGCGCG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCGC
1101 CCAAATCAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGCGC TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGCGCG
1251 CGCGTGGATG AACGACTACA AAGGCCGCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCACCC GCGCGTGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCAGTCAG
1501 TTTATGGAAA ATTTGTTTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGCGGTTT CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGTTT TAGACAGCGT GCGCAAGAA GTCGCCGTG
1751 TCCGACCGCC CGAATACAA CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCGC CTTTGAAGA AAGCGACGAT GTCGCCGCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKRRRRES DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHHLLTQVD ELGVSGINGV EWDVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAANKFQ RGMFLVRQME

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551 FALFDMMIYS EDDEGR LKNW QQVLD SVRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
 651 AAESFKAERG REPSIDALLR HSGFDNAA*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQTHTGWANTVEPLTGIT					
a128	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQTHTGWANTVEPLTGIT					
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNREFTIKNSPEFD					
a128	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNREFTIKNSPEFD					
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	130	140	150	160	170	180
	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSONVLDAFGIY					
m128.pep	-----					
a128	190	200	210	220	230	240
	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
m128.pep	-----					
a128	250	260	270	280	290	300
	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNLFHDL					
m128.pep						140
						YASEKLREAKYAFSETXVKKYFPVGX
a128	310	320	330	340	350	360
	ARRAKPYAEKD LAEVKAFARES LGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	370	380	390	400	410	420
	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPFVGGREARLSHDEILILFHETGHLHLLTQVD					
a128	430	440	450	460	470	480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD					
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWD AVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	490	500	510	520	530	540
	ELGVSGINGVEWD AVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGR LKNWQQVLD SVRKKVAVIQPPEYNRFALSFGHIF					
a128	550	560	570	580	590	600
	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLD SVRKEVAVVRPPEYNRFANSFGHIF					

m128-1.seq

This corresponds to the amino acid sequence <SEQ ID 3092; ORF 128-1>:

m128-1.pgp.

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51 NTVEPLTGIT ERVGRIWGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI

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```

101 GQDIELYNRF KTIKNSPEFD TSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLPQ WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKRRRFS DGTQLQPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDDELPSQ
501 FMENFWWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLLKNW QQVLDVSRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

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The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1 ATGATTGACA ACGACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51 AATCAAAACC GAAGACATCA AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGCGG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCT CCGCACAAAA AACCAAGCTC GATCACGACC
401 TGCGCGATTT CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATCTCT
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGCGATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TAAAAAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAGGTTT TAAATTCCT GCACGACCTC
901 GCCCGCGCGG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCCG GAACACCTCG GTCTCGCCGA CCCGACGCGG TGGGACTTGA
1001 GCTACGCCGG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTTCG
1101 CCAAATCAAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGCGGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGG CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1 MIDNALLHLG EEPFRNQIKT EDIKPAVQTA IAEARGQIAA VKAQTHGTWA
51 NTVERLTGIT ERVGRINGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKTYGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKRRRFA DGTQLQPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

10 20 30 40 50 60

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGTWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAKAQHTGTWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRIGVGVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
m128-1	ERVGRIGVGVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLGSAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLGSAELPPEQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFDNTANIDRTLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDLSYAGEKLRKAYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPQWDLGAYASEKLRKAYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWM
m128-1	VINGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKNFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGCGG GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCACGATC
401 TCGCGGATTT CGTCTCAGC GCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAC CGAAGGCGCG CAACTTCCG CCAAATTCTC

```



```

501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCCTG TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCGCA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCCGCCCG GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCGC
1101 CCAAATCAAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGCGG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGCGCGCGC CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTTAC CTGCTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATCTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAACCG CTTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWAA
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVINFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLPQ WDLGYAGEKL REAKYAFSET
351 EVKKYFPVKG VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKRRRFS DGTQLPLTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHHLLTQVD ELGVSGINGV EWDVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRKKNW QOVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFESDD VAATGKREWF EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

```

          10      20      30      40      50      60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
|||||
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90      100     110     120
a128-1.pep ERVGRWGVVSHLNSVTDTPPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
|||||
m128-1      ERVGRWGVVSHLNSVADTPPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90      100     110     120

          130     140     150     160     170     180

```


a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVNLFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVNLFLHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHGLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDEGRILKNWQQVLDVSRKEVAVVRPEYNNRFAANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDEGRILKNWQQVLDVSRKKVAVIQPPEYNNRFAANSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAAX
	670


```

1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAT AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCGCGCGACA TGGCGGCGGC AAGCCGAAA ATCCCCGACA GCCGCTCAA
351 GCGCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 3098; ORF 206>:

m206.pep..

```

1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3099>:

g206.seq

```

1  atgttttccc ccgacaaaac ccttttcttc tgtctcggcg cactgtctct
51  cgcctcatgc ggcacgacct ccggcaaaca ccgccaaccg aaacccaaac
101 agacagtccg gcaaattcaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctccgactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcgga
251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atcccgcaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcaccatgc ccccggcagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgcaaaaaa
501 ctaccttga ggcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 3100; ORF 206.ng>:

g206.pep

```

1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	LGLIGTPYKW GGSSTATGFDCSGMIQFVYKNALNVKLPR TARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKW GGSSTATGFDCSGMIQLVYKNALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLGAHTFFTE					
g206	IVFFNTGGAH RYSHVGLYIG NGEFIHAPSG GKTIKTEKLS TPFYAKNYLGAHTFFTE					
	130	140	150	160	170	

130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCCGACA GCCGCCTTAA
351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGAAT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
a206	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLSTPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTGT CCCTTTCAGC
51  CTGCGGGGGC GCGGCTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTCTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GCGGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCGGTT
551 CTTCAGATCC CATCCCCGCG TCAAACCTG CACCTGCGAA TGGCGGTAGC
```



```

601 AATTTTGGAA GGGTTGATTT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAAT CAGAATTTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCCGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCCGTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCGGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCCA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCGAG
1201 TTTGCCGCAA AAGTCGATT TCGCAGCAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGCAT GATTTGCATA TGGGTACGCA AAAATTCAA GCCGCCATCG
1301 ATGGAAACGG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTTGCCGGCA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

m287.pep

```

1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMAA
151 DGMQDDPSA GGQNAAGTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NGFRVDLANG VLIDGPSQNI TLTHCKGDSG SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRSLPAE MPLIPVQAD TLIVDGEAVS LTGHSNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTOQFK AADGNFGFK TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

g287.seq

```

1 atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcggtggcg gatcgcccga tgtcaagtcg cgggacacgc
101 cgtcaaaacc ggcgcgcccc gttgttgctg aaaatgccgg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgagc gacgcaaccg ccggaagaag cagccaagat atggcggcag
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaatgat atgccgcaaa atgccgcgca
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaaccctgcc cctgcgaatg gcggtagcga ttttggagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaataaac
501 gttgaccac tgtaaaggcg attcttgtaa tggtgataat ttattggatg
551 aagaagcacc gtcaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaatcgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatc atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttcgggcc
751 gagattccgc tgattcccg caatcaggcc gatacgtga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcggatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttgg
951 cacggccgtg tacaacggcg aagtgtgca tttccatag gaaaacggcc
1001 gtccgtaccc gtcggagcg aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatgaaa cggctttaag gggacttggg
1151 cggaaaatgg cggcggggat gtttcgggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

g287.pep

```

1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV

```


		10	20	30	40	49
m287.pep		MFKRSVIAMACIFALSACGGGGGGSPDVKSADTL	SKPAAPVVSE-----	KETEA		
g287		MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTP	SKPAAPVVAENAGEGVL	PKKEKKDEEA		
		10	20	30	40	60
	50	60	70	80	90	100
m287.pep		KEDAPQAGSQGQ	GAPSAQGSQDMAAV	SEENTGNGGAVTADN	PKNEDEVAQNDMP	QNAAGT
			:	:	:	:
g287		AGGAPQADTQD--	ATAGEGSQDMAAV	SAENTGNGGAATT	DNPKNEDAGAQN	DMPQNA--
		70	80	90	100	110
	110	120	130	140	150	160
m287.pep		DSSTPNHTPDPN	MLAGNMENQATDAGE	SSQPANQPDMA	NAADGMQGDDPS	SAGGQNA
g287		-----				
	170	180	190	200	210	220
m287.pep		AQGANQAGNNQA	AGSSDPIPASNPAP	PANGGNSNFRV	DLANGVLIDGPS	QNITLTHCKGDS
		:::	:	:	:	:
g287		-ESANQTGNNQ	PAGSSDSAPASNP	PANGGSDFGRT	NVNGNSVVIDGPS	QNITLTHCKGDS
		120	130	140	150	170
	230	240	250	260	270	280
m287.pep		CSGNNFLDEEV	QLKSEFEKLSAD	KISKNYKKDGK	NDKFVGLVADSV	QMKGINQYIIFYKP
		:	:	:	:	:
g287		CNGDNLLDEE	APSKSEFEKLSDE	EIKIKRYKKDE	QRENFVGLVAD	RVKKDGTN KYIIFYTD
		180	190	200	210	230
	290	300	310	320	330	340
m287.pep		KPTSFARFR	SARSRRSLPAEM	LIPIVNOADTL	LIVDGEAVSLT	GHSNIFAPEGNYRYLT
			:	:	:	:
g287		KPPT-----	RSARSRRSLPAE	IPIVNOADTL	LIVDGEAVSLT	GHSNIFAPEGNYRYLT
		240	250	260	270	290
	350	360	370	380	390	400
m287.pep		YGAEKLPGG	SYALRVQGEPA	KGEMLAGAAVY	NGEVLHFHTENG	RPYPTRGRFAAKVDFGS
g287		YGAEKLPGG	SYALRVQGEPA	KGEMLVGTAVY	NGEVLHFHMENG	RPYPSSGGRFAAKVDFGS
		300	310	320	330	350
	410	420	430	440	450	460
m287.pep		KSVDGIID	SGDDLHMG	TQKFKAAID	GNFGKGTWTENG	SGDVSGKFYGPAGEEVAGKYSYR
g287		KSVDGIID	SGDDLHMG	TQKFKAAID	GNFGKGTWTENG	GGDVSGRFGYPAGEEVAGKYSYR
		360	370	380	390	410
	470	480	489			
m287.pep		PTDAEKG	GGFGVFAG	KKKEODX		

g287
 |||||:|
 PTDAEKGGFGVFAGKKDRDX
 420 430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3107>:

a287.seq
 1 ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
 51 CTGTGGGGGC GCGGTGGCG GATCGCCGA TGTTAAGTCG GCGGACACGC
 101 TGTCAAAACC TGCCGCCCTT GTTGTACTG AAGATGTCGG GGAAGAGGTG
 151 CTGCCGAAAG AAAAGAAAGA TGAGGAGCG GTGAGTGGTG CGCCGCAAGC
 201 CGATACGCAG GACGCAACCG CCGGAAAGG CGGTCAAGAT ATGGCGGCAG
 251 TTTCGGCAGA AAATACAGGC AATGGCGGTG CGGCAACAAC GGATAATCCC
 301 GAAATAAAG ACGAGGGACC GCAAATGAT ATGCCGCAA ATGCCGCCGA
 351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
 401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATCGGC ACAACCGGCA
 451 AACCAACCGG ATATGGCAA TGCGGCGGAC GGAATGCAGG GGGACGATCC
 501 TCCGCGAGG GAAAATGCCG GCAATACGGC AGATCAAGCT GCAAATCAAG
 551 CTGAAAACAA TCAAGTCGGC GGCTCTCAA ATCCTGCCTC TTCAACCAAT
 601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
 651 TGGCATCAAG CTTGACAGCG GTTCGGAAAA TGTAACGTTG ACACATTGTA
 701 AAGACAAAGT ATGCATAGA GATTCTTAG ATGAAGAAGC ACCACCAAAA
 751 TCAGAAATTTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA
 801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
 851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
 901 TCTTCATCTG CCGGATTCAG GCGTCTGCA CGGTCGAGG GGTGCGTTCC
 951 GGCCGAGATG CCGCTGATT CCGTCAATCA GCGGATACG CTGATTGTCG
 1001 ATGGGGAAGC GGTCAACCTG ACGGGGCATT CCGGCAATAT CTTGCGGCC
 1051 GAAGGGAATT ACCGTATCT GACTTACGGG GCGGAAAAAT TGTCCGGCGG
 1101 ATCGTATGCC CTCAGTGTGC AAGCGGAACC GGCAAAAGGC GAAATGCTTG
 1151 CGGCGACGGC CGGTACAAAC GCGGAAGTGC TGCATTTCCTA TATGGAAAAAC
 1201 GCGCGTCCGT CCCGTCGGG AGGCAGGTTT GCCGCAAAAG TCGATTTCGG
 1251 CAGCAAATCT GTGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
 1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
 1351 TGGACGGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTT ACGGCCCGGC
 1401 CGGCGAAGAA GTGCGGGGAA AATACAGCTA TCGCCGACA GATCGGAAA
 1451 AGGGCGGATT CCGCTGTTT GCCGCAAAA AAGAGCAGGA TTGA

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

a287.pep
 1 MFKRSVIAMA CIVALSACGG GGGGSPDVKS ADTLSKPAAP VVTEDVGEEV
 51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAVSAENTG NGGAATTDNP
 101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
 151 NQPDMAAAD GMQDDPSAG ENAGNTADQA ANQAEENNQVG GSQNPASSTN
 201 PNATNGGSDF GRINVANGIK LDGSENVTL THCKDKVCDR DFLDEEAPPK
 251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIITYKDSAS
 301 SSSARFRRSA RSRRSLPAEM PLIPVNQADT LIVDGEAVSL TGHSGNIFAP
 351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMFEN
 401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGD LHMGTQKFKA VIDGNGFKGT
 451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEKGGFGVF AGKKEQD*

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

m287.pep
 10 20 30 40 49
 MFKRSVIAMACIFALSACGGGGSPDVKSADTLSKPAAPVVSE-----KETEA
 |||||:|
 a287 MFKRSVIAMACIVALSACGGGGSPDVKSADTLSKPAAPVVTEDEVGEEVLPKEKKDEEA
 10 20 30 40 50 60
 50 60 70 80 90 100 109
 m287.pep KEDAPQAGSQGQAPSAGQSDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
 |||:| |:::| |||||:|:|:|:| |||||
 a287 VSGAPQADTQ--DATAGKGGQDMAVSAENTGNGGAATTDNPNKDEGPQNDMPQNAADT
 70 80 90 100 110

m406 . ver

1	ATGCAAGCAC	GGCTGCTGAT	ACCTATTCTT	TTTTCAGTTT	TTATTTTATC
51	CGCCTGCGGG	ACACTGACAG	GTATTCCATC	GCATGGCGGA	GGTAAACGCT
101	TTGCGGTCTGA	ACAAGAACTT	GTGGCCGCTT	CTGCCAGAGC	TGCCGTAAAA
151	GACATGGATT	TACAGGCATT	ACACGGACGA	AAAGTTGCAT	TGTACATTGC
201	CACATAGGCG	GACCAAGGTT	CAGGACATT	GACAGGGGGT	CGCTACTCCA
251	TTGATGCATC	GATTCTGTGC	GAATACATAA	ACAGCCCTGC	CTCCGAGCC
301	GATTACACCT	ATCCACGTTA	CGAAACCACC	GCTGAAACAA	CATCGACGG
351	TTTGACAGGT	TTAACCACTT	CTTTATCTAC	ACTTAATGCC	CCTGCACTCT
401	CTCGCACCCA	ATCAGACGGT	AGCGGAAGTA	AAAGCAGTCT	GGGCTTAAAT
451	ATTGGCGGGA	TGGGGGATTA	TCGAAATGAA	ACCTTGACGA	CTAACCCGCG
501	CGCATAGTCC	TTTCTTTCCC	ACTTGGTACA	GACCGTATTT	TTCTCTGCGG
551	GCACAGACGT	TGTTTCTCCT	GCCAGTCCGC	ATACAGATGT	GTTTATTAAC
601	ATCGACGTAT	TCGGAACGAT	AGCAACACGA	ACCGAAATGC	ACCTATACAA
651	TGCCGAAACA	CTGAAAGCCC	AAACAAAAC	GGAATATTTC	CGAGTAGAC


```

701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTTAA CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGGCAG AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFQVEQEL VAASARAQVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSAGLTG LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSQGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACCTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCCA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTCTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGCAG AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFQVEQEL VAASARAQVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSAGLTG LTSLSTLNA PALSRQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSQGIK PTEGLMVDFS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFQVEQELVAASARAQVKDMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQVEQELVAASARAQVKDMDLQALHGR					

	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
	130	140	150	160	170	180
g406.pep	LTTSLSTLNAPALSRTQSDGSGSRSSSLGNIIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGNIIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	190	200	210	220	230	240
g406.pep	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDPSDIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDPSDIRPYGNHTGNSAPSVEADN					
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```
a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGTCG GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAA CCGACAGAAG GATTAATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGAC GACATAGACA
951 AGGGCAACCT TGA
```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```
a406.pep
1  MOARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVS ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRNTNKKLL IKPKTNAFEA
```


251 AYKENYALWM GPYKVSQGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301 SHEGYGYSDE AVRRHRQGPX *

m406/a406 ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap

m406.pep	10	20	30	40	50	60
	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAQVMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAQVMDLQALHGR					
	10	20	30	40	50	60
m406.pep	70	80	90	100	110	120
	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
	70	80	90	100	110	120
m406.pep	130	140	150	160	170	180
	LTTSLSTLNAPALSRTQSDGSGSKSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTTSLSTLNAPALSRTQSDGSGSKSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
m406.pep	190	200	210	220	230	240
	FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
m406.pep	250	260	270	280	290	300
	IKPKTNAFEAAYKENYALWMGPYKVSQGIKPTGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAYKENYALWMGPYKVSQGIKPTGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
m406.pep	310	320				
	SHEGYGYSDEVVRQHRQGPX					
a406	SHEGYGYSDEAVRRHRQGPX					
	310	320				

EXAMPLE 2

Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm

that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 3

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 4

Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera

were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).. These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 5

Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

Immunol 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 8

Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

Table 2

225 gene variability: List of used <i>Neisseria</i> strains	
Identification Strains number	Source / reference
Group B	
zo01_225 NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225 BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225 NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225 297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225 1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225 BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225 BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225 528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225 NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225 BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225 NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225 NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225 NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225 NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225 SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225 NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225 NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225 BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225 BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225 44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225 MC58	R. Moxon
zo96_225 2996	Our collection
Group A	
zo22_225 205900	R. Moxon
zo23_225 F6124	R. Moxon
z2491 Z2491	R. Moxon / Maiden <i>et al.</i> , 1998
Group C	
zo24_225 90/18311	R. Moxon
zo25_225 93/4286	R. Moxon

Others

zo26_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998
 zo27_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998
 zo28_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998
 zo29_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

Gonococcus

zo32_225 Ng F62 R. Moxon / Maiden *et al.*, 1998
 zo33_225 Ng SN4 R. Moxon

fa1090 FA1090 R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
 NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFRTLGGSRIISHVGLYIGNN
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNPDSRFLN*

Z2491 <SEQ ID 3116>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRVPARRAGNA
 DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFRTLGGSRIISHVGLYIGNNRF
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNPDSRFLN*

Z001_225 <SEQ ID 3117>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFRTLGGSRIISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNPDSRFLN*

Z002_225 <SEQ ID 3118>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFRTLGGSRIISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNPDSRFLN*

Z003_225 <SEQ ID 3119>
 MDSFFKPAVWAVLWLMFAVRLALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFRTLGGSRIISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNPDSRFLN*

Z004_225 <SEQ ID 3120>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVNNRVPARRAGNADELIGNAMGLNEQPVLVNNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSTRFLN*

Z005_225 <SEQ ID 3121>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVNNRVPARRAGNADELIGSAMGLNEQPVLVNNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSTRFLN*

Z006_225 <SEQ ID 3122>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVNNRVPARRAGNADELIGNAMGLNEQPVLVNNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSTRFLN*

Z007_225 <SEQ ID 3123>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVNNRVPARRAGNADELIGNAMGLNEQPVLVNNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSTRFLN*

Z008_225 <SEQ ID 3124>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVNNRVPARRAGNADELIGSAMGLNEQPVLVNNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSTRFLN*

Z009_225 <SEQ ID 3125>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVNNRVPARRAGNADELIGNAMGLNEQPVLVNNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSTRFLN*

Z010_225 <SEQ ID 3126>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVNNRVPARRAGNADELIGNAMGLNEQPVLVNNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSTRFLN*

Z011_225 <SEQ ID 3127>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVNNRVPARRAGNADELIGNAMGLNEQPVLVNNRAPARRAGNA
DELIGNAMGLNEQPVLVNNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSTRFLN*

Z012_225 <SEQ ID 3128>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVNNRVPARRAGNADELIGNAMGLNEQPVLVNNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSTRFLN*

Z013_225 <SEQ ID 3129>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRVARRAGNADELIGNAMGLNEQPVLVINRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFIQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z014_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRVARRAGNADELIGNAMGLNEQPVLVINRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z015_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRVARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z016_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRVARRAGNADELIGNAMGLNEQPVLVINRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z017_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRVARRAGNADELIGNAMGLNEQPVLVINRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z018_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRVARRAGNADELIGNAMGLNEQPVLVINRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z019_225 <SEQ ID 3135>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRVARRAGNADELIGNAMGLNEQPVLVINRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z020_225 <SEQ ID 3136>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRAPARRAGNADELIGSAMGLNEQPVLVINRVARRAGNA
DELIGNAMGLNEQPVLVINRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z021_225 <SEQ ID 3137>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRVARRAGNADELIGNAMGLNEQPVLVINRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z022_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVINRAPARRAG
NADELIGSAMGLNEQPVLVINRVARRAGNADELIGNAMGLNEQPVLVINRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR

SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z023_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z024_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z025_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z026_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z027_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z028_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z029_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z032_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLVPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z033_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRSALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLVPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z096_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDSCGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

Table 3

235 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
Group B	
gnmzq01 NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02 BZ198	Seiler <i>et al.</i> , 1996
gnmzq03 NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04 1000	Seiler <i>et al.</i> , 1996
gnmzq05 1000	Seiler <i>et al.</i> , 1996
gnmzq07 BZ169	Seiler <i>et al.</i> , 1996
gnmzq08 528	Seiler <i>et al.</i> , 1996
gnmzq09 NGP165	Seiler <i>et al.</i> , 1996
gnmzq10 BZ133	Seiler <i>et al.</i> , 1996
gnmzq11 NGE31	Seiler <i>et al.</i> , 1996
gnmzq13 NGE28	Seiler <i>et al.</i> , 1996
gnmzq14 NGH38	Seiler <i>et al.</i> , 1996
gnmzq15 SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16 NGH15	Seiler <i>et al.</i> , 1996
gnmzq17 NGH36	Seiler <i>et al.</i> , 1996
gnmzq18 BZ232	Seiler <i>et al.</i> , 1996
gnmzq19 BZ83	Seiler <i>et al.</i> , 1996
gnmzq21 MC58	Virji <i>et al.</i> , 1992
Group A	
gnmzq22 205900	Our collection

gnmzq23 F6124 Our collection
 z2491 Z2491 Maiden *et al.*, 1998

Group C

gnmzq24 90/18311 Our collection
 gnmzq25 93/4286 Our collection

Others

gnmzq26 A22 (group W) Maiden *et al.*, 1998
 gnmzq27 E26 (group X) Maiden *et al.*, 1998
 gnmzq28 860800 (group Y) Maiden *et al.*, 1998
 gnmzq29 E32 (group Z) Maiden *et al.*, 1998
 gnmzq31 *N. lactamica* Our collection

Gonococcus

gnmzq32 Ng F62 Maiden *et al.*, 1998
 gnmzq33 Ng SN4 Our collection

fa1090 FA1090 Dempsey *et al.* 1991

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>

MKPLILGLAAVLALSACQVRKAPDLDTTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ01 <SEQ ID 3150>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ02 <SEQ ID 3151>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGGLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ03 <SEQ ID 3152>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ04 <SEQ ID 3153>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ05 <SEQ ID 3154>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ07 <SEQ ID 3155>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ08 <SEQ ID 3156>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ09 <SEQ ID 3157>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AEPLEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ10 <SEQ ID 3158>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ11 <SEQ ID 3159>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ13 <SEQ ID 3160>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ14 <SEQ ID 3161>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ15 <SEQ ID 3162>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSARARLVDNRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSNGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ28 <SEQ ID 3173>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ29 <SEQ ID 3174>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ31 <SEQ ID 3175>

MKPLILGLAAVLALSACQVQKAPDFDYTAFKESKPASILVVPPLNESPDVNGTWGMLAST
 AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKAAAYDLLSPYSHNGILKGPRFVEEQPK*

GNMZQ32 <SEQ ID 3176>

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ33 <SEQ ID 3177>

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

Z2491 <SEQ ID 3178>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

Table 4

287 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
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Group B		
287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992
Group A		
z2491	Z2491	Maiden <i>et al.</i> , 1998
Gonococcus		
fa1090	FA1090	Dempsey <i>et al.</i> 1991

References:

- Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

287_14 <SEQ ID 3179>
MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
QGAPSAQGGQDMAAVSEENTGNNGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDCSCGNNFLDEEV
QLKSEFEKLSADAKISNYKKDGKNDKFKVGLVADSVQMKGINQYIIFYKPKPFSFAR
FRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLP
GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPSRGRFAAKVDFGSKSVDGII
DSGDGLHMGTKQFKAAIDGNGFKGTWTENGGGDSVSGKFGYPAGEEVAGKYSYRPTDAEKG
GFGVFAGKKEQD*

287_2 <SEQ ID 3180>
MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
QGAPSAQGGQDMAAVSEENTGNNGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDCSCGNNFLDEEV
QLKSEFEKLSADAKISNYKKDGKNDKFKVGLVADSVQMKGINQYIIFYKPKPFSFAR
FRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLP
GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPSRGRFAAKVDFGSKSVDGII
DSGDGLHMGTKQFKAAIDGNGFKGTWTENGGGDSVSGKFGYPAGEEVAGKYSYRPTDAEKG
GFGVFAGKKEQD*

287_21. <SEQ ID 3181>
MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
QGAPSAQGSQDMAAVSEENTGNNGAAVADNPKNEDEGAQNMPQNAAGTDSSTPNHTPDP
NMLAGNMENQATDAGESSQPANQPDMAANTADGMQGGDDPSAGGQNAAGNTAAQGANQAGNNQ
AAGSSDPIPASNPAPANGGSNFGFVLDLAVGLIDGPSQNTLTHCKGDCSCGNNFLDEEV
QLKSEFEKLSADAKISNYKKDGKNDKFKVGLVADSVQMKGINQYIIFYKPKPFSFARFRRS

ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSV DGIIDSGD
DLHMGTQKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKG GFGV
FAGKKEQD*

287_9 <SEQ ID 3182>

MFKRSVIAMACIVALSACGGGGGSPDVKSADTLSPKPAAPVVTVEDVGEEVLPKEKKDEEA
VSGAPQADTQDATAGKGGQDMAAVSAENTGNGGAATTDNPNKDEGPQNDMPQNAADTDS
STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAAADGMQDDPSAGENAGNTADQA
ANQAENNQVGGSQNPASSTNPATNGGSDFGRIINVANGIKLDSGSENVTLTHCKDKVCDR
DFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNYVIIYKDKSAS
SSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYG
AEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKS
VDGIIDSGDDLHMGTQKFKAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPT
DAEKG GFGVFAGKKEQD*

FA1090 <SEQ ID 3183>

MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA
AGGAPQADTQDATAGSGQDMAAVSAENTGNGGAATTDNPKNEDEGAQNDMPQNAAESAN
QTGNQFAGSSDSAPASNAPANGGSDFGRTNVGNSVVIDGPSQNTLTHCKGDCSNGDN
LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVEKNGTNYVIIYKDKPPT
SARSRRSLPAEIPVQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGS
YALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKSV DGIIDSG
DDLHMGTQKFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPTDAEKG GFG
VFAGKKDRD*

Z2491 <SEQ ID 3184>

MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
QGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGTDSSTPNHTPDP
NMLAGNMENQATDAGESSQPANQPDMAAADGMQDDPSAGGQNAAGNTAAQGANQAGNNQ
AAGSSDPIPASNPAPANGGNSFGRVDLANGVLIDGPSQNTLTHCKGDCSGNNFLDEEV
QLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTSFARFRS
ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSV DGIIDSGD
DLHMGTQKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKG GFGV
FAGKKEQD*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

Table 5

519 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

Group A

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Others

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

Gonococcus

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090_519 <SEQ ID 3185>
MEFFFIILAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAETIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Z2491_519 <SEQ ID 3186>

MEFFIILLVAVVFGFKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV01_519 <SEQ ID 3187>

MEFFIILLVAVVFGFKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV02_519 <SEQ ID 3188>

MEFFIILLVAVVFGFKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV03_519 <SEQ ID 3189>

MEFFIILLVAVVFGFKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV04_519 <SEQ ID 3190>

MEFFIILLVAVVFGFKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV05_519 <SEQ ID 3191>

MEFFIILLVAVVFGFKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV06_519ASS <SEQ ID 3192>

MEFFIILLVAVVFGFKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERK
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV07_519 <SEQ ID 3193>

MEFFIILLVAVVFGFKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV11_519 <SEQ ID 3194>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV12_519 <SEQ ID 3195>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV18_519 <SEQ ID 3196>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV19_519 <SEQ ID 3197>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV20_519ASS <SEQ ID 3198>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM
ISAGMKIIDSSKTAK*

ZV21_519ASS <SEQ ID 3199>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV22_519ASS <SEQ ID 3200>

MEFFIILLVAVVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV26_519 <SEQ ID 3201>

MEFFIILLVAVVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV27_519 <SEQ ID 3202>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV28_519 <SEQ ID 3203>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV29_519ASS <SEQ ID 3204>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSNKTAK*

ZV32_519 <SEQ ID 3205>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV96_519 <SEQ ID 3206>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

Table 6

919 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11asbc	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

Group A

zm22	205900	R. Moxon
zm23asbc	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Group C

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

Others

zm26	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

Gonococcus

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon

fa1090	FA1090	R. Moxon
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References:

- Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3207>

MKKHLRLRSALYGIAAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
YFTPWQVAGNSLAGTGTGYEYEPVLKGDGRRTARFPFIYGIPTDDFISVPLPAGLRGGKN
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA
IDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

Z2491 <SEQ ID 3208>

MKKYLFRAALCGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNSLAGTGTGYEYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELGTSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM01 <SEQ ID 3209>

MKKYLFRAALYGIAAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNSLAGTGTGYEYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM02 <SEQ ID 3210>

MKKYLFRAALYGIAAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNSLAGTGTGYEYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM03 <SEQ ID 3211>

MKKYLFRAALYGIAAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNSLAGTGTGYEYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM04 <SEQ ID 3212>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM05 <SEQ ID 3213>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM06 <SEQ ID 3214>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
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ZM07 <SEQ ID 3215>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM08N <SEQ ID 3216>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
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ZM09 <SEQ ID 3217>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
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KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM10 <SEQ ID 3218>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM11ASBC <SEQ ID 3219>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM12 <SEQ ID 3220>

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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
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KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
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QKTTGYVWQLLPNGMKPEYRP*

ZM13 <SEQ ID 3221>

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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQGTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
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QKTTGYVWQLLPNGMKPEYRP*

ZM14 <SEQ ID 3222>

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LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
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KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSRNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM15 <SEQ ID 3223>

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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM16 <SEQ ID 3224>

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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM17 <SEQ ID 3225>

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 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGKISYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLTPLMGEYAGA
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 QKTTGYVWQLLPNGMKPEYRP*

ZM18 <SEQ ID 3226>

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 LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGKISYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM19 <SEQ ID 3227>

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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
 LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGKISYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM20 <SEQ ID 3228>

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 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGKISYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM21 <SEQ ID 3229>

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 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGKISYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLTPLMGEYAGA
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 QKTTGYVWQLLPNGMKPEYRP*

ZM22 <SEQ ID 3230>

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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
 LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
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 QKTTGYVWQLLPNGMKPEYRP*

ZM23ASBC <SEQ ID 3231>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
 LVRIQRTGKNSGTIDNAGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELQSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTSKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM24 <SEQ ID 3232>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELQSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM25 <SEQ ID 3233>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELQSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM26 <SEQ ID 3234>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQGTSMQGIKAYMQNPORLAEVLGQNPSYIFFRELQSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM27BC <SEQ ID 3235>

MKKYLFRAALYGISAAAILAACQSKSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELQSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM28 <SEQ ID 3236>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQGTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELQSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELQSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATTHPITRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM31ASBC <SEQ ID 3238>

MKKHLFRAALYGIAAAILAACQSKSIQTFPQPDTSIIKGPDRPAGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEVLPKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPYSYVFFRELAGSGNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM32ASBC <SEQ ID 3239>

MKKHLLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEVLPKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKA
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPYSYVFFRELAGSGGDPVGALGTPLMGGYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM33ASBC <SEQ ID 3240>

MKKHLLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEYEVLPKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPYSYVFFRELAGSGNEGPVGALGTPLMGEYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEVLPKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPYSYVFFRELAGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 7: Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF primer Sequence	Restriction sites
001 Forward CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI-
Reverse CCCGCTCGAG-TGCCGTCTTGTCAC	NdeI
003 Forward CGCGGATCCCATATG-GTCGTATTCGTGGC	XhoI
Reverse CCCGCTCGAG-AAAATCATGAACACGCGC	BamHI-
005 Forward CGCGGATCCCATATG-GACAATATTGACATGT	NdeI
Reverse CCCGCTCGAG-CATCACATCCGCCCG	XhoI
006 Forward CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI-
Reverse CCCGCTCGAG-AGTTCGGGCTTTGATGT	NdeI
007 Forward CGCGGATCCCATATG-GCCGACAACAGCATCAT	XhoI
Reverse CCCGCTCGAG-AAGGCGTTCATGATATAAG	BamHI-
008 Forward CGCGGATCCCATATG-AACAACAGACATTTTG	NdeI
Reverse CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009 Forward CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI-
Reverse CCCGCTCGAG-TGGCTTTTGCCACGTTTT	NdeI
011 Forward CGCGGATCCCATATG-AAGACACACCGCAAG	XhoI
Reverse CCCGCTCGAG-GGCGGTCAGTACGGT	BamHI-
012 Forward CGCGGATCCCATATG-CTCGCCCGTTGCC	NdeI
Reverse CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013 Forward CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI-
Reverse CCCGCTCGAG-CTGATTCGGCAAAAAAATCT	NdeI
018 Forward CGCGGATCCCATATG-CAGCAGAGGCAGTT	XhoI
Reverse CCCGCTCGAG-GACGAGGCGAACGCC	BamHI-
019 Forward AAAGAATTC-CTGCCAGCCGGCAAGACCCCGGC	NdeI
Reverse AAAGTGCAG-TCAGCGGGCGGGGACAATGCCCAT	XhoI
023 Forward AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	BamHI-
Reverse AAAGTGCAG-TTACCCCCAAATCACTTAACTGA	NdeI
025 Forward AAAGAATTC-TGCGCCACCCAACAGCCTGCTCC	XhoI
Reverse AAAGTGCAG-TCAGAACGCGATATAGCTGTTCCG	BamHI-
031 Forward CGCGGATCCCATATG-GTCTCCCTTCGCTT	NdeI
Reverse CCCGCTCGAG-ATGTAAGACGGGGACAAC	XhoI
032 Forward CGCGGATCCCATATG-CGGCGAAACGTGC	BamHI-

	Reverse CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
	Reverse CCCGCTCGAG-ATTTGCCGCATCCCGAT	BamHI-
034	Forward CGCGGATCCCATATG-GCCGAAAACAGCTACGG	NdeI
	Reverse CCCGCTCGAG-TTTGACGATTTGGTTCAATT	XhoI
036	Forward CGCGGATCCCATATG-CTGAAGCCGTGCG	BamHI-
	Reverse CCCGCTCGAG-CCGGAATGCGTATCGG	NdeI
038	Forward CGCGGATCCCATATG-ACCGATTTCGCCA	XhoI
	Reverse CCCGCTCGAG-TTCTACGCCGTAAGTCC	BamHI-
039	Forward CGCGGATCCCATATG-CCGTCCGAACCGC	NdeI
	Reverse CCCGCTCGAG-TAGGATGACGAGGTAGG	XhoI
041	Forward CGCGGATCCCATATG-TTCGTGCGCGAACCGC	BamHI-
	Reverse CCCGCTCGAG-GCCCAAAAACCTTTTCAA	NdeI
042	Forward CGCGGATCCCATATG-ACGATGATTGCTTGC	XhoI
	Reverse CCCGCTCGAG-TTTGCAGCCTGCATTTGAC	BamHI-
043	Forward AAAAAAGGTACC-ATGGTTGTTTCAAATCAAATATC	NdeI
	Reverse AAAGTGCAG-TTATTGCGCTTACCTTCCGCCGC	XhoI
043a	Forward AAAAAAGGTACC-GCAAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse AAAAAACTGCAG-TTAATCCTGCAACACGAATTGCCCCGTCCG	Pst I
044	Forward CGCGGATCCCATATG-CCGTCCGACTAGAG	Kpn I
	Reverse CCCGCTCGAG-ATGCGCTACGGTAGCCA	Pst I
046	Forward AAAGAATTC-ATGTGCGCAATGCTCCCGACAAG	BamHI-
	Reverse AAAGTGCAG-TCACTCGGCGACCCACACCGTGAA	NdeI
047	Forward CGCGGATCCCATATG-GTCATCATACAGGCG	XhoI
	Reverse CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	Eco RI
048	Forward AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	Pst I
	Reverse AAAGTGCAG-TCAAGATTCGACGGGGATGATGCC	Eco RI
049	Forward AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	Pst I
	Reverse AAAGTGCAG-AAGGCGTATCTGAAAAAATGGCAG	BamHI-
050	Forward CGCGGATCCCATATG-GGCGCGGGCTGG	NdeI
	Reverse CCCGCTCGAG-AATCGGGCCATCTTCGA	XhoI
052	Forward AAAAAAGAATTC-ATGGCTTTGGTGGCGGAGGAAAC	Eco RI
	Reverse AAAAAAGTGCAG-TCAGGCGGCGTTTTTCACCTTCCT	Sal I
052a	Forward AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTTTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCCAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGAATTTTGCCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTCACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCCTTTTCAATTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTTTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-GTGTCTGCCAGTTTCAG	Eco RI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGAAAGTCAACACCCATTATCC	
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAACTACTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCGTCGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Pst I
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
108a	Forward	AAAAAAGAATTC-GGTAACACATTCGGCAGCTTAGACGGTGG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTATGGG	Eco RI
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTTT	Pst I
111	Forward	CGCGGATCCCATATG-TGTTCTGGAACAAACCGC	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAAA	
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAACTGGAAGTCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	
122	Forward	CGCGGATCCCATATG-GTCATGATTAAATCCGCA	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATTT	
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	Eco RI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	Pst I
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGCACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGCCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-

	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	XhoI
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Eco RI
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCTCGGG	Pst I
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Eco RI
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA	NdeI
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	NdeI
132	Forward	AAAGAATTC-ATGGAACCCCTTCAAAACCTTAATTTG	XhoI
	Reverse	AAAAAACTGCAG-TCACCATGTCTGGCATTGAAAAAC	Eco RI
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	NdeI
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	NdeI
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCAATTCGATCC	XhoI
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	Kpn I
137a	Forward	AAAAAAGAATTC-GGCCGCAAACACGGCATCGGCTTCCT	Pst I
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Eco RI
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTTGGC	Pst I
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Eco RI
141	Forward	AAAGAATTC-ATGAGCTTCAAAACCGATGCCGAAATCGC	Xba I
	Reverse	AAACTGCAG-TCAGAACAAGCCGTGAATCACGCC	Eco RI
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTCATG	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	NdeI
143	Forward	AAAAAAGAATTC- ATGCTCAGTTTCGGCTTTCTCGGCGTTCAGAC	XhoI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	Eco RI
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Pst I
	Reverse	AAAAAATCTAGA-TCGGCATCGGCGGCATATGTCCG	Eco RI
146	Forward	AAAAAAGAATTC- CGCCAAGTCGTCATTGACCACGACAAAGTC	Xba I
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAAACTGGG	Eco RI
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTGGAAC	Pst I
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Eco RI
148	Forward	AAAAAAGAATTC- ATGGCGTTAAAAACATCAAACCTTGGAACACGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Eco RI
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	Xba I
			BamHI-

	Reverse	CCCGCTCGAG-AAACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	NdeI
151	Forward	AAAAAAGAATTC-	XhoI
		ATGAAACAAATCCGCAACATCGCCATCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTAAAGTGGCGGCG	Pst I
152	Forward	AAAAAAGAATTC-	Eco RI
		ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG-	Pst I
		TTACGCCGACGAAATACTCAGACTTTTCGG	
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTTCGGG	XhoI
155	Forward	AAAAAAGAATTC-ATGAAAATCGGTATCCACGCGAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTCAGCAT	Pst I
156	Forward	AAAAAAGAATTC-GCACAGCAAACGGTTTTGAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Pst I
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAAACACAATATCCCCGC	XhoI
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTCCCAAGTTC	Xba I
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTTTGCCCGCCTTCTTT	XhoI
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGCAGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGTTTCCGTCAAACCTGC	XhoI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	BamHI-
			NheI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTCGCG	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	XhoI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	XhoI
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	XhoI
218	Forward	CGCGGATCCCATATG-GTCGCGGTCGATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	XhoI
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	XhoI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	XhoI
226	Forward	AAAGAATTC-CTTGCGATTATCGTGCGCACGCG	Eco RI
	Reverse	AAACTGCAG-TCAAAATCCCAAACGCGGAT	Pst I
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTTGCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	XhoI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	XhoI
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAAGGCGGTTTGGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGGTTTTTCTGATTGCCGCCGC	Pst I
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	XhoI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	BamHI-
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	NdeI
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	XhoI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCC	BamHI-
	Reverse	CCCGCTCGAG-TTTGTCTAAGTTCCTGATATG	NdeI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	EcoRI-
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTC	NdeI
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	XhoI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	BamHI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTG	XhoI
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	BamHI-
243	Forward	CGCGGATCCCATATG-ACGATTTTTCGATGCTGC	NdeI
	Reverse	CCCGCTCGAG-CGACTTGGTTACCGCG	HindIII
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATTT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	BamHI-
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	NdeI
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	XhoI
248	Forward	CGCGGATCCCATATG-CGAAACAGAACACT	BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	BamHI-
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	NdeI
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	XhoI
253	Forward	AAAAAAGAATTC-ATGATTGACAGGAACCGTATGCTGCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I

253a	Forward	AAAAAAGAATTC-AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	AAAAAAGAATTC-ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI-
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	NdeI
			XhoI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	BamHI-
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	NheI
			XhoI
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCCTG	BamHI-
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	NdeI
			XhoI
258	Forward	AAAAAAGAATTC-GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	AAAAAAGAATTC-GCGAAGGCGGTGGCGCAAGGCCA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI-
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	NdeI
			XhoI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	BamHI-
	Reverse	CCCGCTCGAG-AACAGGGCGACACCCT	NdeI
			XhoI
261	Forward	AAAAAAGAATTC-CAAGATACAGCTCGGGCATTTCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	Pst I
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	BamHI-
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	NdeI
			XhoI
264	Forward	AAAAAAGGTACC-GCCGACGCAGTGGTCAAGGCAGAA	Kpn I
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCG	Pst I
265	Forward	AAAAAAGAATTC-GCGGAGGTCAAGAGAAGGTGTTTG	Eco RI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAAATGGG	Pst I
266	Forward	AAAGAATTC-CTCATCTTTGCCAACGCCCCCTTC	Eco RI
	Reverse	AAACTGCAG-CTATCCCTGTTGCGCGTGTGCCA	Pst I
267	Forward	AAAGAATTC-TTCTTCCGATTGATGTTAATCG	Eco RI
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Pst I
269	Forward	AAAGAATTC-TGCAAACCTTGCGCCACGTGCCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
269a	Forward	AAAAAAGAATTC-GACTTTATCCAAAACACGGCTTCGCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
270	Forward	AAAGAATTC-GCCGTCAAGCTCGTTTTGTTGCAATG	Eco RI
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Pst I
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	BamHI-
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	NdeI
			XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTGTTACGGAC	BamHI-
	Reverse	CCCGCTCGAG-TTTGCTTTCAGTATTATTGAA	NdeI
			XhoI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCCATCACGATGATGCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Pst I
277	Forward	AAAAAAGAATTC-ATGCCCCGCTTTGAGGACAAGCTCGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Kpn I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTCGTCATAGTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT	BamHI-
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	NdeI
			XhoI
280	Forward	AAAAAAGGTACC-GCCCCCTGCCGTTGTAAACCAG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	Pst I
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTTCCGG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Pst I
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	BamHI-
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	NdeI
			XhoI
284	Forward	CGCGGATCCCATATG-TTGCCTGCAAAGAATCG	BamHI-
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAACCTG	NdeI
			XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTTCCGAAAA	BamHI-
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	NdeI
			XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	EcoRI-
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC	NheI
			XhoI
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	BamHI-
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	NdeI
			XhoI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCCC	XhoI
	Reverse	CCCGCTCGAG-TTGATTTTTCGGGATGATTT	BamHI-
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTTGTCAGAAC	NdeI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	XhoI
295	Forward	CGCGGATCCCATATG-AAACGGCCGGCCTCC	Eco RI
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	Pst I
297	Forward	AAAAAAGAATTC-GCATAATTGCTTCGACAGAGAG	BamHI-
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	NdeI
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	XhoI
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Eco RI
299	Forward	CGCGGATCCGCTAGC-CTACCTGTCGCCTCCG	Pst I
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	BamHI-
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	NheI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	XhoI
305	Forward	AAAAAAGGTACC-GAATTTTACCGATTTCAGCACCGGA	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCCCAACTTATCCAGCCTGACAG	Pst I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Kpn I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Pst I
306	Forward	CGCGGATCCCATATG-TTTATGAACAAATTTTCCC	Kpn I
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	Pst I
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	BamHI-
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	NdeI
311	Forward	AAAAAAGGTACC-ATGTTTCAGTTTTGGCTGGGTGTTT	XhoI
	Reverse	AAACTGCAG-ATGTTTCATATTCCTTGCCCTCGGC	Kpn I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Pst I
	Reverse	AAACTGCAG-TCAGTTTTTTCATCGATTGAACCGG	Kpn I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Pst I
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Eco RI
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	Pst I
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	BamHI-
402	Forward	AAAAAAGAATTC-GTGCTCAGGCATTTTCATTTACCCTTGC	NdeI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	XhoI
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Xba I
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	Eco RI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	Xba I
			BamHI-
			NdeI
			XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGTGTGATGTTACCC	XhoI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	XhoI
503	Forward	CGCGGATCCCATATG-TGTTGCGGGAAAGGCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI- NdeI
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	HindIII
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	XhoI
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	XhoI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	XhoI
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGCGCCCAGCCGT	XhoI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	Eco RI
	Reverse	AAACTGCAG-TCAAATTCAGACTCTGCCAC	Pst I
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	XhoI
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTAGTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	XhoI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	HindIII
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	BamHI- NdeI

Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
525 Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
527 Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTTCG	Eco RI
Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
529 Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
530 Forward	CGCGGATCCCATATG-AGTGCAGCGCGG	BamHI- NdeI
Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
531 Forward	AAAAAAGAATTC-TATGCCGCCGCCTACCAAATCTACGG	Eco RI
Reverse	AAAAAACTGCAG-TTAAAACAGCGCCGTGCCGACGACAAG	Pst I
532 Forward	AAAAAAGAATTC-ATGAGCGGTTCAGTTGGGCAAAGGTGC	Eco RI
Reverse	AAAAAACTGCAG-TCAGTGTTCGAAGTGGTCGGTATCAAA	Pst I
532a Forward	AAAAAAGAATTC-TTGGGTGTCGCGTTTGAGCCGGAAGT	Eco RI
Reverse	AAAAAACTGCAG-TCAGTGTTCGAAGTGGTCGGTATCAAA	Pst I
535 Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
537 Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
538 Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
539 Forward	CGCGGATCCGCTAGC-GAGGATTTGCAGGAAA	BamHI- NheI
Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
542 Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
Reverse	AAACTGCAG-TTACCGCGAACCGGTCAGGAT	Pst I
543 Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
543a Forward	AAAAAAGAATTC-GGCAAACTCGTCATGAATTTGC	Eco RI
Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
544 Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCGACCTGCACGG	Eco RI
Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
544a Forward	AAAAAAGAATTC- GCAAATGACTATAAAAAACAAAACTTCCAAGTACTTGC	Eco RI
Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
547 Forward	AAAGAATTC-ATGTTCTGTAGATAACGGATTTAATAAAAC	Eco RI
Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
548 Forward	AAAGAATTC-GCCTGCAAACCTCAAGACAACAGTGCGGC	Eco RI

	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCC GCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTGGGAATATGCCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCCAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTCAATTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGTGTCAATTCGCC	XhoI
574	Forward	CGCGGATCCCATATG-TGGTTTGCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCGGG	XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCTG	XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTCGTACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACTTCCCCCGAAGTG	XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	XhoI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCCAGTCGTTGAA	Xba I
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Pst I
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Pst I
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTCTGTFTTGGA	Pst I
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	XhoI
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	BamHI-

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	XhoI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Eco RI
589	Forward	AAAAAAGAATTC-	Pst I
		ATGCAACAAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACGAACGGACTC	BamHI-
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	NheI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	XhoI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCCTGACACTCGCG	Eco RI
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGAGGCGGAGAAAGC	Pst I
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Eco RI
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	Pst I
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	BamHI-
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	XhoI
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	BamHI-
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	NdeI
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	XhoI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	BamHI-
603	Forward	AAAAAAGAATTC-CTGTCCTCGCGTAGGCGGGGACGGGG	NheI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	XhoI
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	Eco RI
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	Pst I
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	BamHI-
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	NheI
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	XhoI
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Eco RI
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCCATCATCAACCG	Pst I
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTGCGGTTT	Eco RI
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	Pst I
			BamHI-
			NdeI

	Reverse	CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward	CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward	CGCGGATCCCATATG-CCGTCTCAAAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward	CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward	CGCGGATCCCATATG-TCCGTCGTGAGCGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward	AAAAAAGAATTC-ATGTCAAACACAATCAAAATGGTTGTCGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward	AAAAAAGAATTC-GGGCTTCTCGCCGCTCGCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTTTTGTGTTTTAAACGAGATA	Pst I
622	Forward	CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGTCCAAATGATAAATCTG	XhoI
624	Forward	CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGATTCGGGCCTGCGC	XhoI
625	Forward	CGCGGATCCCATATG-TTTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCAAAATTACCGCCTT	XhoI
627a	Forward	AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward	AAAAAAGGTACC-GCCTTACAAACATGGATTTTGCGTTC	Kpn I
	Reverse	AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAAA	Pst I
629a	Forward	AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACAACACCGCCGTCCGGTTCAAACC	Pst I
630a	Forward	AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward	AAAAAAGAATTC- ATGACCCAGCGACGGGTCTGGCAAGCAAAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATCCACTATAATCCTGTTGCT	Pst I
638	Forward	AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse	AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward	CGCGGATCCCATATG-ATGCTTTATTTTGTTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward	CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	Eco RI
644	Forward	AAAAAAGAATTC- ATGCCGCTGAAAGGTCGGCGGATTGTTGCCC	Pst I
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Eco RI
645	Forward	AAAAAAGAATTC-GTGGAACAGAGCAACACGTAAATCG	Pst I
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCG	Eco RI
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Pst I
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Eco RI
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Pst I
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Eco RI
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCCACCG	Pst I
	Reverse	AAAAAACTGCAG-TTAACGGCGGAACTGCCGCCGTC	Eco RI
650	Forward	AAAAAAGAATTC-ATGTCCAACTCAAAACCATCGC	Pst I
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Kpn I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Pst I
	Reverse	AAAAAACTGCAG-TTATTTGCCAGTTGGTAGAATGCGGC	Eco RI
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGGTAATTTTCATCGG	Pst I
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCGA	Eco RI
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Pst I
	Reverse	AAAAAACTGCAG-CTACGATTTCCGCGATTTCACATCGT	Eco RI
657	Forward	AAAAAAGAATTC-GCAGAATTTGCCGACCGCCATTTGTGCGC	Pst I
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	BamHI- NdeI XhoI
658	Forward	CGCGGATCCCATATG-GTGTCCGGAATTGTG	Eco RI
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	Pst I
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	BamHI- NdeI XhoI
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTCCGCCGTCGGGC	Eco RI
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	Pst I
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	BamHI- NdeI XhoI
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	Eco RI
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	Pst I
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTTGCCGACGATTT	Eco RI
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Eco RI
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTTCGTATTCGTCCG	Pst I
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTAAAAAACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-A AAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTAGGAGCTTTTGGAACGCGTCGGACTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTTCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCGC	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAATAAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTTCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI

694	Forward	CGCGGATCCCATATG-TTGGTTTCCGCATCCGG	BamHI-
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	NdeI
695	Forward	CGCGGATCCCATATG-TTGCCTCAAACCTCGTCCG	XhoI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	BamHI-
696	Forward	CGCGGATCCCATATG-TTGGGTTGCCGGCAGG	NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC-GCATCGACAGACGGTGTGTCGTGGAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTTGGATACTTC	BamHI-
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	NdeI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	XhoI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Eco RI
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	Pst I
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	BamHI-
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	NheI
	Reverse	AAAAAACTGCAG-TTAGTTTTGCCGGATAATATGGCGGGTGCG	XhoI
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	Eco RI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	Pst I
708	Forward	CGCGGATCCGCTAGC-CCTTTTAAGCCATCCAAAA	BamHI-
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	NheI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	XhoI
	Reverse	CCCGCTCGAG-AACGGTTTCGGTCAG	BamHI-
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	NdeI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	XhoI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	BamHI-
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATAACC	NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI-
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	NdeI
			XhoI

725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI-
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	NdeI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAAC	XhoI
	Reverse	CCCGCTCGAG-GCCGATGTTTACGCTCC	BamHI-
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI-
	Reverse	GCCCAAGCTT-TTTGTCGGTTTGGGTATC	NdeI
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	HindIII
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	BamHI-
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	NheI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	EcoRI-
	Reverse	CCCGCTCGAG-TCGCTTGCCCTCCTTTAC	NdeI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	XhoI
	Reverse	CCCGCTCGAG-TTTGAGATTTTGAATCAAAGAG	BamHI-
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI-
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	NdeI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACC GAACA	XhoI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGCGAGAATT	BamHI-
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCC GAAG	NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI-
	Reverse	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	NdeI
743	Forward	CGCGGATCCCATATG-GACGGTGTGTGCCTGTT	XhoI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	BamHI-
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-

	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
747	Forward	CCGGAATTCTAGCTAGC-CTGACCCCTTGGG	XhoI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	EcoRI-
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	NheI
	Reverse	CCCGCTCGAG-TTTC AAGCCGAGTATGC	HindIII
750	Forward	CGCGGATCCCATATG-TGTTCCGCCGAACCTG	BamHI-
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCAA	NdeI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGTT	XhoI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	BamHI-
759	Forward	CGCGGATCCGCTAGC-CGCTTCACACACACCAC	NdeI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	BamHI-
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	NdeI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	XhoI
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	BamHI-
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	NdeI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTAA	XhoI
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTCTGTACAGCAGGGG	NdeI
768	Forward	CGCGGATCCCATATG-GCCCCGAAAAACCCG	XhoI
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	BamHI-
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	NdeI
	Reverse	CCCGCTCGAG-GCGTTTGTGCGAGATTTTC	XhoI
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	BamHI-
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	NdeI
772	Forward	CGCGGATCCCATATG-TTTCGGCGTTGGTGG	XhoI
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	BamHI-
774	Forward	CGCGGATCCCATATG-TCCGTTTACCCGTTTC	NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	BamHI-
			NdeI

Reverse	CCCGCTCGAG-GGCGTTGTTCCGATTTCG	XhoI
900 Forward	CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI-
Reverse	CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	NdeI
901 Forward	CGCGGATCCCATATG-CCCGATTTTTTCGATG	XhoI
Reverse	CCCGCTCGAG-AAAATGGAACAATACCAGG	BamHI-
902 Forward	CCGGAATTCTACATATG-TTGCACTTTCAAAGGATAATC	NdeI
2		XhoI
Reverse	CCCGCTCGAG-AAAAATGTACAATGGCGTAC	EcoRI-
903 Forward	CCGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	NdeI
Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
904 Forward	AAAAAAGGTACC-ATGATGCAGCACAAATCGTTTC	Kpn I
Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
904a Forward	AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
905 Forward	CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI-
Reverse	CCCGCTCGAG-CCACTGATAACCGACAGAT	NdeI
907 Forward	CGCGGATCCCATATG-GGCGCGCAACGTGAG	XhoI
Reverse	CCCGCTCGAG-ACGCCACTGCCAGCG	BamHI-
908 Forward	AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	NdeI
Reverse	AAACTGCAG-TTAATATGGTTTTGTCTGTTTCG	XhoI
909 Forward	CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	Eco RI
Reverse	CCCGCTCGAG-TCGGTTTTGAAACTTTGGTTTT	Pst I
910 Forward	AAAGAATTC-GCATTTCGCGGCGACTCTGCCGAGCG	BamHI-
Reverse	AAACTGCAG-TCAGCGATCGAGCTGCTCTTT	NdeI
911 Forward	AAAGAATTC-GCTTTCCGCGTGGCCGGCGGTGC	XhoI
Reverse	AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTTCCGC	Eco RI
912 Forward	AAAAAAGAATTC- CAAATCCGTCAAACGCCACTCAAGTATTGAG	Pst I
Reverse	AAAAAACTGCAG-TTACAGTCCGTCCACGCCTTTCGC	Eco RI
913 Forward	CGCGGATCCCATATG-GAAACCCGCCCCCGC	Pst I
Reverse	CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	BamHI-
915 Forward	CGCGGATCCCATATG-TGCCGGCAGGCGGAA	NdeI
Reverse	CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
914 Forward	AAAGAATTC-GACAGAATCGGCGATTTGGAAGCACG	Eco RI
Reverse	AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
916 Forward	CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI-
Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	NdeI
		XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCCGCCTTCACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG	NdeI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	XhoI
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	BamHI-
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCCGTGAATCC	NdeI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	XhoI
922	Forward	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	Eco RI
	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	Pst I
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NheI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	XhoI
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTT	BamHI-
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	NdeI
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	XhoI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Eco RI
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTGCCCCGACAACAACGCGACG	Eco RI
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAACCGCCAATCCGCCGACAC	Eco RI
936	Forward	CGCGGATCCCATATG-GCCGCCGTCGGCGC	Pst I
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	BamHI-
937	Forward	AAAAAAGAATTC-CCGTTTACATTCAAACCGGCGCAAC	NdeI
	Reverse	AAAAAACTGCAG-TTAAAATGTATGCTGTACGCCAAA	XhoI
939a	Forward	AAAAAAGAATTC-GGTTCCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	NdeI
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	XhoI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	BamHI-
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	NdeI
			XhoI
			BamHI-

	Reverse CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
	Reverse GCCCAAGCTT-GGGTCGTTTGTTCGTC	BamHI-
959	Forward CGCGGATCCCATATG-CACCACGACGGACACG	NdeI
	Reverse CCCGCTCGAG-GTCGTCGCGGCGGGA	HindIII
961	Forward CGCGGATCCCATATG-GCCACAAGCGACGACG	BamHI-
	Reverse CCCGCTCGAG-CCACTCGTAATTGACGC	NdeI
972	Forward AAAAAAGAATTC- TTGACTAACAGGGGGGGAGCGAAATTAAAAAC	XhoI
	Reverse AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Eco RI
973	Forward AAAAAAGAATTC-ATGGACGGCGCACAACCGAAAAC	Xba I
	Reverse AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Eco RI
982	Forward CGCGGATCCCATATG-GCAGCAAAGACGTAC	Pst I
	Reverse CCCGCTCGAG-CATCATGCCGCCCATCC	BamHI-
983	Forward CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	NdeI
	Reverse CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
	Reverse CCCGCTCGAG-TAATAAACCTTCTATGGGC	NdeI
988	Forward CGCGGATCCCATATG-TCTTTAAATTTACGGGAAAAAG	XhoI
	Reverse GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	BamHI-
989	Forward CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	NdeI
	Reverse CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	HindIII
990	Forward. CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	EcoRI-
	2	NdeI
	Reverse CCCGCTCGAG-AAACAGCCATTTGAGCGA	XhoI
992	Forward CGCGGATCCCATATG-GACGCGCCCGCCCG	BamHI-
	Reverse CCCGCTCGAG-CCAAATGCCCAACCATTC	NdeI
993	Forward CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	XhoI
	Reverse CCCGCTCGAG-GAACACATCGCGCCCG	BamHI-
996	Forward CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	NdeI
	Reverse CCCGCTCGAG-TCTAAACCCCTGTTTTCTC	XhoI
997	Forward CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	EcoRI-
	Reverse CCCGCTCGAG-GACGGCATCGCTCAGG	NheI
		XhoI

g001.seq

1	ATGCTGCCGC	AGGGGAAGGC	GGCGCGGAGG	GTGTCGGCGA	ACGAGGTGTC
51	CGCGCAGGCT	TGCGCCCGGA	TGGTGTGTGT	CATCTGCCAG	ACGCTGCCG
101	AACCGCATAC	TTTAAACGCG	TCCGGTACGC	ATACTTTACC	GGTTTGGGCG
151	ATTTTGCCGA	GGTCGTTGCG	CAGCAAAATC	ACAAATCATCA	CGTTTTCCGC
201	GCGGTTTTTC	GGGTTCGTTT	GTAACTCGCG	GGCGCGGCGT	TCGTCTTGTC
251	CGTCGCCCAA	AGATCGGCGCG	GTGCGCTTCA	TCGGTTCCGT	GCTGATGGTG
301	CCGTCTGAAG	CAATGTTGAG	GAAAGAGTTG	GCGCAGAAAC	ACACGCTCCA
351	CGCGGATTGC	CCGGCTTCAT	CGGGCAGGTG	GGACAATACG	CGATAG

g001.pap

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1  MLPQGKAARR VSANEVSGRA CARMVLVICQ TLPKRDTLNG SGHTHTLPVWA
51 ILPRSLRSKS TIITFSARFF GSVCNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEAMLRKSS GEKHSVHADC PASSGRWDNT A*

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m001.seq

1	ATGCTGCCGC	AGGGGAAGGC	GGCGCGGAGG	ATGTCGGCGA	ACGAGGTGTG
51	CGGcAssCTT	ss.GCTTGA	yGGTGCTGCT	CATCTGCCAA	ACGTCGCCGA
101	AACCGCATAC	TTTAAACCGT	TCGGGTACGC	ATACTGTGCC	GGTTTGGGCG
151	ATTTTGGCCGA	GATCGTTACG	CAGCAAAATCG	ACAATCATCA	CGTTTTCGCG
201	GCGGTTTTC	GGGTGCGCTT	GCAACTCGGC	GGCGCGGCGT	TCGTCTTGTC
251	CGTCGCCCAA	AATCGGCGCG	GTGCGCTTCA	TCGGTTTCGGT	GCTGATGGTG
301	CGCTGCCGAAC	CGATTTTGAG	GAAAGATTTCG	GGCGAGAAAC	ACACGCTCCA
351	CGCGGATTGC	CCCTCCGCAT	CGGGCAGGTG	GCACAAGACG	CGATAG

m001.pap

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1  MLPGQKAARR MSANEVCGXL XAWXVLVICO TLPKRDITNG SGTHTVPVWA
51  ILPRSLRKS  TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*

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a001.seq

1	ATGCTGCCGC	AGGGGAAGGC	GGCGCGGAGG	ATGTCGGCGA	ACGAGGTGTG
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101	AACGC GATAC	TTTAAACGGT	TCCGGATACG	ATACTGTGCC	GGTTGGGGCG
151	ATTTTGGCCGA	GGTCGTTACG	CGCAAAATCG	ACAAATCATCA	C67TTTTCGGC
201	GCGGTTTTTC	GGGTGCGCTT	GCAACTCGGC	GGCGCGGCGT	TCGTCTTGTC
251	CGTCGCCCCAA	AATCGGCGCG	GTGCGCTTTCA	TCGGTTCGGT	GCTGATGGTG
301	CCGTCCGAAC	CGATTTTGAG	GAAAGATTTC	GGCAGAAAAC	ACACGCTCCA
351	CGCGGATTGC	CCTTGTGTCAT	CGGCGAGGTG	GGACAAAACG	CGATAG

a001.pcp

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1  MLPQGKAARR MSANEVCGKA WAMMVLVICO TLPKRDITNG SGTHTVPVWA
51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHADC PCASGRWDKT A*

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m001/a001 96.2% identity over a 131 aa overlap

10 20 30 40 50 60
 m001.pep MLPQGKAARRMSANEVCGXLA^WVLVLCQTLPKRD^TLN^GSG^THTVPVWAILPRSLR^SK^S
 |||||
 a001.pep MLPQGKAARRMSANEVCGKAW^WMLVLCQTLPKRD^TLN^GSG^THTVPVWAILPRSLR^SK^S

	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPIILRKSSGEKHSVHADC					
a001.pep	TIIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPIILRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
a001.pep	PCASGRWDKTAX					
	130					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 001 shows 89.3% identity over a 131 aa overlap with a predicted ORF (ORF 001.ng) from *N. gonorrhoeae*:

m001/g001

	10	20	30	40	50	60
m001.pep	MLPQGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS					
g001	MLPQGKAARRMSANEVSGRACARMVLVICQTLPKRDTLNGSGTHTLPVWAILPRSLRSKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPIILRKSSGEKHSVHADC					
g001	TIIITFSARFFGSVCNSAARRSSCPSPKIGAVPFIGSVLMVPSEAMLRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
g001	PASSGRWDNTAX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 7>:

g003.seq

```

1  ATGGTCGAT  TCGTGGCTGA  AGGCGTATTC  GGTCCGCTG  TTTTGGGTCA
51  CTTGGTATTG  CTCTTCGGTC  AGGGTGCCTT  TGAGTTCGGC  GTCACCTCGG
101  TTTTATACG  TTGCCGCGTC  GAAGCCTTTG  CCTTGCCTG  CGGCTTTGGT
151  TTTGCCCGGC  AGCGGTTCTG  CGGCTTTGCG  GATGTCGATG  TGGCAGTAGC
201  CGTTGGGGTT  TTTAATCAGG  TAGTCCTGAT  GGTATTCCTC  GGCCTCGTAG
251  AAGTTTTTCA  GCGGTTCTGT  TTCAACAACG  AGGGGCAGTT  GGTATTTTGT
301  CTGCTCGCGT  TTGAGGGCGG  CGGCGATGAC  GGCTTTTTCG  GCGGGGTCGG
351  TGAGTACAC  GCGGCTGCGG  TATTGCGTGC  CGGTGTCGTT  ACCCTGTTTG
401  TTGAGGCTGG  TCGGATCAAC  GACGCGGAAA  TAATATTGCA  GGATGTCGTC
451  CAGGCTGagt  TTGTCGGCAT  CGTaggtcac  tTTGACGGTC  TCGGCATGAC
501  CCGTATGGCG  GTaggacact  tctTCgtanc  TcGGGtTTTC  CGTgttGCCC
551  TTGGCgttac  cGGATACCGC  gtcaACCACG  CCGTcgatgc  gttggaAATA
601  ggCTTCCAAg  ccccaaaagc  agccgccggc  gaagtaaagt  gtgcccgtgt
651  tcatgattGC  TGa

```

This corresponds to the amino acid sequence <SEQ ID 8; ORF 003.ng>:

g003.pep

```

1  MVVFVAEGVF  GRAVLGHLVL  LFGQGAFFFG  VTRFFIRCRV  EAFALRCGFG
51  FARQRFVGFA  DVDVAVAVGV  FNQVVLMLVL  GVVEVFQRFV  FNNEGQLVFL
101  LLAFEGGGDD  GFFGGVGVVH  AAALRAGVV  TLFVEAGRIN  DAEIILQDVV

```


151 QAEFVGIVGH FDGLGMTRMA VGHHFVRVFR VAVGVTGYRV NHAVIDALEIG
201 FQAPKAAAGE VNGARVHDC

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

m003.seq

```

1   ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCCGCGCTG TTTTGGGTAA
51  CTGTGATTG CTCTTCGGTC AGGGTGCCTT TGAGTTCGGC GTCACCTCGT
101 TTTTATACG TTGCCCGGTC GAAGCCTTTG CCTTCCGGG CCGTCTTGGT
151 TTTGCCCGGC AGCGTTTCGT CAGCkTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGk CGGCGATGAC GGCTTTTTTCG kCGGGGTCGG
351 TGTAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCTGT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGCG
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA
601 GGCTTCCAAG CCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT
651 TCATGATTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

m003.pep Length: 221

```

1   MVVFVAEGIF GRAVLGNLXL LFGQGAFFFG VTRFFIRCRV EAFALRGGLG
51  FARQRFVSXA DVDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFFGXGDD GFFXGVGVVH AAALRTGVV ALFVEAGRIN DAEEILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RAVGVAGYR VNHAVIDALEI
201 GFOAPEAAXG EVNGARVHDF *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

a003.seq

```

1   ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCCGCGCTG TTTTGGGTAA
51  CTTGGTATTG CTCTTCGGTC AGGGTGCCTT TGAGTTCGGC GTCACCTCGT
101 TTTTATACG TTGCCCGGTC GAAGCCTTTG CCTTCCGGT CCGTCTTGGT
151 TTTGCCCGGC AGCGTTTCGT CCGCTTTGCG GATATCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTTCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTTCG GCGGGGTCGG
351 TGTAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCTGT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGCG
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA
601 GGCTTCCAAG CCCAGAAGC AGCCGCCGGC GAGGTAGATG GTGCGCGTGT
651 TCATGATTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

a003.pep

```

1   MVVFVAEGIF GRAVLGNLVL LFGQGAFFFG VTRFFIRCRV EAFALRCGLG
51  FARQRFVGFA DIDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFFEGGGDD GFFGGGVGVH AAALRTGVV ALFVEAGRIN DAEEILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RAVGVAGYR VNHAVIDALEI
201 GFOAPEAAAG EVDGARVHDF *

```

m003/a003 95.9% identity over a 220 aa overlap

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXL LFGQGAFFFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
a003	MVVFVAEGIFGRAVLGNLVL LFGQGAFFFGVTRFFIRCRVEAFALRCGLGFARQRFVGFA					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
a003	DIDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGGDDGFFGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
a003	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALFQAEPAAXGEVNGARVHDFX					
a003	RVAVGVAGYRVNHAVDALFQAEPAAXGEVNGARVHDFX					
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVFVFAEGIFGRAVLGNLXLLFQGQAFEFVTRFFIRCRVEAFALRGGLGFARQRFVXSX					
g003	MVFVFAEGVFGRAVLGHLVLLFQGQAFEFVTRFFIRCRVEAFALRCGFGFARQRFVGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
g003	DVDVAVAVGVFNQVVLVFLGVVEVFQRFVNNQQLVFLLLAFEGGDDGFFGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
g003	AAAVLRAGVVTLFVEAGRINDAEIILQDVVQAEFVGIVGHFDGLGMRMAVGHFFV-RVF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALFQAEPAAXGEVNGARVHDFX					
g003	RVAVGVAGYRVNHAVDALFQAPKAAAGEVNGARVHDC					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

```

1  .ATGgtagAAC GGCATATCCA GCATTTCGG AACGGTCATC TTCATTGAT
51  GCGCCCATGC CAACAagtga gccAAAtgtT CCGCGGCAGG GCCTacgatt
101 TCCGCGCCGA TAAagcgccc gGTGgctTTT tcgGCataca ggcgcaTatg
151 gCCTTTGTTT ACCAgcatca cgcggctgcg accttgattT TTGAACGATA
201 CTTCGCCgaT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTCGgga ctggtaaACA CCACGCCAAT
301 GGTgctgcgg cGCAAAACCG TGCCGATAtt cgGtagcgg ccccgcgta
351 ttgcccggca atcttacctt ggtcggcgcc ttcatGCAGC AGGGGCagtt
401 ggttgacgc gtgcggcgca ataAAGATAT GCGGAATgct ggtCTGCATg
451 gtCAGCGGAT CGGCAACGGG tacgccgcgc gcgtctttgT CGATATTGAT
501 GTTTTCCAAA CCGATAttgT CAACGTTCCG ACGGCgACCT ACGGCTGCCA

```



```

551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTTG ACCTCGGTTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTCGCCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCCG ATGATTCCGC CCAAACCGAA AATTTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

```

g004.pep
  1 MVERHIQHLR NGHLMRPC QQVSQMFGR AYDFRADKAA GGFFGIQAHM
 51 AFVYQHHAHA TLIFERYFAD DKFVGLVLRG NLRVFQDKA DLRTGKHHAN
101 GAAQAATAADI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTFR ASLSILMFSK PILSTFGRRP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMP MIPPKPKIST
251 FTFKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

```

m004.seq
  1 ATGGTAGAAC GGCATATCCA GCATTGCGG AACGGTCATC TTCATTTGAT
 51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTC ACCAGCATCA CGCGGCTGCG GCCTTGGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTAGAC CGACAAAGCC GATTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTTCG CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTCCGAAAT GCCGCCGATG ATTCCGCCCA AACCGAAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

```

m004.pep
  1 MVERHIQHLR NGHLMCPS QQVRQMFGR AYDFRADKAA GGFFGIQAHM
 51 AFVHQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQDKA DLRTGKHHAD
101 GAAPQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPAM KICGILVCMV
151 SGSATGTTPRA SFSILIFSKP ILSTFGRRP AASIYSATNT PFSPPSCSQWT
201 STLPSASSLT SVLASRCSFN SSPNTAFASS ETTGSEMPPM IPPPKKISTF
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

```

a004.seq
  1 ATGGTAGAAC GGCATATCCA GCATTGCGG AACGGTCATC TTCATTTGAT
 51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCCCG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTC ACCAGCATCA CGCGGCTGCG GCCTTGGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCTTGGT CGGCAGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCCCGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGTT
501 TTCCAAACCG ATATTGTCAA CGTTCGACG GCGGCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCTC GAGTTTGGCC TCGGTTTTCG CATCCAAATG
651 CAGTTTCAAT TCTTCACCGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTCCGAAAT GCCGCCGATG ATGCCACCCA AACCGAAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```


This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

a004.pep

```

1  MVERHIQHLR NGHLMCPSP QQVRQMFGR TYDFCADEAA GGFFGIQAHM
51 AFVYQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGEHYAD
101 GAAQAATAADI RVAAALSPAI LPWSAASCSR GSWLDASPAI KICGILVCIV
151 SGSATGTPRA SFSILMFSPK ILSTFGRRPT AASIYSATNT PFSPSCSQWT
201 STLPSASSLA SVLASKCSFN SSPNTAFASS ETTGSEMPPM MPPKPKISTF
251 TPKRCNA*

```

m004/a004 94.9% identity over a 257 aa overlap

m004.pep	10	20	30	40	50	60
	MVERHIQHLRNGHLMCPSPQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA					
a004	MVERHIQHLRNGHLMCPSPQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVYQHHAHA					
m004.pep	70	80	90	100	110	120
	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI					
a004	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGEHYADGAAQAATAADIRVAAALSPAI					
m004.pep	130	140	150	160	170	180
	LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFSILIFSILSKPILSTFGRRPT					
a004	LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFSILMFSPKILSTFGRRPT					
m004.pep	190	200	210	220	230	240
	AASIYSATNTPFSPSCSQWTSTLPSASSLTVLASCFSNPPNTAFASSETTGSEMPPM					
a004	AASIYSATNTPFSPSCSQWTSTLPSASSLTVLASKCSFNPPNTAFASSETTGSEMPPM					
m004.pep	250					
	IPPKPKISTFTPKRCNAX					
a004	MPPKPKISTFTPKRCNAX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

m004/g004

m004.pep	10	20	30	40	50	60
	MVERHIQHLRNGHLMCPSPQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA					
g004	MVERHIQHLRNGHLMRCPQQVSMFGGRAYDFRADKAAGGFFGIQAHMAFVYQHHAHA					
m004.pep	70	80	90	100	110	119
	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA					
g004	TLIFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHANGAAQAATAADIRVAAPRYCPA					
m004.pep	120	130	140	150	160	179
	ILPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFSILIFSILSKPILSTFGRRP					


```

g004      |||||:||||:|||||:||||:|||||
          ILPWSAASCSRGSWLDASPAIKICGMLVCMVSGSATGTPRASLSILMFSKPILSTFGRRP
          130      140      150      160      170      180

m004.pep  180      190      200      210      220      230      239
          TAASIYSATNTPFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
          |||:|||||:|||||:|||||:|||||:|||||:|||||
g004      TAANIYSATNTPFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
          190      200      210      220      230      240

m004.pep  240      250
          MIPPKPKISTFTPKRCNAX
          |||||:|||||:|||||
g004      MIPPKPKISTFTPKRCNA
          250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 19>:

```

g005.seq
1  ATGGGGATGG ACAATATTGA TATGTTTCATG CCTGAACAAG AGGAAATCCA
51  ATCAATGTGG AAAGAAATTT TACTGAATTA CGGTATTTTC CTGCTCGAAC
101 TGCTTACCGT GTTCGGCGCA ATTGCGCTGA TTGTGTTGGC TATCGTACAG
151 AGTAAGAAAC AGTCGGAAG CGGCAGTGTC GTACTGACAG ATTTTTCGGA
201 AAATTATAAA AAACAGCGGC AATCGTTTGA AACATTCTTT TTAAGCGAGG
251 AAGACACAAA ACATCAGGAA AAAAAAGAAA AGAAAAAGGA AAAGGCGGAA
301 GCCAAAGCAG AGAAAAAGCG TTTGAAGGAG GCGGGGAGA AATCTGCCGA
351 AACGCAAAAA TCCCGCCTTT TTGTGTTGGA TTTTGACGGC GATTTGTATG
401 CACACGCCGT AGAATCCTTG CGTCATGAGA TTACGCGCGT GCTTTTGATT
451 GCCAAGCCTG AAGATGAGGT TCTGCTCAGA TTGGAAGTTC CGGGCGCGT
501 GGTTCACGGT TACGGTTTGG CGGCTTCGCA GCTTAGGCGT TTGCGCGAAC
551 GCATATTCC GCTGAccgtc gccgTCGATA AGGTCGCGGC AAGCGgcggc
601 tatatgatgg cgtgtgtgGC GGATAAAATT GTTTCCGCTc cgtttgcggc
651 catcggttcg gtgggtgtgg tgGcggaagt gcCGAATATC CAccgCctGT
701 TGAAAAAACA TGATATTGAT GTGGATGTGA TGACGCGCGG CGAATTAAAG
751 CGCACGGTTA CTTTATGGG TGAAATACG GAAAGGGCA AACAGAAATT
801 CCGGCAGGAA CTGAGGAAA CGCATCAGT GTTCAAGCAG TTTGTCACTG
851 AAAACGCCCC CGGGTTGGAT ATTGAAAAA TAGCGACGGG CGAGCATTGG
901 TTCGGCCGGC AGGCGTTGGC GTTGAAGTTC ATTGACGAGA TTTGACCAG
951 TGATGATTG TTGTTGAAAG CGTTGAAAA CAAACAGGtt aTCGAAGTGA
1001 AATATCAGGA GAAGCGAAGC CTGATCCAGC GCATTGGTTT GCAGGCGGAA
1051 GCTTCCGTTG AAAAGTTGTT TGCCAAACTT GTCAACCGGC GAGCGGATGT
1101 GATGTAG

```

This corresponds to the amino acid sequence <SEQ ID 20; ORF 005.ng>:

```

g005.pep
1  MGMDNIDMF PEQEEIQSMW KEILLNYGIF LLELLTVFGA IALIVLAIVQ
51  SKQSESGSV VLTDFSENYK QQRQSFETFF LSEEETKHQE KKEKKKEKAE
101  AKAEKRLKE GGEKSAETQK SRLFVLDFDG DLYAHAVESL RHEITAVLLI
151  AKPEDEVLLR LESPGGVVHG YGLAASQLRR LRERNIPLTV AVDRVAASGG
201  YMMACVADKI VSAPFAVIGS VGVVAEVPNI HRLKHKHDID VDVMTAGFEK
251  RTVTFMGENT EKGKQKFRQE LEETHQLFKQ FVSENRPGLD IEKIATGEHW
301  FGRQALALNL IDEISTSDDL LLKAFENKQV IEVKYQEKRS LIQRIGLQAE
351  ASVEKLFACL VNRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 21>:

```

m005.seq
1  ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51  GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCCTGCTC GAACTGCTTA
101  CCGTGTTCGG CGCAATGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151  AAACAGTCGG AWAGCGGCAG TGTCGTAAGT ACGGATTTT CCGAAAATTA
201  TAAAAAACAG CGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251  CACAACATCA GGAAAAAGAG GAAAAGAAA AGGAAAAGGC GGAAGCCAAA

```



```

301 GCAGAGAAAA A. CGTTTGAA GGAGGGTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGCTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAAAG GGCAAACAGA AATTCCGACA
801 GGAAGTGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTG AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCTG CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATTCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTTCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTCAAC CGGCGGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

m005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQXSGSVVL TDFSENYKKQ RQSFEEFFLS GEEAQHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFVLXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTSDLLL KAFENKQVIE VKYQEQSLI QRIGLQAEAS
351 VEKLFALKVN RRADV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

a005.seq

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTCTCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AAAGCGGCAG TGTCGTAAGT ACGGATTTTT CGGAAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAAACATCA GAAAAAGAG GAAAAAGAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGGTGGG GAGAAATCTT CCGAAACGCA
351 AAAATCCCGC CTTTTTGTGT TGGATTTTGA CGGCGATTGT TATGCACACG
401 CCGTAGAATC CTTGCGTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCGCT TAGATTGGAA AGTCCGGGCG GCGTGGTTCA
501 CGGTTACGGT TTGGCGGCTT CGCAGCTTAG GCGTTTGCGC GAACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTTGTAGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAAAG GGCAAACAGA AATTCCGACA
801 GGAAGTGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTG AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCTG CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATTCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTTCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTCAAC CGGCGGGCGG ATGTGATGTA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

a005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSESGSVVL TDFSENYKKQ RQSFEEFFLS GEEAQHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFVLDGDL YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRLR ERNIPLTVAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```


301 RQALALNLID EISTDDLLL KAFENKQVIE VKYQEQSLI QRIQLQAEAS
 351 VEKLFKLVN RRADM*

m005/a005 79.2% identity over a 366 aa overlap

m005.pep	MDNIDMFPEQEEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSVVL	10	20	30	40	50	60
a005	MDNIDMFPEQEEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESXSGSVVL	10	20	30	40	50	60
m005.pep	TDFSENYKKQRSFEAFFLSGEEAQHQEKEKKKEKAEAKAEKKRLKEGGEKSAETXKSR	70	80	90	100	110	120
a005	TDFSENYKKQRSFEAFFLSGEEAKHQEKEKKKEKAEAKAEKKRLKEGGEKSSSETQKSR	70	80	90	100	110	120
m005.pep	LFVLXX	130	140	150	160	170	180
a005	LFVLDFDGDLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPGGVVHGYGLAASQLRRLR	130	140	150	160	170	180
m005.pep	XXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSGVVAEVPNIHRLKKHDIDVD	190	200	210	220	230	240
a005	ERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAIVGSGVVAEVPNIHRLKKHDIDVD	190	200	210	220	230	240
m005.pep	VMTAGEFKRTVTFMGENTEGKGQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHWFG	250	260	270	280	290	300
a005	VMTAGEFKRTVTFMGENTEGKGQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHWFG	250	260	270	280	290	300
m005.pep	RQALALNLIDEISTDDLLLKAFENKQVIEVKYQEQSLIQRIGLQAEASVEKLFKLVN	310	320	330	340	350	360
a005	RQALALNLIDEISTDDLLLKAFENKQVIEVKYQEQSLIQRIGLQAEASVEKLFKLVN	310	320	330	340	350	360
m005.pep	RRADMVX						
a005	RRADMVX						

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

m005.pep	MDNIDMFPEQEEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSV	10	20	30	40	50
g005	MGMDNIDMFPEQEEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESXSGSV	10	20	30	40	50
m005.pep	VLTDSENYKKQRSFEAFFLSGEEAQHQEKEKKKEKAEAKAEKKRLKEGGEKSAETXK	60	70	80	90	100
g005	VLTDSENYKKQRSFETFFLSEETKHQEKKEKKKEKAEAKAEKKRLKEGGEKSAETQK	60	70	80	90	100

	120	130	140	150	160	170
m005.pep	SRLFVLXX					
			:			
g005	SRLFVLDFDGDLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPGGVVHGYGLAASQLRR					
	130	140	150	160	170	180
	180	190	200	210	220	230
m005.pep	XXXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDID					
	:					
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
	190	200	210	220	230	240
	240	250	260	270	280	290
m005.pep	VDVMTAGEFKRTVTFMGENTEKQKQFRQEELEETHQLFKQFVSENRPQLDIEEVATGEHW					
g005	VDVMTAGEFKRTVTFMGENTEKQKQFRQEELEETHQLFKQFVSENRPGLDIEKIATGEHW					
	250	260	270	280	290	300
	300	310	320	330	340	350
m005.pep	FGRQALALNLIDEISTSDDLLKAFENQVIEVKYQEKQSLIQRIGLQAEASVEKLFACL					
g005	FGRQALALNLIDEISTSDDLLKAFENQVIEVKYQEKRSIQRIGLQAEASVEKLFACL					
	310	320	330	340	350	360
	360					
m005.pep	VNRRADVMX					
g005	VNRRADVMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

```

g006.seq
1   ATGCTGCTGG TGCTggaatt ttggttCGGc gtGtCGGCGG TGGGCatact
51  tgCGTGTGTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCGG CCTGAACAAC AGCTTGGAAC gCGACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GTACCGCCAT TACGGACTGG TTTCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGGCTCGGCG
251 CGCGGATGGG TATTTGTTC GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACGGCA GCGCGGGGCA TATTTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATG AGTTTGGACG ATGTGCCGCG ATTGGTCGAA CAATATCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTCCGAAcG GAACATCAA
451 GCCGGAACTT GA

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

```

g006.pep
1   MLLVLEFWFG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDERQLYRH YGLVSRLRVL ISNREAFGYL CVGAAMGILF GFAFVMTLK
101 GYGSAGHIYS VGTYLWMFAM SLDDVPRLVE QYSLNKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

```

.m006.seq
1   ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGCGTGTGTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCGG CCTGAACAAC AGCTTGGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACC GCGCGCAGCT GTACCGCCAT TACGGACTGC TTTCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGGCTCGGCA
251 CGCGGATGGG TATTTGTTC GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT

```


351 GTTTGCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
 401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
 451 GCCGGAAC TTGA

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

m006.pep

1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
 51 KGDRRQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMTLK
 101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSNLKDIGO RIEWSERNIK
 151 AGT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

a006.seq

1 ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
 51 TCGTGTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
 101 TGTATTTCCG CCTGAAGAAC AGCTTGGAAC GCGACAACCA CTTTATCCGA
 151 AAAGCGCAGC AGCGGCAGCT GGACCGCCAT TACGGACTGC TTGCGCGCCT
 201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGCTCGGCA
 251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
 301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT
 351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
 401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
 451 GCCGGAAC TTGA

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

a006.pep

1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR
 51 KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMTLK
 101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSNLKDIGO RIEWSKRNIK
 151 AGT*

m006/a006 96.7% identity over a 153 aa overlap

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDRRQLYRH					
a006	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLKNSLERDNHFIRKGDERQLDRH					
	10	20	30	40	50	60
m006.pep	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMTLKGYSSAGHVYSVGTYLWMFAM					
a006	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMTLKGYSSAGHVYSVGTYLWMFAI					
	70	80	90	100	110	120
m006.pep	SLDDVPRLVEQYSNLKDIGO RIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSNLKDIGO RIEWSKRNIKAGTX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

m006/g006

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDRRQLYRH					

g006-1.seq

g006-1.pep

m006-1.seq

1	ATGTGGAAAA	TGTTGAAACA	CATAGCCCAA	ACCCACCGCA	AGCGATTGAT
51	TGGCACAATT	TCCCTGGTCG	GACTGGAAAA	CCTTTTGATG	CTGGTGTATC
101	CGGTGTTTGG	CGGCCGGGCG	ATCAATGCCG	TGATTGCGGG	GGAGGTGTGG
151	CAGGCGTTGC	TGTACGCTTT	GGTTGTGCTT	TTGATGTGGC	TGGTGGGTGG
201	GGTGC GCGCG	ATTGCCGATA	CGCGCACGTT	TACGCGGATT	TATACCGAAA
251	TCGCGGTGCC	GGTCGTGTTG	GAACAGCGGC	AGCGACAAGT	CCCGCATTTC
301	GCGGTAACTG	CCGCGGTTGC	CCTGTGCGGT	GAGTTTGTCA	GCTTTTTTGA
351	AGAAACCTGC	CCGATTGCCG	GCACATCCGT	CGTATCCATA	TTCGCGCGCT
401	GCATCATGCT	GCTGGTGTCT	GAATTTTGGG	TGCGCGTGTG	GCGGTTGGGC
451	ATACTGTGCT	TGTTTTTATG	GCTTTTGCCA	CGTTTTTGCC	CCATCAGCGA
501	AAACCTGCAT	TTCGCGCTGA	ACACAGTACT	GGAACGCGAC	AACCACTTTA
551	TCCGAAAAGG	GCACCGGCGG	CAGCTGATCC	GCCATTACGG	ACTGCTTTGG
601	CGCCTGCGTG	TGCTGATTTC	CAACCGCGAA	GCGTTGCGCT	ATCTCTGCGT

m006-1.pep

m006-1/g006-1 **95.5% identity in 288 aa overlap**

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 35>:

a006-1.seq (partial)

1	..	AGCCAAAACC	ACCGAAGCG	ATTGATTGGC	ACATTTTTTC	TGGTCGGACT
51		GGAAAACCTT	TTGATGCTGG	TGTATCCGGT	GTTTGCGCGC	TGGGCGATTA
101		ATGCCCGTAT	TGCGGGGACG	GCCTGGCAGG	CGTGCTGTGA	CGCTTTGGTT
151		TGTGCTTTTGA	TGTGGCTGGT	CGGTGCGGCG	CGGCGGATTG	CCGATACGCG
201		CACGTTTACG	CGGATTTATA	CGAAATCGC	CGTGCCGGTT	GTTGTGGAAC
251		AGCGCGAGCG	GCAAGTCCCG	CATTGCGCGG	TAACTGCGCG	GGTTGCCCTG
301		TCGCGTGAAT	TTGTCAGCTT	TTTTGAAGAA	CACCTGCCGA	TGCGCCGCAC
351		ATCCGTCGTA	TCCATATTCC	CGCGCTGCAT	CATGCTGCTG	GTGCTGGAAT
401		TTTGGGTCCG	CGTGTCCGCG	TGGGCATAC	TTCGCTTGTT	TTTATGGCTT
451		TTGCCACGTT	TTGCCGCCAT	CAGCGAAAAC	CTGTATTTC	CCCTGAAGAA
501		CAGCTTGGAA	CGCGACAACC	ACTTTATCCG	AAAAGGCGAC	GAGCGGCAGC
551		TGGACCGCCA	TTACGGACTG	CTTGGCGCGC	TGCGTGTGCT	GATTTCCAAC
601		CGCGAAGCCT	TCGGCTATCT	TGCGCTGGC	AGCGCGATGG	GTATTTTGTT
651		CGGCTTTGCT	TTTGTGATGA	TGACGCTCAA	AGGCTACAGC	AGCGCGGGGG

701 ATGCTCTATTC GGTCCGGCACT TATCTGTGGA TGTTCGCCAT AAGTTTGGAC
 751 GACGTGCCGC GATTGGTCCA ACAATATTCC AATTGAAAG ACATCGGACA
 801 ACGGATAGAG TGGTCGAAAC GGAACATCAA AGCCGGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

a006-1.pep (partial)

1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL
 101 SREFVSFFEE HLPAAATSVV SIFGACIMLL VLEFWVGVS VGLALFLWL
 151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRVLISN
 201 REAFGYLCVG TAMGILFGFA FVMMTLKGYS SAGHVYSVGT YLWMFAISLD
 251 DVPRLVEQYS NLKDIGQRIE WSKRNIKAGT *

a006-1/m006-1 95.7% identity in 280 aa overlap

	10	20	30	40	50
a006-1.pep	SQNHRKRLIGTFFLVGLENLMLVYPVFGGWAINAVIAGQAWQALLYALVVL				
m006-1	MWKMLKHIAQTHRKRLIGTFFSLVGLENLMLVYPVFGGRAINAVIAGEVWQALLYALVVL				
	10	20	30	40	50
	60	70	80	90	100
a006-1.pep	LMWLVGAAARRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
m006-1	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
	70	80	90	100	110
	120	130	140	150	160
a006-1.pep	PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLKNSLERD				
m006-1	PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERD				
	130	140	150	160	170
	180	190	200	210	220
a006-1.pep	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYS				
m006-1	NHFIRKGDERRQLRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYS				
	190	200	210	220	230
	240	250	260	270	280
a006-1.pep	GHVYSVGTYLWMFAISLDDVPRLVEQYSNLKDIGQRIEWSKRNIKAGTX				
m006-1	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

g007.seq

1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGcgC
 51 CGCcGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT
 101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
 151 ACTGCGtTTC CTccgctTTT CCggtcgGac tgtattatga acaAACCGCa
 201 cgTCCTgctg cacagcatgg tcaaaggcAt cgacgggaca ttcaaagtgg
 251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgcca tcagcgATGC
 301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

g007.pep

1 MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
 51 TAFPLFRSD CIMNKPVLL HSMVKGIDGT FKVERQNLRR IYARNRHQRC
 101 GHCRRRLHYH ERL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:

This corresponds to the amino acid sequence <SEQ ID 40; ORF 007>:

m007.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 41>:

a007.seq

This corresponds to the amino acid sequence <SEQ ID 42; ORF 007.a>:

a007.pap

m007/a007 97.3% identity over a 113 aa overlap

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m007/g007

```

      10      20      30      40      50      60
m007.pep  MNTTRLPTALVLGCFCAAASADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD
          |||||::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g007      MNTTRLPTAFILCCLCAAASADNSIMTKGQKVYESNCIACHGKKGEGRGTAFFPLFRSD
          10      20      30      40      50      60

      70      80      90     100     110
m007.pep  FIMKKPQVLLHSMVKGINGTIKVXRQNLQRIHARNRHQRCGHCRRRHLYHERLX
          ||::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


g007 CIMNKPVLLHSMVKGIDGTFKVERQNLRRYARNRHQRCGHCRRRHLYHERL
 70 80 90 100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 43>:

g007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCATCGCC TGCCACGGCA AGAAAGGGA AGGCGCGGC
151 ACTGCGTTTC CTCGCTTTT CCGGTCGGAC TATATTATGA ACAAACGCA
201 CGTCCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCC CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGGC AAAAAAAC.
```

This corresponds to the amino acid sequence <SEQ ID 44; ORF 007-1.ng>:

g007-1.pep (partial)

```

1  MNTTRLPTAF ILCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
51  TAFPPLFRSD YIMNKPVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKG KKN...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 45>:

m007-1.seq

```

1  ATGAACACAA CCCGACTGCC GACCGCCTTC GTCTTGGGCT GCTTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGBA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCC CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGC AAAAAAACT
401 AA
```

This corresponds to the amino acid sequence <SEQ ID 46; ORF 007-1>

m007-1.pep

```

1  MNTTRLPTAL VLGCFCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51  TMFPPLYRSD FIMKKPVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKS KKN*
```

m007-1 / g007-1 91.7% identity in 133 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD					
	10	20	30	40	50	60
g007-1	MNTTRLPTAFILCLCAAASAADNSIMTKGQKVYESNCIACHGKKGEGRGTAFPPLFRSD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPVLLHSMVKGINGTIKVNKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	70	80	90	100	110	120
g007-1	YIMNKPVLLHSMVKGINGTIKVNKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
	130					
g007-1	TEKDVQAKGKKN					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 47>:

a007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCTTC GTCTTGGGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
```



```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

a007-1.pep (partial)

```

1  MNTRLPTAL VLGLCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51  TMFPPLYRSD FIMKKPVLL HSMVKINGT IKVNGKTYNG EMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTRLPTALVLGLCAAAS	ADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
a007-1	MNTRLPTALVLGLCAAAS	ADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
	10	20	30	40	50	60
m007-1.pep	FIMKKPVLLHSMVKINGT	IKVNGKTYNGFMPATAISD	DIAAVATYIMNAFDNGGGSV			
a007-1	FIMKKPVLLHSMVKINGT	IKVNGKTYNGFMPATAISD	DIAAVATYIMNAFDNGGGSV			
	70	80	90	100	110	120
m007-1.pep	TEKDVQAKSKKNX					
a007-1	TEKDVQAKSKKNX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

g008.seq

```

1  ATGAACAACA GACATTTTGC CGTCATcgCC TTGGGCAGCA ACCTTGACAA
51  CCCCACACAA CAAATacgcg gcgcattaga cgcgctctcg tccatectg
101 acatccggct tgaaCaggtt tcctcactgt aTatgaccgc acctgtcggg
151 tacgAcaaTC agcccgATTT CATCaatgcc gTCTgcaccg TTCCACCAC
201 CtTGGACGGC ATTGcccTGC TTGCCgaACT CAaccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGCC TTACCCTGCC
351 GCATCCGCGC GCGCAGGAAC GCAGTTTCGT CATAcGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAATAACG GAAAGGTTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGACA GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

g008.pep

```

1  MNNRHFAVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51  YDNQPDFINA VCTVSTLDG IALLAELNRI EADFGRRSF RNAPRTLDEL
101 IIDFDGISSD DPRLLPHPR AHERSEVIRP LAEILPDFIL GKYGKVVELS
151 KRLGNQGIRL LPDR*-

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

m008.seq

```

1  ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51  CCCTGCTCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTT TGTCaATGCC GTCTGCACCG TTTCCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAct CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GkATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACCTTGCC

```



```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTGTTTGA GGAAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAAAT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

m008.pep

```

1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRRERF RNAPRTLXL
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHKQVAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 53>:

a008.seq

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTGC TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTT CGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAAC CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGAC TCACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

a008.pep

```

1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRRERF RNAPRTLDLD
101 IIDFDGISSD DRLTLPHPR AHERSFVIRP LAEILPDFIL GKHKQVAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHDPDIRLKQASSLYMTAPVGYNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHDPDIRLKQASSLYMTAPVGYNQPDFVNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRRERFARNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRRERFARNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
	130	140	150	160		
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

m008/g008

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHDPDIRLKQASSLYMTAPVGYNQPDFVNA					
g008	MNNRHFAVIALGSNLDNPAQQIRGALDALSSHDPDIRLEQVSSLYMTAPVGYNQPDFINA					

183

	10	20	30	40	50	60
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDDIIDFDGISSDDTLTLPHPR					
g008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
	130	140	150	160		
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
g008	AHERSFVIRPLAEILPDFILGKYGVVLSKRLGNQGIRLLPDRX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

g009.seq
 1 ATGCCCCGCG CTGCCGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
 51 CGAACAAAAT ACCCATCGCC GCGCCGACGC AGAGATAGCC GAAGGCTTCG
 101 CGGTTGGAAA TCAGCACACG CAGGCGCGAA ACCAGTCCGT AATGGCGGTA
 151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTcg cGTTCCAAGC
 201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
 251 AaaaGCCATA A

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

g009.pep
 1 MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFAVGNQHT QARNQSVMAV
 51 QLPLVAFSDK VVVAFOAVVQ AEIQVFADGG KTWQKP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

m009.seq
 1 ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
 51 CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
 101 CGGTTGGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTA
 151 CAGCTGCCGC CGGTCGCCTT TTCGGATAAA GTGGTTGTcg CGTTCCAAGC
 201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
 251 AAAAGCCATA A

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

m009.pep
 1 MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFAVGNQHT QARKQSVMAV
 51 QLPPVAFSDK VVVAFOAVVQ AEIQVFADGG KTWQKP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

m009/g009

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
g009	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFOAVVQAEIQVFADGGKTWQKPX					
g009	VVVAFOAVVQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAT  ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAT TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGTGCCGCG TCGTCGCCTT TTCGGATAAA GTGGTTGTCG CGTTCCAAGC
201 TGTTCCTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
1  MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
51  QLPVAFSDK  VVVAFAQVLQ AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
a009	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFAQVQAEIQVFADGGKTWQKXPX					
a009	VVVAFAQVLQAEIQVFADGGKTWQKXPX					
	70	80				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
1  ATGGGTTTTC CTGTTGCGAA GTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GCGCGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTGC TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGCGAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGGCGAG GGCGGTATTC TGTGAacgc
801 cgacggcgaa cgcTTTATGG AAcgetatgc GCcgACCGta aAagaCTTGG
851 CTTCTCGCga cgtGGTTTCA CgcgcGatgG CGatggaAat ctatgaaggt
901 cgcggctgTG GtaaaAAcaA agaCCacgtC TTAactGAAAA TCgACcAtAt
951 cggTGcAGAA AAAATTATGG AAAAaCTGCC GGGCATCCGC GAGATTTCCA
1001 TTCagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc ggttgTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTcgc aCCAATTATC ACGGTGAAGT
1101 TGTGTTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep


```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRDWHMY DTVKGSWLIG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENGDVVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDFIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

```

m010.seq (PARTIAL)
1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTTGT CTAAAGTGTT
51  CCCGACCCGT TCGCATAACG TAGCGGCGCA GGGCGGTATT TCCGCCTCTn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCGTG
151 AAAGGTTCCG ACTGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAAA ATTTATCAGC GTCCTTTCGG CGGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAGAACGC GYCTGTGCGG TTGCCGACCG
351 TACAGGTCAT GCGATGCTGC ATACTTTGTA CCAACAAAAC GTCGTGCCA
401 ATACGCAATT CTTTGTGGAA TGGACGGCAC AAGATTTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACCGCCATG GAAATGGAAA CCGCGGAAGT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGCGCGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCGC CGATGGTTTG
601 GGTATTTGTG CGCGTGCAGG TATCCCCTTG GAAGACATGG AATTCTGGCA
651 ATTCCAGCCG ACCGGCGTGG CGGGTGCGGG CGTGTGATT ACCGAA....

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

```

m010.pep (PARTIAL)
1  ..XQLSKSGLNC AVLSKVFPTR SHTVAAQGGI SASXGNVQED RWDWHMYDVT
51  KGSIDLGDQD AIEFMCRAP EAVIELEHMG MPFDRVESGK IYQRFPGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQQN VRANTQFFVE WTAQDLIRDE
151 NGDVVGVTAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMFWQFQP TGVAGAGVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

```

a010.seq
1  ATGGGCTTTC CTGTTGCAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATAACCGT AGCGGCGCAG
151 GCGGATATT CCGCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTGGGG GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACCGG
401 CCGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGCGCATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGCGGCGG TATTTATGCG TCTTCTACCA ATGCCATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGCGGTGTC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGCGCAG GCGGCTATTC TGTGAATGC
801 CGACGCGGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTGTTTTCC CGCGCATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CCGCGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCT
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGTATTCAG ACCCACTACC ATGGCGAAGT
1101 TGTCGTTTCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAATCCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAG TTCATCAAAG AGCAAAGCGA CTGGAACCTT TTGCCTGCTA

```



```

1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGA CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAATCAT GCGGATGTC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TCGGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
  1 MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKV F PTRSHTVAAQ
 51 GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR A APEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLSR DVVS RAMAMEIYEG
301 RGCCKNKD H V LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESGAHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

m010.pep                                10      20      30
                                XQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASXGNV
a010                                |||
MGFPVRKFDAVIVGGGGAGLRAXLQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV
      10      20      30      40      50      60

m010.pep      40      50      60      70      80      90
QEDRWDWHMYDTVKGSDWLGDQDAIEFMCR A APEAVIELEHMGMPFDRVESGKIYQRPFG
a010      |||
QEDRWDWHMYDTVKGSDWLGDQDAIEFMCR A APEAVIELEHMGMPFDRVESGKIYQRPFG
      70      80      90      100     110     120

m010.pep      100     110     120     130     140     150
GHTAEHGKRAVERXC A VADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V
a010      |||
GHTAEHGKRAVERAC A VADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V
      130     140     150     160     170     180

m010.pep      160     170     180     190     200     210
TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
a010      |||
TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
      190     200     210     220     230     240

m010.pep      220     230
FQPTGVAGAGVLITE
a010      |||
FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPT VKDLSR DVVS RAMAMEIYEG
      250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 010 shows 98.7% identity over a 231 aa overlap with a predicted ORF (ORF 010.ng) from *N. gonorrhoeae*:

m010.pep/g010.pep

m010.pep				10	20	30	
				XQLSKSGLNCAVL	SKVFPT	RSHTVAAQGGISASXGNV	
g010	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCAVL	SKVFPT	RSHTVAAQGGISASLGNV				
	10	20	30	40	50	60	
m010.pep	40	50	60	70	80	90	
	QEDRWDWHMYDTVKGS	DWLGDQDAIEFMCRAA	PEAVIE	LEHMGMPFDRVESGKIYQRPFG			
g010	QEDRWDWHMYDTVKGS	DWLGDQDAIEFMCRAA	PEAVIE	LEHMGMPFDRVESGKIYQRPFG			
	70	80	90	100	110	120	
m010.pep	100	110	120	130	140	150	
	GHTAEHGKRAVERXCAVADRTGHAM	LHTLYQQNVRANTQFFVEWTAQDLIRDENG	DVVGV				
g010	GHTAEHGKRAVERACAVADRTGHAM	LHTLYQQNVRANTQFFVEWTAQDLIRDENG	DVVGV				
	130	140	150	160	170	180	
m010.pep	160	170	180	190	200	210	
	TAMEMETGEVYIFHAKAVMEFATGGG	GRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
g010	TAMEMETGEVYIFHAKAVMEFATGGG	GRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
	190	200	210	220	230	240	
m010.pep	220	230					
	FQPTGVAGAGVLITE						
g010	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPT	VKDLASRDVVSRAAMEIYEG					
	250	260	270	280	290	300	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

```

1  ATGGGTTTTC CTGTTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTGTGC TAAAGTGTTT CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCAGGATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCGCA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCT TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGTTTGG GCATTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGGCGAG GCGGTATTC TGTGTAACGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTGTTTCA CCGCGATGG CGATGGAAAT CTATGAAGGT
901 CGCGGCTGTG GTAAAAACAA AGACCACGTC TTACTGAAAA TCGACCATAT
951 CGGTGCAGAA AAAATTATGG AAAAAGTGCC GGGCATCCGC GAGATTTCCT
1001 TTCAGTTTGC CGGTATCGAT CCGATTAAAG ACCCGATTCC GGTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTATC ACGGTGAAGT
1101 TGTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT

```


1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDMHY DTVKGSWLG DQDAIEFMCR AAEAVIELE
101 HMGMPPDRVE SGKIYQRPFG GHTAENGKRA VERACAVADR TGHAMLHTLY
151 QQNVRAANTQF FVEWTAQDLI RDENGDVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPPIVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

g010-1 / P10444

sp|P10444|DHS_A_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942
 (AB000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 191/303 (63%), Positives = 238/303 (78%)

```

Query: 1 MGFPVRKFDAVIVXXXXXXXXXXXXXSKSLNCVLSKVFPTRSHTVAAQGGISASLGNV 60
M PVR+FDVAV++ S+SG CA+LSKVFPTRSHTV+AQGGI+ +LGN
Sbjct: 1 MKLPPREFDAVIVGAGGAGMRAALQISQSGQTALLSKVFPTRSHTVSAQGGITVALGNT 60

Query: 61 QEDRWDMHYDITVKGSWLGQDQDAIEFMCRAAPEAVIELEHMGMPDRVESGKIYQRPFG 120
ED W+WHMYDITVKGS++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG
Sbjct: 61 HEDNWEWHMYDITVKGSYIGDQDAIEYMCKTGPEALLEHMGGLPFSRLDDGRIYQRPFG 120

Query: 121 GHTASHGKRAVERACAVADRTGHAMLHTLYQQNVRAANTQFFVEWTAQDLIRDENGDVVG 180
G + G R A ADRTGHA+LHTLYQQN++ +T F EW A DL+++++G VVG
Sbjct: 121 GQSKNFGGQAARTAAADRTGHALLHTLYQQNLKNTTIFSEWYALDLVKNQDGAUVGC 180

Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240
TA+ +ETGEV P A+A + ATGG GRIY S+TNA++NTGDG+G+ RAG+P++DME WQ
Sbjct: 181 TALCIETGEVVYFKARATVLTATGGAGRIYQSTTNAHINTGDGVGMARAGVVPQDMEMWQ 240

Query: 241 FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG 300
FHPTG+AGAGVL+TEG RGECC LLN GERFMERYAP KDLA RDVV+R++ +EI EG
Sbjct: 241 FHPTGIAGAGVLVTEGCRGEGGYLLNKHGERFMERYAPNAKDLAGRDVVARSIMIEIREG 300

Query: 301 RGC 303
RGC
Sbjct: 301 RGC 303

```

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 53/102 (51%), Positives = 62/102 (60%)

```

Query: 309 HVLLKIDHIGAEKIMEKLPGIREISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368
H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +
Sbjct: 310 HAKLKLDHLGKEVLESRLPGILELSRTFAHVDPVKEIPVIPTCHYMMGGIPTKVTGQAL 369

Query: 369 VPQGEYEVVKGLYAAGECACASVHGANRLGTNSLLDLVVF 410
+V V GL+A GE AC SVHGANRLG NSLLDLVVF
Sbjct: 370 TVNEKGEDVVVPGFLAVGEBIACVSVHGANRLGNSLLDLVVF 411

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..

```

1  ATGGGTTTTC CTGTTGCGAA GTTGTATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTGC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTCCGCG GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCGGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC

```


451 CAACAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGTG TATTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 TGTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTCTCGCGA CGTTGTTTCC CGGCGATGG CGATGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTACTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTCC GGGCATCCGC GAGATTCCA
1001 TTCAGTTCCG CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTACC ACGGCGAAGT
1101 TGTCTGTTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAATA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACCCACTCCC TGTGGACTT GGTGGTATC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGAAACCT TTGCCTGCTA
1301 ATGCAGGTGA GTTGACCCGC CAACGTATCG AGCGTTTGGG CAACCAAACC
1351 GATGGTGAAA ACGTTGATGC ATTGCGTCGC GAACGTCAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTGATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAG
1601 AATCACGCGG TCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATCA GATATCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAAGCT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pep..

1 MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51 GGISASLGNV QEDRWDMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QONVRANTQF FVEWTAQDLI RDENGDVVGV TAMEMETGEV YIFHAKVMP
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RGCGRNKNDHV LLKIDHIGAE KIMEKLP GIR ESIQFAGID PIKDFIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGEDYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVOLHA GVFRTEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPPERDDE
551 NWMKHLYHS DINTLSYKPV HTKPLSVEYI KPAKRVY*

m010-1 / g010-1 99.5% identity in 410 aa overlap

	10	20	30	40	50	60
m010-1.pep	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVF	PTRSHTVAAQGGISASLGNV				
g010-1	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVF	PTRSHTVAAQGGISASLGNV				
	10	20	30	40	50	60
m010-1.pep	QEDRWDMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG	TGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDVVGV				
g010-1	QEDRWDMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG	TGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDVVGV				
	70	80	90	100	110	120
m010-1.pep	GHTAEHGKRAVERACAVADRTGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDVVGV	TGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDVVGV				
g010-1	GHTAEHGKRAVERACAVADRTGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDVVGV	TGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDVVGV				
	130	140	150	160	170	180
m010-1.pep	TAMEMETGEVYIFHAKVMPATGGGGRIYASSTNAYMNTG	DGLGICARAGIPLEDMEFWQ				
g010-1	TAMEMETGEVYIFHAKVMPATGGGGRIYASSTNAYMNTG	DGLGICARAGIPLEDMEFWQ				
	190	200	210	220	230	240

190

	190	200	210	220	230	240
m010-1.pep	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
g010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
	250	260	270	280	290	300
m010-1.pep	310	320	330	340	350	360
	RGCGRKNDHVLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
g010-1	RGCGRKNDHVLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
	310	320	330	340	350	360
m010-1.pep	370	380	390	400	410	420
	TNYHGEVVVPQGEDYEVPVKCLYAAGECACASVHGANRLGTSLLDLVVFGKAAGDSMIK					
g010-1	TNYHGEVVVPQGEDYEVPVKCLYAAGECACASVHGANRLGTSLLDLVVFRPTPRX					
	370	380	390	400	410	
m010-1.pep	430	440	450	460	470	480
	FPIKEQSDWKPLPANAGELTRQRIERLDNQTDGENVDALRRELQSVQLHAGVFRTEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1.seq..

```

1  ATGGGCTTTC CTGTTTCGCAA GTTGTATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTTGT CTAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGCGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACCGG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGCGAAGTTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCGG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGCGGT ACGCGGCGAG GGCGGTATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCT
1001 TFCAGTTTCG CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCGC
1051 ACTACCCACT ATATGATGGG CGGTATTCCG ACCAACTACC ATGGCGAAGT
1101 TGTCTGTTCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCCGCGCA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAATCAT GGCGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATCA GATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1.pep..

```

1  MFFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDMHY DTVKGSWDLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHATAHGKRA VERACAVADR TGHAMLHTLY

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151 QQNVRAQTQF FVEWTAQDLI RDENGDVVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RCGGKNKDHV LLKIDHIGAE KIMEKLP G IREISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWK P LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMIAA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

m010-1 / a010-1 99.3% identity in 587 aa overlap

a010-1.pep	10	20	30	40	50	60
a010-1	MGFPVRKFD	AVIVGGGGAGL	RAXLQLSKS	GLNCAVL	SKVFPTR	SHTVAAQGGISASLGNV
	10	20	30	40	50	60
a010-1	MGFPVRKFD	AVIVGGGGAGL	RAALQLSKS	GLNCAVL	SKVFPTR	SHTVAAQGGISASLGNV
	70	80	90	100	110	120
a010-1.pep	QEDRWDMHY	DTVKGSDWL	GDQDAIEF	MCRAAPEA	VIELEHMG	MPFDRVESGKIYQRPF
m010-1	QEDRWDMHY	DTVKGSDWL	GDQDAIEF	MCRAAPEA	VIELEHMG	MPFDRVESGKIYQRPF
	70	80	90	100	110	120
a010-1.pep	130	140	150	160	170	180
a010-1	GHTAEHGK	RAVERACA	VADRTGH	AMLHTLY	QQNVRAQT	QFFVEWTAQDLIRDENG
	130	140	150	160	170	180
m010-1	GHTAEHGK	RAVERACA	VADRTGH	AMLHTLY	QQNVRAQT	QFFVEWTAQDLIRDENG
	130	140	150	160	170	180
a010-1.pep	190	200	210	220	230	240
a010-1	TAMEMETGE	VEVYIFHA	KAVMFATG	GGGRIYAS	SSTNAYMN	TG DGLGICARAGI
	190	200	210	220	230	240
m010-1	TAMEMETGE	VEVYIFHA	KAVMFATG	GGGRIYAS	SSTNAYMN	TG DGLGICARAGI
	190	200	210	220	230	240
a010-1.pep	250	260	270	280	290	300
a010-1	FHPTGVAG	AGVVLITE	GVRGEGG	ILLNADGE	RFMERYAP	TVKDLASRDVVS
	250	260	270	280	290	300
m010-1	FHPTGVAG	AGVVLITE	GVRGEGG	ILLNADGE	RFMERYAP	TVKDLASRDVVS
	250	260	270	280	290	300
a010-1.pep	310	320	330	340	350	360
a010-1	RCGGKNK	DHVLKID	HIGAEK	IMEKLP	GIREISIQ	FAGIDPIKDPIPVVP
	310	320	330	340	350	360
m010-1	RCGGKNK	DHVLKID	HIGAEK	IMEKLP	GIREISIQ	FAGIDPIKDPIPVVP
	310	320	330	340	350	360
a010-1.pep	370	380	390	400	410	420
a010-1	TNYHGEV	VVPQGDE	YEVVPV	KGLYAAGE	CACASVH	GANRLGTNSLLDLV
	370	380	390	400	410	420
m010-1	TNYHGEV	VVPQGDE	YEVVPV	KGLYAAGE	CACASVH	GANRLGTNSLLDLV
	370	380	390	400	410	420
a010-1.pep	430	440	450	460	470	480
a010-1	FIKEQSD	WKPLPAN	AGELTRQ	RIERLDN	QTDGENV	DALRRELQ
	430	440	450	460	470	480
m010-1	FIKEQSD	WKPLPAN	AGELTRQ	RIERLDN	QTDGENV	DALRRELQ
	430	440	450	460	470	480
a010-1.pep	490	500	510	520	530	540
a010-1	KGVREVM	IAERVKR	TEIKDK	SKVWNTA	RIEAL	EALDNLIEVAKAT
	490	500	510	520	530	540
m010-1	KGVREVM	IAERVKR	TEIKDK	SKVWNTA	RIEAL	EALDNLIEVAKAT
	490	500	510	520	530	540
a010-1.pep	550	560	570	580		
a010-1	SDDHPER	DDENWM	KHTLYH	SDANTLS	YKPVHTK	PLSVEYIKPAKRVYX


```
g011.seq
1  ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51  GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAA CCGCCTTACC GAAGATATGA AAACCCGCGAT GCGCGCCAAA
151 GATCAAGTTT CCTCTGGCAC CATCGCCTC ATCAATGCCG CCGTCAAACA
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACGCCCA
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGGCGCGAA AATCTACACT
301 GARGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT
351 CTGTCACCGC TACCTGCCCG AAATGCTCTC CGCCGGCGAA ATCCGACCCG
401 CCGTCGAAGC AGCCGTGTGC GAAACCGGCG CGGCAGGTAT GGCGGATATG
451 GGCAAAGTGA TGGTCGTATT GAAAAccgc CTCGCGCGCA AAGccgATAT
501 GGGCGAAGTC AACAAATCT TGAAAAccGt aCTGACCGCC tga
```

```
g011.pep
1 MKTHRKTCSA VCFAFQTASF PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFV DERTEADDAK ITAILTKMVK QRKDGAKIYT
101 EAGRQDLADK LAEIDVLHR YLPQMSAGE IRTAVEAAVA ETGAAGMADM
151 GKVMVVLKTR LAGKADMGEV NKILKTVLTA *
```

```
m011.seq (partial)
1  ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51  GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAA CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCGC CCGTCACAAA
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCAGGTT
351 ATGCAACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG
401 AGGTCGAAGC TCCGTTGCCG GAAACCGGCG CGCAGGTTAT GGCGGATATG
451 GGTAAAGTCA TGGGGCTGCT GAAAACCCGC CTCGCAGGTA AAGCCGA...
```

```
m011.pep (partial)
  1  MRTHRKTCSA  VCFAFQTASK  PAVSIRHPSE  DIMSLKIRLT  EDMKTAMRAK
51  DQVSLGTIRL  INAAVKQFEV  DERTFADDAK  ITAILTKMVK  QRKDSAKIYT
101 EAGRQDLADK  ENAEIEVLHR  YLPQMSLAGE  IRTEVEAAVA  ETGAAGMADM
151 GKVMGLLKTR  LAGKA.....
```

```

m011/g011
      10      20      30      40      50      60
m011.pep  MRTHRKTCSAVCFAFQTASKPAVSIRHPSEDIMSLKIRLTEDMKTAMRAKDQVSLGTIRL
g011      MKTHRKTCSAVCFAFQTASKPAVSIRHPSEDIMSLKTRLTEDMKTAMRAKDQVSLGTIRL
      10      20      30      40      50      60
m011.pep  INAAVKQFEVDERTEADDAKITAILTKMVKORKDSAKIYTEAGRODLADKENAEIEVLHR
g011      INAAVKQFEVDERTEADDAKITAILTKMVKORKDGAKIYTEAGRODLADKENAEIDVLHR

```


193

	70	80	90	100	110	120
	130	140	150	160		
m011.pep	YLPQMLSAGEIRTEVEAAVAETGAAGMADMGKVMGLLKTRLAGKA					
					:	
g011	YLPQMLSAGEIRTAEEAAVAETGAAGMADMGKVMVVLKTRLAGKADMGEVKNILKTVLTA					
	130	140	150	160	170	180
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

g012.seq

```

1  ATGCTCGCCC GTCGCTATTT TTTCAATATC CAACCCGGGG CGGTTTTCAC
51  TGACAAACTG CTGGAACAAC TGATGCGTTT CCTCCAGTTC CTGCCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACa
201 gGcggTGGAT ATTCGgcact tccgCcacca caccaccga accgatgacc
251 gcaaacggaG CGGAACAAT TTTATCCGcC acacacgcca tcatatagcc
301 gcCGCTTGCC GCGACCTTAT CGAcggcgac ggTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TCGGTTTCG
551 GCAGATTCTT CCCCGCCTC CTTCAAACGC TTTTCTCTG CTTGGGCTTC
601 CGCCTTTTCC TTTTCTTTT CTTTTTTTTC CTGATGTTTT GTCTCTTCTC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

g012.pep

```

1  MLARRYFFNI OPGAVFTDKL LEQLMRFLQF LPEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRFRHHHTR TDDRKRSGNN FIRHTRHHIA
101 AACRDIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKRRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPAL LQTLFLCFGF
201 RLFLFLFFFF LMFCLFLA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

m012.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGTGGAT ATTCGGTACT TCCGCCACCA CACCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
501 nnnnnnnnnn nnnnnnnnnnC AACACAAAAA GGCGTGATT nTGGGTTTCG
551 GCAGATTCTT CCCACCTC CTTCAAACGT TTTTCTCTG CTTGGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTGT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

m012.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRHHHTR TDNRKRSGSN FIRHTRHHIT
101 AARXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXQHKKA*F XRFGRFLPTL LQTFFLCFGF
201 RLFLFLFLFF LMLCLFPA*

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTGCGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGCGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCCTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAATTCGCC GTCAAAATCC AACACAAAAA GCGGGGATT TTGCGTTTCG
551 GAAGATTCTC CCCACCCCTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
1  MLARCHFLNI QLRVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAQVD IRYFRYNTHR TNRKRSGNN FIRHTRHHIT
101 TARRHLIDGD QQRNIAFAQT PKLRSRQTVT VNHAARTFQS QQLNIFRLGN
151 QKRRRLMTQ GFYGVCIQIA VKIQHKAGF LRFRFLPTL LQTLFLCFGF
201 RLFLFLFF LMFLFPA*
```

m012/a012 64.2% identity over a 218 aa overlap

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
a012	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAQVDIRYFRHHTHRTDNRKRSGNSNFIHTRHHITAARXXXXXXXXXXXXXXXXXXXX					
a012	NIMFFQQAQVDIRYFRYNTHRTDNRKRSGNNFIHTRHHITTARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
m012.pep	130	140	150	160	170	180
	XXXQHKKAXF					
a012	PKLRSRQTVTVAHAARTFQSKQNLIFRLGNQKRRRLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
m012.pep	190	200	210	219		
	XRFRFLPTLLQTFFLCFGRFLFLFLFLFLMLCLFPAX					
a012	LRFRFLPTLLQTLFLCFGRFLFLFLFLFLMFLCLFPAX					
	190	200	210			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					

195

	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHHTRTDNRKRSNSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXXXX					
	: : : : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHHTRTDDRKRSGNNFIRHTRHHIAAACRDLIDGQGQRNIAFAQT					
m012.pep	130	140	150	160	170	180
	XXXQHKKAXF					
	:	:	:	:	:	
g012	130	140	150	160	170	180
	PKLRSRQTVTVNHAARTFQSEQNLIIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
m012.pep	190	200	210	219		
	XRFGRLPTLLQTFFLCFGRFLFLFLFLFLMLCLFPAX					
	: : : : : :					
g012	190	200	210			
	LRFGRLPALQLFLCFGRFLFLFLFLFLMFLCLFLAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

m012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAACTG  CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGGTGGAT ATTCGGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CyTAAGCTGC GAAGCCGCCA AACCCTAACC GTGAACCAAG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GCGGGGATT TTGCGTTTCG
551 GCAGATTCTC CCCACCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

m012-1.pep

```

1  MLARCHFLNI QLRVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHTHR TDNRKRSNSN FIRHTRHHIT
101 AARRHLIDGD GQRNIAFAQT XKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFG
201 RLFLFLFLFF LMFCLFPA*

```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	: : : : : :					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
m012-1.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHHTRTDNRKRSNSNFIRHTRHHITAARRHLIDGQGQRNIAFAQT					
	: : : : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHHTRTDDRKRSGNNFIRHTRHHIAAACRDLIDGQGQRNIAFAQT					
m012-1.pep	130	140	150	160	170	180
	XKLRSRQTVTVNHAARTFQSEQNLIIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	: : : : : :					
g012	PKLRSRQTVTVNHAARTFQSEQNLIIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					

196

	130	140	150	160	170	180
	190	200	210	219		
m012-1.pep	LRFG	RFLP	TLQL	TLFL	CFGR	FLFLFLFLMFCFLFPAX
g012	LRFG	RFLP	ALLQ	TLFL	CFGR	FLFLFLFLFLMFCFLFLAX
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GCGGGGATT TTGCGTTTCG
551 GAAGATTCTC CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVID IRYFRYNTHR TDNRKRSNGN FIRHTRHHIT
101 TARRHLIDGD GORNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKRRNLMTQ GFYGVCIQIA VKIQHKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCFLFA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60
a012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
m012-1	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
a012-1.pep	NIMFFQQAVIDIRYFRYNTHRTDNRKRSNGNFIRHTRHHITTARRHLIDGDGORNIAFAQT					
m012-1	NIMFFQQAVIDIRYFRHHTHRTDNRKRSNGNFIRHTRHHITAARRHLIDGDGORNIAFAQT					
	70	80	90	100	110	120
a012-1.pep	NIMFFQQAVIDIRYFRYNTHRTDNRKRSNGNFIRHTRHHITTARRHLIDGDGORNIAFAQT					
m012-1	NIMFFQQAVIDIRYFRHHTHRTDNRKRSNGNFIRHTRHHITAARRHLIDGDGORNIAFAQT					
	70	80	90	100	110	120
a012-1.pep	PKLRSRQTVT VNHAARTFQSKQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKAGF					
m012-1	XKLSRQTVT VNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKAGF					
	130	140	150	160	170	180
a012-1.pep	PKLRSRQTVT VNHAARTFQSKQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKAGF					
m012-1	XKLSRQTVT VNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKAGF					
	130	140	150	160	170	180
a012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLFLFLFLMFCFLFPAX					
m012-1	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLFLFLFLMFCFLFPAX					
	190	200	210	219		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1  aTgcctttga ccatgctgtg cagcaGGAcg tGCGGTTtgt tcataatata
51  gtCcagaccGG AAAagcggAG GAAaCGCAGT GCCGCGCCCT TCCCCTTTCT
101 TGCCGTGGCA GCGGATGCag tTgGATTTCGT ACACTTTTTG CCCTTTtGtc

```



```

151 atgatGCTgt tgtcggCGGC AGAAGCgGCG GcgCAGAGGC AGCACAAGAT
201 GAAGGCGGTC GGCAGTCGGG TTGTGTtcat tGgcgTTTCC cctaattgttt
251 tgaaaccttg ttttttgatt Ttgcctttac ggggtgaaaa gtttttTtgg
301 cccaaatccg gaatttag

```

This corresponds to the amino acid sequence <SEQ ID 88; ORF 013.ng:

g013.pep

```

1 MPLTMLCSRT CGLFIIQSDR KSGGNAVPRP SPFLPWQAMQ LDSYTFCPFV
51 MMLLSAAEAA AQRQHKMKAV GSRVVFIVGS PNVLKPCFLI LPLRGEKFFW
101 PKSGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 89>:

m013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TGCGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCACGCAG TTGGATTTCG ACACCTTTTG CCCTTTTGTC
151 ATGATGCTGT TGTCCGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTCAT TGGTGTTCCT TTCATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT TTTGCCGAAT
301 CAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 90; ORF 013>:

m013.pep

```

1 MPLTMLCSST CGFFMMKSER XSGGNMVPRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQKQPKTRAV GSRVVFIVGS FMFETLLLLL RSGXKIFLNP
101 Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 91>:

a013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TGCGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCACGCAG TTGGATTTCG ACACCTTTTG CCCTTTTGTC
151 ATGATGCTGT TGTCCGCGGC AGAAGCGGCG GCGCAGAGGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTCAT TGGTGTTCCT TTAATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT CTTGCCGAAT
301 CGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 92; ORF 013.a>:

a013.pep

```

1 MPLTMLCSST CGFFMMKSER *SGGNMVPRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIVGS LMFETLLLLL RSG*KIFLNP
101 R*

```

m013/a013 97.0% identity over a 101 aa overlap

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVPRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
a013	MPLTMLCSSTCGFFMMKSERXSGGNMVPRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFIVGSFMFETLLLLILRSGXKIFLNPQX					
	:					
a013	AQKQPKTRAVGSRVVFIVGSLMFETLLLLILRSGXKIFLPNRX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:


```

      10          20          30          40          50          60
m013.pep    MPLTMLCSSTCGFFMKSERXSGGNMVP RPSPFLPWQATQLDSYTCF PFVMMLLSAAEEA
             ||||| |:::|| | | | | | | | | | | | | | | | | | | | | | |
g013         MPLTMLCSRTCGLFI IQSDRKSGGNAV RPSPFLPWQAMQLDSYTCF PFVMMLLSAAEEA
              10          20          30          40          50          60

              70          80          90          100
m013.pep    AQKQP KTRAVGS RVVFIGVS F-MFET LLLILR-SGXKIFLPNQX
             ||:| |:||||| :| | | | | | | | | | | | | | | | | | | |
g013        AQRQHKKAVGS RVVFIGV SPNVLKP CFIPL PLRGKF FWPKSGIX
              70          80          90          100

```

g015.seq

1	ATGCAGTATC	TGATTGTCAA	ATACAGCCAT	CAATCTTCG	TTACCATCAC
51	CATTTTGGTA	TTCAACATCC	GTTTTTTCCT	ACTTTGGAAA	AATCCAGAAA
101	AGCCCTTGGT	CGGCTTTTGG	AAAGCACTGC	CCCACCTCAA	CGACACGATG
151	CTGCTGTTTA	CGGGATTGTG	GCTGATGAAG	ATTACCCATT	TCTCCCGGTT
201	CAACGCGCCT	TGGCTCGGCA	CAAAAATCCT	GCTCCTGTTT	GCCTACATCG
251	CACCTGGGCAT	GGTAATGATG	CGCGCCCGTC	CGCGTTCGAC	CAAGTTCTAC
301	ACCTGTTTACC	TGTCGCTAT	TGTGTGCATC	GCCTGCATCG	TTTACCTTGC
351	CAAAACCAAA	GTCCTGCCAT	TCTGA		

g015.pcp

1 MQYLIVKYSH QIFVTITILV FNIRFLLWK NPEKPLVGFW KALPHLNDTM
51 LLFTGLWLWK ITHFSPFNAP WLGTKILLF AYIALGMVMM RARPRSTKFY
101 TVYLLAMCCI ACIVYLAKTK VLPF*

m015.seq

```

1      . . AAAATCAGAA AAGCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51     CGACACCATG CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101    TCTCCCGCTT CAACGCGCCT TGCTCGGTA CAAAAATCCT GCTTCTGCTC
151    GCCTATATCG CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTTCGAC
201    ACGTTTCTAC ACGGTTTACC TGCTGCACAT GTGTGCGGTC GCCTGCATCG
251    TTTACCTTGC CAAAACCAA GTCTGCCTT TCTTGA

```

m015.pep (partial)

1 ..KIRKALAGFW KALPHLNDTM LLFTGLWLMK ITHFSPFNAP WLGTKILLLL
51 AYIALGMMMM RARPRSTKEY TVYLLAMCCV ACIVYLAKTK VLPF*

a015.seq

1 ATGCAGTATC TGATTGTCAA ATACAGCCAT, CAAATCTTCG TTACCATCAC
51 CATTTTGGTA TTCAACATCC GTGTTTTNT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGC GGGCTTTTGG AAGCGATGCC CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGATTGFG CGTGATGAAA ATTACCATT TCTCCCGTT
201 CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTGGGTAT GATGATGATG CGCGCCCGTC CGGTTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTGCAGC CTGTTTGCCTC ACCTGCATCG TTTACCTTGC
351 CAAACCAAA GTCTCGCCTT TCTGA

a015.pap

1 MQYLIVKYSH QIEVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM
 51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY
 101 TVYLLAMCCL TCIVYLAKTK VLPF*

m015/a015 96.7% identity over a 91 aa overlap

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
a015	LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
a015	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCLTCIVYLAKTKVLP				
	70	80	90	100	110	120
m015.pep	FX					
a015	FX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng) from *N. gonorrhoeae*:

m015/g015

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
g015	LIVKYSHQIFVTITILVFNIRFLLWKNPEKPLVGFVKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
g015	FSPFNAPWLGTKILLLLAYIALGMMVMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
	70	80	90	100	110	120
m015.pep	FX					
g015	FX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

g018.seq

1 atGCAGCAGG GGCagttggt tggacgcgtc gcccgcaata AAGATATGCG
 51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGgtac gccgcgcgcg
 101 tctttgTCGA TATTGATGTT TTCCAAACCG ATATgtTCAA CGTTCGGACG
 151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTTCGC
 201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC
 251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT
 301 CGCCTCGTCT GA

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

g018.pep

1 MQQGQLVGRV ARNKDMRNAG LHGQRIGNGY AARVFVDIDV FQTDIVNVRT
 51 ATYGCQHIFG NKYAFAILL PMDFYIACV EFDLGFSIQM QFQFFSEHGF

m018.seq

m018.ppt

a018.seq

a018.pap

```

      10      20      30      40      50      60
m018.pep  MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGQHIFG
          ||| ||||:| ::|||:|||||:| |||:| |||:|||||||:|:|||||
g018      MQGGQLVGRVARNKDMRNLHGQRIGNGYAARVFDIDVFQTDIVNVRTATYGCQHIFG
          10      20      30      40      50      60

```


	70	80	90	100
m018.pep	NKYAFFAILLPMDFYIAVCI	FDLGFSIQMQFFAEHGVRLVX		
g018	NKYAFFAILLPMDFYIAVC	VEFDLGFSIQMQFFSEHGFRLVX		
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

g019.seq (partial)

```

1  ..ctgctggcgg ccctggtgct tgccgcgtgt tcttcgACAA ACaactGCC
51  AGCCGGCAAG ACCCGGCAG ACAATATAGA AActgcGgAC CTTTCGGCAA
101 GCGTTCCAC ccgcCTGCC GAACCGAAG GAAAAACGCT GGCAGATTAC
151 GGCGCTACC CGTCCGCACT GGATGCAGTG AAACAGAAAC ACGATGCGGC
201 AGCCGCGGCC TATTGGAAA Acgcaggaga cagCGcgatg gcGGAAAtg
251 tccgcaagga gtgGCTGa

```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

g019.pep (partial)

```

1  ..LLAALVLAAC SSTNTLPAGK TPAADNIETAD LSASVPTRPA EPEGKTLADY
51  GGYPALDAV KQNNDAASAAA YLENAGDSAM AENVKRWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

m019.seq (partial)

```

1  ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGCTGCTGG CGGCCCTGGT
51  GCTTGCCGCG TGTTCTTCGA CAAACACACT GCCAGCCGCG AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCCGCCCT
151 GCCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCAGCAG ACAGTGGACG CTGTTTGAC AGGAATACGC
351 CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451 AAACTGCCTT CGGGCTGCAC CAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTGTGTTGAC GGCAACGACG CCTGGAGGCG CGTGCGCGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAGAGG GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTAAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CTGCGCGCCT TGGACTATTA
801 CGGCAAGGTT GCCGACCGCC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACCCCGCGCG CGCCTTGCGC GCCCGACGTT GGGACGAGCT GGCCTCCGTT
901 ATCTCGCATA TGCCCGAAAA ACTGCAAAAA AGCCCGACCT GGCTCTACTG
951 GCTGGCACGC AGCCGCGCGC CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GGCGGCAGCG ACGGGCAGGA ATTTTATGCG GGTGCTGGCA
1051 GGGGAAGAAT TGGGTGCGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAAACGCG
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG GCGTTTGGCC ACACGCGGCT TGACGAAGA
1251 CAAGCTGCTG ACCGCCGCGC AAACCGCGTT CGACCACGGT TTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTTG
1351 CGCTATATTT CGCCGTTTAA AGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTGCTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCGGCG AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCCGACG GG...

```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

m019.pep (partial)

```

1  MYLPSMKHSL PLLAALVLAA CSSTNTLPAG KTPADNIETA DLSASVPTRP

```



```

51  AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSCGCKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYXGKV ADRRQLTDDQ IEWYARAALR ARRWDDELASV
301 ISHMPEKLQK SPTWLYWLAR SRAATGNTQE AEKLYQAAA TGRNFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQV SQSAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

```

a019.seq
1  ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCTGGT
51  GCTTGCCGCG TGTCTTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAACTGCC GACCTTTCGG CAAGCGTTCC CACCNGCCCT
151 GCCGAACCCG AANGAAAAAC GTNGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CAGAGCCGAA CGACTATACG CGTGCCGCGC AACTGGTCAA AAATACGGGC
451 AAAGTGCCTT CCGGCTGCAC CAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCAGGGA CTGCTGGCCG
551 GCGCCCAAA CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTGCGCGGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAGAGG GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCTT TGGACTATTA
801 NGGCAAGGTT GCCGACCGCC GCGCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCCTNNNGC NNCGNNGTT NGNANGANTT GGCNNCCGNN
901 ANCNCGNNNN TGCNNGANAA ACNNNNNNAN AGNCNNANNT NGNTNNANTG
951 NNTGGCACGC AGCCGCGCCG CNACGGGCAA CACGCAANAN GCGGANAAAC
1001 TNTACAAACA GGCGGCAGCA NCGGGCANGA ATTTTATATG NGTGCTGNCN
1051 GGGGAAGAGT TGGGGCGCAN AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAANC AGCGTCTCTC GTATGGCGGA AGACGGCGCG ATTAAGCGCG
1151 CGCTGGTGCT GTTCCGAAAC AGCCGAACCG CCGCGGATGC GAAAATGCGC
1201 CGTCNNGGCTC AGGCGGAATG GCGTTTCGCC ACACGCGGCT TCATGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGT CGACACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTTG
1351 CGCTACATTT CGNNNNNTNA NGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCGTGGG TTTACGGGCT GATTTCGTAG GAAAGCCGCT
1451 TCGTTATGGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCTTGCCA CCGCGCGGCA AATCGCCGCG AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCGGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCCGCTTG CAAAACAACG AAGTCCTCGC CACCGCAGGC
1651 TATAACGCCG GTCCCGGCGAG GCGCGCGCGA TGGCAGGCGG ACACGCCCTT
1701 CGAAGGCGCG GTATATGCCG AAACCATCCC GTTTTCCGAA ACGCGCGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCTT ACTACGCTC CTCTTCGCG
1801 GCGCCGCACA TCCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

```

a019.pep
1  MYPPSLKHSI PLLVLVLAA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51  AEPEKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSCGCKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYXGKV ADRRQLTDDQ IEWYARAAXX XXXXXXAXX
301 XXXXXXKXXX XXXXXXKXAR SRAATGNTQX AXKLYQAAA XGNFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFVN SRTAGDAKMR
401 RXAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL

```


451 RYISXXD TV IRHAQNVNVD PAWVYGLIRQ ESRFVMGAQS RVGAQGLMQV
 501 MPATAREIAG KIGMDAAQLY TADGNIRMG T WYMADTKRRL QNNEVLATAG
 551 YNAGPGRARR WQADTFLEGA VYAETIPFSE TRDYVKKVMA NAAYYASLFG
 601 APHIPLKQRM GIVPAR*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLPSMKHSLPLLAALVLAACSSNTL	PAGKTPADNIETADLSASVPT	TRPAEPEPKTLAD			
a019	10	20	30	40	50	60
	MYPPSLKHSLPLLVXLVLAACSSNTL	SADKTPADNIETADLSASVPT	TXPAEPEKTXAD			
m019.pep	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARRQWTL	FAQEYAKLE				
a019	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARRQWTL	XAXEYAKLE				
m019.pep	130	140	150	160	170	180
	PAGRAQEVECYADSSRNDYTRAAELVKNTGKLP	SGCTKLLEQAAASGLLDGND	AWRRVRG			
a019	130	140	150	160	170	180
	PAXRAQEVECYADSSRNDYTRAAELVKNTGKLP	SGCTKLLEQAAASGLLDGND	AWRRVRG			
m019.pep	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALL	SEMESGLSL				
a019	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALL	SEMESGLSL				
m019.pep	250	260	270	280	290	300
	EQRSFAWGVLGHYQSQNLNVPAAALDYXGKVADRRQLTDDQIEWYARAAL	RARRWDELASV				
a019	250	260	270	280	290	300
	EQRSFAWGVLGHYQSQNLNVPAAALDYXGKVADRRQLTDDQIEWYARAAXX	XXXXXXXXXX				
m019.pep	310	320	330	340	350	360
	ISHMPEKLQKSPTWLYWLARSRAATGNTQAEKLYKQAAATGRNFYAVLAGEEL	GRKIDT				
a019	310	320	330	340	350	360
	XXXXXXXXXXXXXXXXXARSRAATGNTQAXKLYKQAAAXGXNFYAVLXGEEL	GRXIDT				
m019.pep	370	380	390	400	410	420
	RNNVPDAGKNSVRRMAEDGAVKRALVLFQNSQSAGDAKMRRQAQAEWR	FATRGFDEDKLL				
a019	370	380	390	400	410	420
	RNNVPDAGKXSVLRMAEDGAIKRALVLFNRNRTAGDAKMRRXAQAEWR	FATRGFDEDKLL				
m019.pep	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLN	YTLRYISPFKDTVIRHAQNVNVDPAWVYGLIRQ				
a019	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLN	YTLRYISXXXDTVIRHAQNVNVDPAWVYGLIRQ				
m019.pep	490	500	510	520		
	ESRFVIGAQSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADG					
a019	490	500	510	520	530	540
	ESRFVIGAQSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADGNIRMG	TWYMA	TKRRL			
a019	550	560	570	580	590	600
	QNNEVLATAGYNAGPGRARRWQADTFLEGA	VYAETIPFSE	TRDYVKKVMA	NAAYYASLFG		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

g019/m019

		10	20	30	40	49
g019.pep		LLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTRPAEPEGKTLAD				
m019	MYLP	SMKHS	LP	LLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTRPAEPEKTLAD		
		10	20	30	40	50 60
	50	60	70	80	89	
g019.pep	YGGYPSALDAVKQNNDAAAAYLENAGDSAMAENVRKEWL					
	: : : : :					
m019	YGGYPSALDAVKQNDAVAAYLENAGDSAMAENVRNEWLKSLGARRQWTLFAQEYAKLE					
		70	80	90	100	110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 111>:

g023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  AATGCAGCGT GCGACTGCGG TTATTATGTT GATTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAG CTTGGGTAAA AGTATTTACC CAAGTGAGCT TTATCGCCGT
201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCCTCGG CGTGCCTTTG TTTTTCAGG TTGCCACCAT TGtctGGCTG
301 GTCGGCTGCC TCGTGATTTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 023.ng>:

g023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFAI PKEYPAWQAF
51  FSQAWVKVFT QVSFIAVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

m023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  GATGCAACGT GCGACTGCGG TTATTATGTT GATTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTCCCTG CCTAAAGAAT ATTCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT
201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCCTCGG CGTGCCTTTG TTTTTCAGG TTGCCACCAT CGTTTGGCTG
301 GTCGGCTGTC TCGTGATTTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 023>:

m023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFSI PKEYSAWQAF
51  FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

a023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GGGATTGGGC
51  GATGCAACGT GCGACCGCGG TTATTATGTT GATTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCTCTG CCTAAAGAAT ATTCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT

```


201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA
 251 AACCCITCGG CGTGCGTTT TTTTGCAGG TTGCCACCAT CGTCTGGCTG
 301 GTCGGCTGCT TGGTGTATTC AATTAAAGTA ATTTGGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVLFL PKEYSAWQAF
 51 FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYXKPFVRL FLQVATIVWL
 101 VGCLVYSIKV IWG*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYT VALLVVLFLSLPKEYSAWQAFFSQTWVKVFT					
a023	MVERKLTGAHYGLRDWVMQRATAVIMLIYT VALLVVLFLSLPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWL VGCLVYSVKVIWGX					
a023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWL VGCLVYSIKVIWGX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYT VALLVVLFLSLPKEYPAWQAFFSQAQWVKVFT					
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYT VALLVVLFLSLPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWL VGCLVYSVKVIWGX					
m023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWL VGCLVYSVKVIWGX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq

1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TTGCCGCTCT
 51 GTTGGGCGGT TGcgCCACCC AACAGCCTGC TccTGTCATT GCAGGCAATT
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA
 151 ACGCCGTACA ATGCGCTCC TGCCGCCAac gatgcGCCgT ATGTGCCGCC
 201 CGTGCAAact ggcgcgggttT ATTCCGCTCC TGCTTATGTT CCGCcgTCTG
 251 CACCTGCCGT TTCGGgtaca tatgtTCCTT CTTACGCACC CgtcgACATC
 301 aacgCGGCGa cgCataCTAT TGTGCGTGGC GACACgGtgt acaACATTTc
 351 caaAcgCtac CATATCTCTC AAGACGATT CCGTGCGTGG AACGGCATGA
 401 CCGACAATAC GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCaggA
 451 TATGCCGCAC CGAAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC
 501 TGCCGCGCAA ACCCCTGTGA AACCCGCCGC gcaACCGCCC GTTCAGTCCG
 551 CGCCGCAACC TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC
 601 GCGCCCGCCC CGCAATCTCC TGCCGCTTCG CCTTCCGGCA CGCGTTCGGT
 651 CGCGGCATT GTTTGGCAGC GTCCGACCCA AGGTAAAGTG GTTGGCCGATT


```

701 TCGGCGGCGG CAACAAGGGT GTCGATATTG CCGGCAATGC CGGACAACCC
751 GTTTTGGCGG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAA TTGCTGGTCG GCGAAGGTCA GCAGGTCAAA
901 CGCGGTGAGC AGGTTGCTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTC GAGGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

g025.pep

```

1 MLKQTLLAA CTAVAALLGG CATQQPAPVI AGNSGMQTVS SAPVYNPYGA
51 TPYNAAPAA DAPYVPPVQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHITVRG DTVYNISKRY HISQDDFFRAW NGMTDNTLSI QQIVKVKPAG
151 YAAPKTAAVE SRPAVPAAAQ TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQGV VADFGGNGK VDIAGNAGQP
251 VLAAADGKVV YAGSGLRGY NLVIIQHNS FLTAYGHNQK LLVGEGQQVK
301 RQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

m025.seq (partial)

```

1 ..GTGCGCGCGG TGCAAAGCGC GCCGGTTTAT ACGCCTCTG CTTATGTTC
51 GCCGTCTGCA CCGCGCGTTT CGGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGCGGACG CATACTATTG TGCGCGGCGA CACGGTGTAC
151 AACATTTCCA AACGCTACCA TATCTCTCAA GACGATTTCC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCGGCACCG AAAGCCGAG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CCGCGCAACC GCCCGTACAG TCCGCACCCG TCGACATTAA
351 CGCGCGGACG CATACTATTG TGCGCGGCGA CACGGTGTAC AACATTTCCA
401 AACGCTACCA TATCTCTCAA GACGATTTCC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACCGCAG CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCCTGTGAAA CCCGCCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCGC TGCGGAAAT AAAGCGGTTT CCGCGCCCGC
651 CCCGCAATCT CCTGCCGCTT CGCCTTCCGG CACGCGTTCC GTCGCGGCGA
701 TTGTTTGGCA GCGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCCGCGGC
751 AACACAAGG GTGTCGATAT TGCCGGTAAT GCGGACAGC CCGTTTGGC
801 GGCGGCTGAC GGCAAAGTGG TTTATGCCGG TTCAGGTTG AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCTGAC CGCATACGG
901 CACAACCAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACCGGTC
951 GCAGGTTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGGTGCG TCAAAACGGC AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

m025.pep (partial)

```

1 ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
51 NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNMLSIGQIV KVKPAGYAAP KTAAVESRPA VPAAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRPT QGKVVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVVYAGSGL RGYGNLVIIQ HNSSF LTAYG
301 HNQKLLVGEG QQVKRQQQVA LMGNTDASRT QLHFEVRQNG KPVNPN SYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

a025.seq

```

1 ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACCGCCC TTGCCGCTCA
51 GTTGGGCGGA TGCCCCACCC AACACCCTTC TCCTGTCATT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAATCC TTATGGCGCA

```



```

151 ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCGCC
201 GGTGCAAAGC GCGCCGGTTT ATANGCCTCC TGCTTATGTT CCGCCGCTCTG
251 CACCTGCCGT TTCGGGTACA TACGTTCTTT CTTACGCANC CGTCGCATC
301 AACGCGGCGA CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351 CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCCTGG AACGGCATGA
401 CCGACAATAC GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA
451 TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC
501 TGCCCGGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACCGGCGGA
551 CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601 CATATCTCTC AAGACGATTT CCGTGCCTGG AACGGCATGA CCGACAATAC
651 GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701 CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC TGCCGTGCAA
751 ACCCTGTGA AACCGCGCGC GCAACCGCCT GTGCAGTCCG CGCCGCAACC
801 TGCCCGGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCGCCC GCCCGCAAT
851 CTCCTGCCGC TTCGCCTTCC GGCACGCGTT CCGTCGGCGG CATTGTTTGG
901 CAGCGTCCGA CGCAAGGTAA AGTGTTGCC GATTTCGGCG GCAACAACAA
951 GGGTGTCGAT ATTGCAGGAA ATGCGGGACA GCCCGTTTGG GCGGCGGCTG
1001 ACGGCAAAGT GGTATTATGCA GGTTCGGTT TGAGGGGATA CGGCAATTTG
1051 GTCATCATCC AGCATAATTC TTCCTTCTTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGGCGAAG GCCAGCAGGT CAAACGCGGG CAGCAGGTCTG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTGAGGTG
1201 CGGCAAAACG GCAAACCGGT TAATCCGAAC AGCTATATCG CGTCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

a025.pep

```

1 MLTP TTL*VA CTALAAQLGG CPTQHPSPI AGNSGMQTV SAPVYNPYGA
51 TPYNAAPAA DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101 NAATHITVRG DTVYKISKCY HISQDDFAW NGMTDNTLSI GQIVKVKPAG
151 YAAPKAAAVK SRPAVPAAQ PLVQSAPVDI NAATHITVRG DTVYNISKRY
201 HISQDDFAW NGMTDNTLSI GQIVKVKPAG YAAPKAAAVK SRPAVPAAVQ
251 TPVKPAAQPP VQSAPQPAAP AAENKAVPAP APQSPAASPS GTRSVGGIVW
301 QRPTQKVVV DFGGNNKGVD IAGNAGQPVL AAADGKVVA GSGLRGYGNL
351 VLIQHNSFL TAYGHNQKLL VEGEQVKRG QVALMGNT EASRTQLHFEV
401 RQNGKPVNPN SYIAF*

```

m025/a025 97.4% identity over a 351 aa overlap

```

                                10      20      30
m025.pep                                VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                |||:|||||
a025      GMQTVPSAPVYNPYGATPYNAAPANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
              40      50      60      70      80      90

              40      50      60      70      80      90
m025.pep      YAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMTDNTLSIGQIVKVKPAGYAAP
|||:|||||
a025      YAXVDINAATHITVRGDTVYKISKCYHISQDDFAWNGMTDNTLSIGQIVKVKPAGYAAP
              100      110      120      130      140      150

              100      110      120      130      140      150
m025.pep      KAAAVKSRPAVPAAQPPVQSAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMT
|||:|||||
a025      KAAAVKSRPAVPAAQPLVQSAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMT
              160      170      180      190      200      210

              160      170      180      190      200      210
m025.pep      DNLSIGQIVKVKPAGYAAPKTAAVESRPVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
|||:|||||
a025      DNTLSIGQIVKVKPAGYAAPKAAAVKSRPAVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
              220      230      240      250      260      270

              220      230      240      250      260      270
m025.pep      KAVPAPQSPAASPSGTRSVGGIVWQRPTQKVVADFGGNNKGVDIAGNAGQPVLAAAD
|||:|||||

```



```

a025      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLAAD
           280      290      300      310      320      330

m025.pep      280      290      300      310      320      330
GKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDASRT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a025      GKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTASRT
           340      350      360      370      380      390

m025.pep      340      350
QLHFEVRQNGKPVNPNSYIAFX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a025      QLHFEVRQNGKPVNPNSYIAFX
           400      410

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 025 shows 75.6% identity over a 353 aa overlap with a predicted ORF (ORF 025.ng) from *N. gonorrhoeae*:

m025/g025

```

m025.pep      10      20      30
VPPVQSAPVYTTPPAYVPPSAPAVSGTYVPS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      GMQTVSSAPVYNPYGATPYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
           40      50      60      70      80      90

m025.pep      40      50      60      70      80      90
YAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMTDNTLSIGQIVKVKPAGYAAP
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      YAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMTDNTLSIGQIVKVKPAGYAAP
           100     110     120     130     140     150

m025.pep      100     110     120     130     140     150
KAAAVKSRPAVPAAQPPVQSAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMT
|
g025      K-----

m025.pep      160     170     180     190     200     210
DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVAAVQTPVKPAAQPPVQSAPQPAAPAAEN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      -----TAAVESRPAPVAAVQTPVKPAAQPPVQSAPQPAAPAAEN
           160     170     180     190

m025.pep      220     230     240     250     260
KAVPAPAP--QSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      KAVPAPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
           200     210     220     230     240     250

m025.pep      270     280     290     300     310     320
ADGKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDAS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      ADGKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDAS
           260     270     280     290     300     310

m025.pep      330     340     350
RTQLHFEVRQNGKPVNPNSYIAFX

```


RTQLHFEVRQNGKPVNPNSYIAFX
320 330

g031.seq

g031.per

m031.seq (partial)

m031.pep (partial)

a031.seq

a031.pep (partial)

1 IRLFTQAVIE FPQTAEHCRR TRDQHQERRN RQGFRRPVQH VGRRNQQQRH
51 SQTGQSGRN HAQKQCATR O

210

m031/a031 100.0% identity over a 71 aa overlap

```

          10      20      30      40      50      60
m031.pep  RLKHGVLHGFYSAIRLFTQAVIEFFQTAEHCRRTDQHQERRNRQGFRRPVQHVGRNRQQ
          |||||
a031      IRLFTQAVIEFFQTAEHCRRTDQHQERRNRQGFRRPVQHVGRNRQQ
          10      20      30      40

          70      80
m031.pep  QRHSQTCGQSGRNHAQKQCCATRQ
          |||||
a031      QRHSQTCGQSGRNHAQKQCCATRQ
          50      60      70

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

```

          10      20      30
m031.pep  RLKHGVLHGFYSAIRLFTQAVIEFFQTAEH
          |::|: : |||||
g031      NQQRQHHHGKRHIKQQVRIGNAHQRHHRQNRNYGSSQAQPTDIRLFTQAVIEFFQTAEH
          60      70      80      90      100     110

          40      50      60      70      80
m031.pep  CRRTRDQHQERRNRQGFRRPVQHVGRNRQQQRHS-QTCGQSGRNHAQKQCCATRQ
          |:|||||:|||||:| ||| :|: |:: ::: | :|:
g031      CQRTDQHQERRNRQGFRRPVQHAGGRNQOTEHDEQSLRQPSQTVHHTQNVFRRTVALV
          120     130     140     150     160     170

g031      TDNDAGKVNRRQKAAAYGIGKRKHKQPARHNRVQTFRTHLQFFINVIASRVKMFFTS
          180     190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032.seq

```

1  ATGCGGCGAA  ACGTGCCTGC  CGTCGCCGTA  TTGCGCCGCC  CACGATTCCA
51  GCGGTTTTTG  GATTTGGCGT  TGGCTCAGGC  GCGTGCCGTT  CCTGCCGGTA
101 AACAGGGCTT  TGCCGTCCGA  TGCCGTCTGA  CGCAGCGGCA  GATAGTTTTT
151 CAAGGCTTCC  ACGCTTTTGC  CGGTCAGCGG  AACCTGACGC  TGCTTGCGCC
201 CTTTGCCGGT  AACGTGTACC  CACGCTTCGT  CCAAATATAC  ATCATCTGCA
251 TTCAAGCCGT  GTATCTCGCT  CACGCGCAAA  CCGCTGCCGT  ACATCAGCTC
301 GAACAGCGCG  TGGTCGCGCA  CCGCCAGCGG  GTCGCCGCCG  TCCACGGGCA
351 AATCCAACAT  CCGGTTTACG  CATTCCTGCG  GCAGGGCTTT  GGGTACGCGC
401 TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  GTCGGGTCGG  CGCGCATCAG
451 CCCGCGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCCACGCC  GACAGCTTGC
501 GCGCCAGCGT  CCGACCGTCC  AAACCGCGCT  GCGACAGCCG  CCGCAACGCC
551 GccgTAAAT  CGCGCCGCGA  CAAGTCCTGC  GGCACGCgc  ctgcaTCTTC
601 AGACGGCATT  TGTGCCAACA  GTGCAACAG  TTCTTCCAAA  TCGCGCCGGT
651 ATGCCGCAAC  CGTGTGCTCC  GACTTGCCCT  CGCGCACGAT  GTTTTCCAAA
701 TAAGCGTCAA  AATacgcgc  AAACccgTCC  AAAACCATAA  CCGTCCCA
751 CAAATATCAA  AAAACAGTG  A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 032.ng>:

g032.pep

```

1  MRRNVPAAV  LRRPRFEAF  L  DLALAQARAV  PAGKQGF  AVR  CRLTQRQIVF
51  QGFHAFAGQ  R  NLTLAPFAG  NVYPRFVQIY  IICIQAVYLA  HAQTAAVHQL

```



```

101 EQRVVAHRQR VAAVHGQIQH PVQPFRLQGF GYALGLLRRF DVGGRVGAHQ
151 PAFDQPGAIL PPRRLARQR PTVQTALRQP PQRRLKIAFR QVLRHAACIF
201 RRHLCQCKQ FFQIAPVCRN RVLRLALAHF VFQISVKIRR KPVQNHNRPT
251 QISKNQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

m032.seq (partial)
  1 ATGCGGCGAA ACGTGCmTGC mGTGCGCGTT kTGCGCCGCC CATTGCGCCA
 51 AACGTTTTTG GATTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGACCAGCGG CACCTGCCGC TgTT.GCGCC
201 CTTTGCCGAT AAcGTGTACC CACGCyTCGT CCAAATAGAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGCTGCCGT ACATCAGTTC
301 GAACAGGGCG TGGTCGCGCA CCGCCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTcAGC CATTCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGCG GTCGGGTCGG CGTGCACTAG
451 GCCGCGCTTT ACCAGCCAAA CGCAATACTG CCGCCAAGAC GAAAGCTTGC
501 GAGCCAGCGT CCGTCCCCC AAACCGCG...

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 032>:

```

m032.pep (partial)
  1 MRRNVXAVAV XRRPLRQTF LALAAQARAV PAGKQGFVAV CRLTQRQIVF
 51 QGFHAFADQR HLPLXAPFAD NVYPRXVQID IICIQAVYLA HAQTAAVHQF
101 EQGVVAHRQR VAAVHGQIQH PVQPFRLQGF GYALGLLRRF DVGGRVGVHQ
151 AALYQPNAIL PPRRLASQR PFPQTA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

```

a032.seq
  1 ATGCGGCGAA ACGTGCCTGC CGTGCCTGTT TTGCGCCGCC CATTGCGCCA
 51 AACGTTTTTG GATTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGGTCAGCGG AACCTGCCGC TGCTTGCGTC
201 CTTTGCCGAT AACGTGTACC CACGCCTCGT CCAAATATAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGCGCG TGATCGCGCA CCGCCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTcAGC CATTCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGCG GTCGGGTCGG TATGACGAG
451 ACCGCGTTTG ACCAGCCAGG CGCAATACTG CCGCCAAGAC GACAGCTTGC
501 GCGCCAGCGT CCGCGCATT CAAACCGCGT GCGACAGCCG CCGCAACGCC
551 GCCGTAATAA CGGCTGCGA CAAGCCCTGC GGCACGCCGC CTGCATCTTC
601 AGACGGCATT TGTGCCAACA GCGCAAACAG TTCTTCCAAA TCGCGCCGGT
651 ATGCCGCCAC CGTGTGCTCC GACTTGCCCT CGCGCAGCAT GTTTTCCAAA
701 TAAGCGTCAA AATGCGCCGC AAACCGTCC AAAACCATAA CCGCCCCACA
751 CAAATATCAA AAAACAGTG A

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 032.a>:

```

a032.pep
  1 MRRNVPAVAV LRRPLRQTF LALAAQARAV PAGKQGFVAV CRLTQRQIVF
 51 QGFHAFAGQR NLPLASFAG NVYPRLVQIY IICIQAVYLA HAQTAAVHQF
101 EQRVIAHRQR VAAVHGQIQH PVQPFRLQGF GYALGLLRRF DVGGRVGMQQ
151 TAFDQPGAIL PPRRLARQR PRIQTALRQP PQRRLKIALR QALRHAACIF
201 RRHLCQQRKQ FFQIAPVCRH RVLRLALAHF VFQISVKMRR KPVQNHNRPT
251 QISKKQ*

```

m032/a032 88.1% identity over a 176 aa overlap

```

          10      20      30      40      50      60
m032.pep MRRNVXAVAVXRRPLRQTFDLALAAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFADQR
          ||||| ||||| ||||| ||||| ||||| |||||
a032      MRRNVPAVAVLRRPLRQTFDLALAAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFAGQR
          10      20      30      40      50      60

```


212

	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQVRVAAVHGQIQH					
a032	NLPLLASFAGNVYPRLVQIYIICIQAVYLAHAQTAAVHQFEQVRVIAHRQVRVAAVHGQIQH					
	70	80	90	100	110	120
m032.pep	PVQPFRLRQGFYALGLLRRFDVGGVRGVHQAALYQPNAILPPRRKLASQRPFQTA					
a032	PVQPFRLRQGFYALGLLRRFDVGGVRGMQQTAFDQPGAILPPRRQLARQRPRIQTALRQP					
	130	140	150	160	170	180
a032	PQRRRKIALRQALRHAACIFRRHLCQQRKQFFQIAPVCRHRVRLALAHDFQISVKMRR					
	190	200	210	220	230	240

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng) from *N. gonorrhoeae*:

m032/g032

	10	20	30	40	50	60
m032.pep	MRRNVXAVAVXRRPLRQTFDLALAQARAVPAGKQGFVRCRLTORQIVFQGFHAFADQR					
g032	MRRNVPAAVAVLRRPRFEAFDLALAQARAVPAGKQGFVRCRLTORQIVFQGFHAFAGQR					
	10	20	30	40	50	60
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQVRVAAVHGQIQH					
g032	NLTLLAPFAGNVYPRFVQIYIICIQAVYLAHAQTAAVHQLEQVRVVAHRQVRVAAVHGQIQH					
	70	80	90	100	110	120
m032.pep	PVQPFRLRQGFYALGLLRRFDVGGVRGVHQAALYQPNAILPPRRKLASQRPFQTA					
g032	PVQPFRLRQGFYALGLLRRFDVGGVRGAHQPAFDQPGAILPPRRQLARQRPVQTALRQP					
	130	140	150	160	170	180
g032	PQRRRKIAPRQVLRHAACIFRRHLCQQCKQFFQIAPVCRNRVRLALAHDFQISVKIRR					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

g033.seq

```

1   ATGGCGGCGG CGGACAACT CTTGGGCGGC GACCGCCGCA GCGTCGCCAT
51  CATCGGAGAC GCGCGATGA CGCGGGGCA GCGGTTGAA GCCTTGAATT
101 GCGCGGGCGA TATGGATGTG GATTGCTGG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAAGT CGCGCGTTG CCCAAATATC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTAG TACCGTCAA GCGCAAACgg
251 GCAAGGTAT T AGACAAAATA CCCGGCGCGA TGGagtTTGC CCAAAAAGTC
301 GAACACaaaa TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCGCTG TTTGAAAATT TCGGCTTCCG CTACACCGGC CCCGTGGACG
401 GACACAACGT CGAGAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCcg tcaAATACCA CGCCGTCGcc aACCTGCcta
551 AAGAAGGCGG GCGCAAATg ccGTCTGAAA AAGAACCCAA GCCCGCCgCc
601 aaaccgACCT ATACCCAAGT ATTCGCCAAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG

```



```

701 GACTGGTGA GTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT tacCTTTGCC GCGGGTTTGG CGTGCGAAGG
801 CATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTGCCCGT TTTGTTTGCC
901 GTCGACCGTG CGGGCATCGT CCGCGCGGAC GGTCCGACCC ATGCCGGCTT
951 GTACGATTTG AGCTTCTTGC GCTGTGTGCC GAACATGATT GTTCCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCCTGCTGC TTTCGACCTG CTATCAGGCG
1051 GATGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CCGGCGCGCC
1101 GGTTCAGAC GGCATGAAA CCGTGGAAT CCGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCC TcatTGCCT TCGGCAGTAT GGTCCGCCACC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTt
1251 cgtcaaacCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCAcg
1301 accGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGGTCTTGG AAGTGTGGC GAAACACGGC ATCTGCAAA CCGTTTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGAACA CGGCGATCCG AAAAACTTT
1451 TGGACGATT GGGTTTGAGT GCCGAAGCGG TGGAACGCCG GGTGCGCGAG
1501 TGGCTGCCGG ACCGTGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

g033.pep

```

1 MAAADKLLGG DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLLKDLRSR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKEGGAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAT
401 ALAVAEKLNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLILLGV ADTVTEHGDP KLLDDLGLS AEAVERRVRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

m033.seq

```

1 ATGGCGCGCG CAGACAAACT CTTGGGCAGC GACCGCGCA GCGTCGCCAT
51 CATCGCGGAC GCGCGGATGA CCGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCaG.CGA TATGGATGTt GATTTGCTrG TCGTCTCAA CGACAACGAA
151 ATGTGCGATT CCCCCAACGT CCGCGCGCTG CCGAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GCCTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGAGTTTGC CCAAAAAGTC
301 GAACACAAAA TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCTTTG TTTGAAAAC TCGGCTTCCG CTACACCGGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCCG TCAAATACCA CGCCGTGCGC AACCTGCCTA
551 AAGAAAGCGC GCGCGAAATG CCGTCTGAAA AAGAACCCTA GCCCGCCGCC
601 AAACCGACCT ATACCAAGT GTTCGGCAAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTACCCGT TTTGTTTGCC
901 GTCGACCGCG CGGGCATCGT CCGCGCGGAC GGCCCGACCC ATGCCGGTCT
951 GTACGATTTG AGCTTTTTCG GCTGCGTGCC GAACATGATT GTCGCGCGC
1001 CGAGCGATGA AAACGAATGC CGCCTGTTGC TTTCGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CCGGCGCGCC
1101 GGTTCAGAC GGCATGAAA CCGTGGAAT CCGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTCCGCCCC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG

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1301 ACCGCATCGT TACCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATT GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCCG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

m033.pep

```

1  MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51  MSISPNVGAL PKYLASNVVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLDLRLSR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGK IIRREGKTA FIAFGSMVAP
401 ALAVAELKNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLVLLGV ADTVTGHGDP KLLLDLGLS AEAVERVRRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

a033.seq

```

1  ATGGCGCGCG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51  CATCGGCGAC GCGCGGATGA CGCGGGTCA GCGGTTTGAA GCCTTGAAC
101 GCGCGGGCGA TATGGATGTG GATTGCTGG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAACGT CGGTGCGTTG CCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCGGCGCGCA TGGAGTTTGC CCAAAAAGTC
301 GAACATAAAA TCAAACCCCT TGCCGAAGAA GCCGAACACG CCAACAGTC
351 ACTGTCTTTG TTTGAAAAC TCGGCTTCCG CTATACCGGC CCGGTGGACG
401 GACACAACGT CGAAAATCTG GTCGATGTAT TGGAAGACCT GCGCGGACGC
451 AAAGGCCCGC AGCTTCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGATCCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCGAAATG CCGTCTGAAA AAGAACCCTA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAA TGGCTGTGCG ACCGGGCGCG
651 GGCAGATTCC CGACTGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GGCGGTTTGG CTTCGCAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAA ACCTGCCCGT TTTGTTTGCC
901 GTCGACCGCG CGGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCCGTTT
951 GTACGATTTA AGCTTTTTGC GCTGCATTCC GAATATGATT GTCGCCGCGC
1001 CGAGCGATGA AAATGAATGC CGCCTGCTGC TTTCGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCGTCCG CTATCCGCGC GGCACGGGTA CCGGCGTGCC
1101 GGTTCAGAC GGCATGAAA CCGTGAAAT CGGCAAGGCG ATTATCCGCC
1151 GCGAAGGTGA GAAACCGCA TTCATTGCC TCGGCAGTAT GGTGCGCCCT
1201 GCATTGGCGG TCGCCGAAA ACTGAACGCC ACCGTCGCCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG
1301 ACCGCATCGT TACCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTGGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATT GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCCG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

a033.pep

```

1  MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51  MSISPNVGAL PKYLASNVVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLEDLRLR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA

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301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA
 351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAP
 401 ALAVAGKLN TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS
 451 AVLEVLAKHG ICKPVLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
 501 WLSDRDAAN*

m033/a033 98.4% identity over a 509 aa overlap

m033.pep	10	20	30	40	50	60
	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISPNVGAL					
a033	MAAADKQLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISPNVGAL					
	10	20	30	40	50	60
m033.pep	70	80	90	100	110	120
	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
	70	80	90	100	110	120
m033.pep	130	140	150	160	170	180
	FENFGFRYTGFPVDGHNVENLVDVLKDLRSRKGFPQLLHVITKKNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGFPVDGHNVENLVDVLEDLRGRKGFPQLLHVITKKNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
m033.pep	190	200	210	220	230	240
	NLPKESAAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
m033.pep	250	260	270	280	290	300
	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLVLF					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLVLF					
	250	260	270	280	290	300
m033.pep	310	320	330	340	350	360
	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
m033.pep	370	380	390	400	410	420
	GTGTGAPVSDGMETVEIGKGIIRREGKTAFAFGSMVAPALAVAEKLNATVADMRFVKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREGKTAFAFGSMVAPALAVAGKLNATVADMRFVKP					
	370	380	390	400	410	420
m033.pep	430	440	450	460	470	480
	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLGVADTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGSAVLEVLAKHGICKPVLLGVADTVTGHGDP					
	430	440	450	460	470	480
m033.pep	490	500	510			
	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
	490	500	510			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng) from *N. gonorrhoeae*:

m033/g033

m033 . pep	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVLLVVLNDNEMSISPNVGAL	60
g033	MAAADKLLGGDRRSVAIIGDGAMTAGQAFEALNCAGDMDVLLVVLNDNEMSISPNVGAL	60
m033 . pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEEAEHAKQSLSL	120
m033 . pep	FENFGFRYTGPDGHNVENLVDVLKDLRSRKGPKQLLHVITKKGNGYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPDGHNVENLVDVLKDLRSRKGPKQLLHVITKKGNGYKLAENDPVKYHAVA	180
m033 . pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRSLVAITPAMREGSGLVEFEQ	240
g033	NLPKEGGAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRSLVAITPAMREGSGLVEFEQ	240
m033 . pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA	300
m033 . pep	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR	360
m033 . pep	GTGTGAPVSDGMETVEIGKGIIRREGKTAFFAFGSMVAPALAVAELNATVADMRFVKP	420
g033	GTGTGAPVSDGMETVEIGKGIIRREGKTAFFAFGSMVATALAVAELNATVADMRFVKP	420
m033 . pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTGHGDP	480
g033	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTEHGDP	480
m033 . pep	KKLLDDLGLSABAVERRVRAWLSDRDAANX	510
g033	KKLLDDLGLSABAVERRVREWLPRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034 . seq

1	ATGAGCCGTT	TATGGTTTTT	TGCCGTAAAA	AACATTATAA	TCCGCCTTAT
51	TTACCTATTG	CCCAAGGAGA	CACAAATGGC	ACTCGTATCC	ATGCGCCAAC
101	TGCTTGACCA	CGCCGCCGAA	AACAGCTACG	GCCTGCCCGC	GTTCAACGTC
151	AACAACCTCG	AACAAATGCG	CGCCATTATG	GAAGCCGCCG	ACCAAGTCAA
201	CGCGCCCGTC	ATCGTACAGG	CGAGCGCAGG	TGCGCGCAAA	TACGc9gGCG
251	CGCCGTTTTT	GCGCCACCTG	ATTCTGGCGG	CAGTCAAGA	ATTTCCGCAC
301	ATCCCCGTCG	TGATGCACCA	AGACCACGGC	GCATCGCCCG	ACGTgtgCCA
351	ACGCTCCATC	CAACTGGGCT	TCTCCTCCGT	GATGATGGAC	GGCTCTTTGC
401	TCGAAGACGG	CAAAACCCCT	TCTTCTTACG	AATACAACGT	CAACGCCACC
451	CGTACCGTCG	TCAACTTCTC	CCACGCCTGC	GGCGTGTCCG	TCGAAGGCGA
501	AATCGGCGTA	TTGGGCAACC	TCGAAACCGG	CGAAGCAGGC	GAAGAAGACG
551	GAGTGGGCGC	GGCAGGCAAA	CTCTCACACG	ACCAAATGCT	CACCAGCGTT
601	GAAGATGCCG	TGCGTTTCGT	TAAAGATACC	GGCGTTGACG	CATTGGCGAT
651	TGCCGTCGGC	ACCAGCCACG	GCGCATACAA	ATTACCCCGT	CCGCCACACG


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701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGgctCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CCGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAT CAAACCTGTT TCGTTGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

g034.pep

```

1 MSRLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLLDGKTP SSYEYNVNAT
151 RTVVNFSSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKI NEYGGNIGET YGVFVEEIVE GIKHGVRKVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

m034.seq (partial)

```

1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA WACAGCTACG GCYTGCCGGC GTTCAACGTC
151 AACAACTCG WACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCCGTC ATCGTACAGG CGAGTGCCGG TGCGCGCAAA TATGCGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGCGCG CTGTCGAAGT ATTTCCACAC
301 ATCCCGTCG TCATGCACCA AGACCACGGC GCATCACCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAACCTCTC CCACGCTTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GCGGTTGACG CATTTGGCTAT
651 TGCCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCCACAG
701 CGCATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

m034.pep (partial)

```

1 MSCLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE XSYGLPAFNV
51 NNLXQMRAIM EAADQVDA PV IVQASAGARK YAGAPFLRHL ILAAVEVFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFSSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

a034.seq

```

1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCGCG GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCCG ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGCGCG CTGTCGAAGA ATTTCCGCAC
301 ATCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TTTCTCTTATG AATACAACGT CAACGCCACC
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

```



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451 CGTACCGTGG TTAATTTCTC CCACGCCTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TCGGTTTCGT TAAAGATACC GCGGTTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGCGTACAA ATTCAACCGT CCGCCACAG
701 GCGACGTGTT GCGTATCGAC CGCATCAAAG AAATCCACCA AGCCTGCCC
751 AATACACACA TCGTGATGCA CGGCTCCAGC TCCGTTCCGC AAGAATGGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAC ACGGCGTGCG TAAAGTCAAC
901 ATGATACCG ACTTGGCCT TGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAC CCGTCCGACT TCGATCCGCG CAAATATTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GCTACCTCGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCGGTT TCCTTGAAA AAATGGCAA
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

a034.pep

```

1 MSRLWFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRVFKDT GVDALAIAGV TSHGAYKFTR PPTGVDLRLD RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVKRVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL SKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

m034.pep	10	20	30	40	50	60
	MSCLWFFAVKNIIRLIYLLPKETQMALVSMRQLLDHAAE NSYGLPAFNVNNLXQMRAIM					
a034	MSRLWFFAAKNIIRLIYLLPKETQMALVSMRQLLDHAAE NSYGLPAFNVNNLEQMRAIM					
	10	20	30	40	50	60
m034.pep	70	80	90	100	110	120
	EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI					
a034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI					
	70	80	90	100	110	120
m034.pep	130	140	150	160	170	180
	QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHACGVSVEGEIGVLGNLETGDAG					
a034	QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHACGVSVEGEIGVLGNLETGEAG					
	130	140	150	160	170	180
m034.pep	190	200	210	220	230	240
	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSHGAYKFTRPPTGVDLRLD					
a034	EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSHGAYKFTRPPTGVDLRLD					
	190	200	210	220	230	240
m034.pep	250					
	RIKEIHQALPNTHIVMH					
a034	RIKEIHQALPNTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVKRVN					
	250	260	270	280	290	300

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

m034/g034

m034 . pep	MSCLWFFAVKNI IIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAM	60
g034	MSRLWFFAVKNI IIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAM	60
m034 . pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILA AVEVFPHIPVVMHQDHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILA AVEEFPHIPVVMHQDHGASPDVCQRSI	120
m034 . pep	QLGFSSVMDGSLMEDGKTPSSYEYNVNATRTVVNF SHACGVSVGEIGVLGNLETGDAG	180
g034	QLGFSSVMDGSLLEDGKTPSSYEYNVNATRTVVNF SHACGVSVGEIGVLGNLETGEAG	180
m034 . pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAI AVGTS HGAYKFTRPPTGDVLRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAI AVGTS HGAYKFTRPPTGDVLRID	240
m034 . pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSV PQEWLKVINEYGGNIGETYGVPVEEIVEG IKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

g036 . seq

1	ATGCTGAAGC	CGTGTTCGGT	ATACAGTGCC	TGTGCGGCGG	cgttgccTGC
51	GCGGACTTCG	AGCAGCAGGC	GTTGCGTGCC	TTCGGGCAGA	TGTGCGTACC
101	AATATTCGAG	CAGGGCGGAC	GCAACGCCCC	GTCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCACTTC	GGATTCGTCG	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCTGCCGT	CTTTTCCGC	AAGGAAAACC	TGTTCCGACG
251	GCGAAACAAG	CGCGGACTCA	AATTGGCGTT	GCGTCCACGC	GGACGGGTTG
301	CAGACGGTAT	CGAGCGCGGC	CAGTGCGGCG	CAGTCGGACG	GTGAGGCTGG
351	GCGGATGTTT	ATGTTCTGTC	CTTCCGTTC	GCCTGTTCTT	TGGCAGTCAG
401	GGCGATTTTG	TGCGGACGTC	AGAGCAGTTC	GGCGTGTGCC	GCGCCAGTTG
451	CGGGATAGCC	GCCGCCGAGG	GCGAGCGCGA	GAAAATCGGC	GGCGGTCGGC
501	ATATCGGGTT	TGCCTGAGAA	GGGCGGACGG	TTTCCAGTGC	CGAACGCACT
551	GCCGATGCCG	TCTGAAAAGA	CGTACCCCTC	GGGAGGGGCA	ATGTCTGCCG
601	CCCTACCGAC	TTGATAATCG	CTCAAACGGC	GGCGGTTTCA	CGTGTCCGAC
651	CACGCATAAA	ACACTTCGCC	CATACGCGCG	TCCGCAGCGG	CGAGTATGCA
701	GCTTTGCGGC	GGCGGCAGCG	AGGCGGCGGC	ATCGAGCGTG	GGGATGCCGA
751	TTAAAGGCGT	GTCGAACGGC	GTTGCCAAAC	CTTGCGCCAC	GCCGATGCCG
801	ATACGCAGTC	CGGTAA			

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

g036 . pep

1	MLKPCLVYSA	CAAALPARTS	SSRRCVPSGR	CAYQYSSRAD	ATPRRRHSGA
51	VAIRCSSDSS	GRFCQTIKAA	ILPSFSARKT	CSDGETSADS	NWRCVHADGL
101	QTVSSAASAA	QSDGEAGRMF	MFVPSVPPVL	WQSGRFCCGR	RAVRRVPRQL
151	RDSRRRGRAR	ENRRRSAYRV	CLRRADGFPV	RTHCRCLKR	RTPRGGQCLP
201	PYRLDNRSNG	GSACRTTHK	TLRPYARPQR	RVCSFAAAAA	RRRHRAWGCR
251	LKACRTALPN	LAPRRCRYAV	R*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

m036 . seq

1	ATGCTGAAGC	CGTGCGCCGT	GTACAGTGCC	TGTGCGGCGG	TGTTGCCTGC
51	ACGGACTTCG	AGCAGCAGGC	GTTGCGTGTC	TTCGGGCAGA	TGTGTGAACC
101	AATATTCGAG	CAGGGCGGAC	GCAATTCCTT	GGCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCACTTC	GGATTCGTCG	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCCG . CGT	CTTTTCCGC	AAGGAAAACC	TGTTCCGACG
251	GCGAAACAG	TGCGGACTCA	AATTGGCGTT	GCGTCCATGC	GGACGGGTTG
301	CAGACGGCAT	CGAGTGCGGC	CAGTCCTCA	CAATCGGCAC	AAACGGCAGC


```

351 GCGGATGTTC ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GGCGATTTTG TTGCGGACGT AGAGCAAACC GGCCTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA ACACCTTCGCC CATACGAGCG TCCGTAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGGT ATCAAACGGC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

m036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMR ESRRQSAYPV CLRTAELLPA RTRCLRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

a036.seq

```

1 ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCTGCTG
51 ACGGACTTTC AGCAGCAGGC GTTCCGTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTTCGAG CAGGGCGGAC GCAATTCCCTT GCGGCGCGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCT GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCGCGCGT CTTTTCCGC AAGGAAAACC TGTTCGGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCAGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTC ACAGGCGCGC CCTCCGTTCC GCCTGTTCTT TGGCAGTCAA
401 GGCGATTTTG TTGCGGACGT AGAGCAGCTC GGCGTGTGCC GCAGCGACGG
451 CGGGAAAACC GCCTTCAGCC GCCAGATTGA GGAAGTCGGC GGCGGTTCGGC
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGCG CGAACGCATT
551 GCCGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGTCTGCCG
601 CCCGACCGAC CTGATAATCG CTCAAACGGC GGCGGTTTCA CGTGTGCAAC
651 CATGCATAAA ACACCTTCGCC CATACGTGCG TCCGCGAGCG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAAGGAGT ATCAAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

a036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRFFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFPA RTHCRCLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

m036/a036 85.6% identity over a 270 aa overlap

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS					
a036	MLKPCAVYSACAAVLPARTSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m036.pep	GRFCQTIKAAIPXSFSAKRTCSNWDGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
a036	GRFCQTIKAAIPXSFSAKRTCSNWDGETSADSNWRCVHADGLQTASSAASAAQSAXTARRMF					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMPRESRRQSAYPVCRLRTAELLPA					
a036	TGAPSVPPVLWQSGRRFCCGRRRAARRVPQRRRENRLQPPDXGSRRRSAYRVCLRRADGFFA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERXPXQGCSEFAAAAA					
a036	RTHCRCLKRRILPAAGCLPPDRPDNRSNGGGSACRTMHKTLRPYVRPQRQGCSEFAAAAA					
	190	200	210	220	230	240
	250	260	270			
m036.pep	RRRHRARVRLRGYQTALPNPELHRCRYAVRX					
a036	RRRHRARVRLKEYQTALPNLAPRRCRYAVPX					
	250	260	270			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 036 shows 74.9% identity over a 271 aa overlap with a predicted ORF (ORF 036.ng) from *N. gonorrhoeae*:

m036/g036

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRVCNQYSSRADAI PWRRHSGAVAIRCSSDSS					
g036	MLKPCLVYSACAAALPARTSSSRRCVPSGRCAQYSSRADATPRRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m036.pep	GRFCQTIKAAIPXSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
g036	GRFCQTIKAAILPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMPRESRRQSAYPVCRLRTAELLPA					
g036	MEFVSPVPPVLWQSGRFCCGRRARRVPRQLRDSRRRGRARENRRRSAYRVCLRRADGFPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERXPXQGCSEFAAAAA					
g036	RTHCRCLKRRTPRGGQCLPPYRLDNRSNGGGSACRTTHKTLRPYARPORRVCSEFAAAAA					
	190	200	210	220	230	240
	250	260	270			
m036.pep	RRRHRARVRLRGYQTALPNPELHRCRYAVRX					
g036	RRRHRRAWGCRLKACRTALPNLAPRRCRYAVRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 133>:

m036-1.seq

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTTGCCTGC
51  ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTTCGAG CAGGCGCGAC GCAATTCCTT GGCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCGCGCGT CTTTTCCTCG AAGGAAAACC TGTTGCGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGCAGC CAGCTCCTCA CAATCGGCAC AAACGGCACG

```



```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GCGGATTTTG TTGCGGACGT AGAGCAAACC GGCCTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA ACACTTCGCC CATACGAGCG TCCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

```

m036-1.pep
  1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
 51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMR ESRQSAYPV CLRTAELLPA RTRCLRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*

```

m036-1/g036 76.8% identity in 228 aa overlap

m036-1.pep	10	20	30	40	50	60
	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIIRCSSDSS					
g036	MLKPCLVYSACAAALPARTSSSRRCVPSGRCAQYSSRADATPRRRHSGAVAIIRCSSDSS					
	10	20	30	40	50	60
m036-1.pep	70	80	90	100	110	120
	GRFCQTIKAAIPPSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
g036	GRFCQTIKAAIIPPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF					
	70	80	90	100	110	120
m036-1.pep	130	140	150	160	170	180
	TGALSVRPVLWQSGRFCCGR RANRRVRHGRQDNRPWLPMRESRQSAYPVCLRTAELLPA					
g036	MEFVPSVPPVLWQSGRFCCGR RAVRRVPRQLRDSRRRGRARENRRRSAYRVC LRRADGFPV					
	130	140	150	160	170	180
m036-1.pep	190	200	210	220	229	
	RTRCLRLKRRIPPAAGCLP PARPDNRSNGGSSAYRTMHKTLRPYERPX					
g036	RTHCRCRLKRRTPRGGQCLPPYRLDNRSNGGGSACRTHKTLRPYARPQRRVCSFAAAAA					
	190	200	210	220	230	240
g036	RRRHRAWGCRLKACRTALPNLAPRRCRYAVRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

```

g038.seq
  1 ATGACTGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51 TTTGAAATTC GCGGAATTTA CCACCAAAGC CGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTC AACGACGGCG CGTCCACGCT GCAACTGGCA
151 AAATTCTATG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCCTACAAAG GCATTATTTT GGCGGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC GCGGCGAAGG CGGCGTGTG GTCCGCGCGC CGCTTAAAGG
351 GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCAATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGCG CGGTGTCGCC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTAATTTGT CCGCCGTTCA
501 GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTTGTT TATCCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCCTC
601 GAACCCGTCG GCACCTACCG CCGGCAGTAC GGCGTAGAAT AA

```


This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDRGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GKLSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRTYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GCGCAATTCA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGTCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGCG CGGTGTCGCC
451  ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAA AAACAATACG GCTGCCCCGT CGCCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GCGCAATTCA CCACCAAGGC CGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGCG CGGTGTCGCC
451  ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAA AAACAATACG GCCTGCCCCGT CGCCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```

          10      20      30      40      50      60
m038.pep  MTDFRQDFLK FSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
```


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```

|||||
a038      MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
          10      20      30      40      50      60
          70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          |||||||
a038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          70      80      90      100     110     120
          130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
          |||||||
a038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
          130     140     150     160     170     180
          190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRRYRRQYGVEX
          |||||||
a038      ASLNDLFILLQNNPEFGQFLEPVRRYRRQYGVEX
          190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng) from *N. gonorrhoeae*:

m038/g038

```

          10      20      30      40      50      60
m038.pep  MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
          |||||||
g038      MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGASTLQLAKFYAQSIIES
          10      20      30      40      50      60
          70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          |||||||
g038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
          70      80      90      100     110     120
          130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
          |||||||
g038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQEVEKQYGLPVAPI
          130     140     150     160     170     180
          190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRRYRRQYGVEX
          |||||||
g038      ASLNDLFILLQNNPEFGQFLEPVRTYRRYRRQYGVEX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

g039.seq

```

1  ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51 CGAGAAAACA TCATGCCCGC CTGTTTCTGT CCGCACTGCA AAACCCGCCT
101 CTGGGTCAAA GAAAcccagC TCAAcgtCgC ccaagGCTTC GTCGTCTgcc
151 aaAAAtgcga agGGCTgttt aaAgccaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaaact gtttcgggat gTcaaaCTCG

```


225

```

251 TCcaccgcaT cggcacgcac gccattagca aGAaacagat gtcccgcgac
301 gaaatCgccg ataatcctcaa cggcgggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGcaggTT TCCGTACCGC
401 CCGCCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCCT GTTCGCACCT
451 ATCGTCCTCA TTATGCAGCT TTCTACCTC TTCATCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

g039.pep

```

1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSA
51 KNAKGCLKPK TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKKQMSRD
101 EIADILNGGT TLHDTTPATA AAAPAAAPQV SVPPARQEGE NWTIATLFL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

m039.seq

```

1 ATGCCGTCCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCCTGCA AAACCCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CGnnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCT GTGACGAAAT CGCCGGCATC CTCAACGGCG GTACAACCCA
351 GCCCGATATT CCGCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCCCGCGCG CCCGCCGTC AGGATGGGT CAACTGACG
451 ATTGCAACCC TGTTCGCCCT TATCGTCCTC ATTATGCAGC TTCTCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

m039.pep

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPPXXXXX
51 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LNGGTTPDI PPATAATPAA APQVTVPAA PARQDGFNWT
151 IATLFLALIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

a039.seq

```

1 ATGCCGTCCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCCTGCA AAACCCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CCAAGGCTTC GTCGTCTGCC
151 AAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCAGGAAA
201 GAACCCATAT TCAACGATT. TGCCCGAAGC TGTTCGGAT GTCAAACCTG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCCGCC
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGGTTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTTC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

a039.pep

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSA
51 KNAKECLKPK TIWQARKNPY STIXPEAVSD VKLVHRIGTS AIGKKQISR
101 EIAGILNGGT TQDIPPATA ATPAAAPQV VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLVIL*

```

m039/a039 79.4% identity over a 170 aa overlap

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPDTHEEIPC					
a039	MPSEPPYASDGIKPDTHEEIPC					

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	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRI	GT	RAIGKKQISRDEI	AGILNGGTTQ	PDI
a039	TIWQARKNPFYSTIX----	PEAVSDVKLVHRI	GT	SAIGKKQISRDEI	AGILNGGTTQ	PDI
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAATPAAAPQVT	PPAAPARQDGFN	WTIATL	FALIVLIMQ	LSYLVLIX	
a039	PPATAATPAAAPQVT	PPAAPARQDGFN	WTIATL	FALIVLIMQ	LSYLVLIX	
	120	130	140	150	160	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 039 shows 60.8% identity over a 171 aa overlap with a predicted ORF (ORF 039.ng) from *N. gonorrhoeae*:

m039/g039

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPD	THEEIPC	PPVSA	PAPTAKPV	SGSKPNS	MSPXXXXXXXXXXXXXXXXXXXX
g039	MPSEPPAASDGIKPT	HTTEKTS	CPPVSV	RTAKPAS	SGSKP	SSTSPKASSAKNAKGLKPK
	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRI	GT	RAIGKKQISRDEI	AGILNGGTTQ	PDI
g039	TIWQARKNLYSTIG----	PKLFRDVKLVHRI	GT	HAISKQMSRDEI	ADI	LNGGTTLLHDT
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAAT-PAAAPQVT	PPAAPARQDGFN	WTIATL	FALIVLIMQ	LSYLVLIX	
g039	PPATAAAAPAAAPQV	SVPPA---RQ	EGLNWTIATL	FALIVLIMQ	LSYLFILX	
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 147>:

g040.seq

```

1  ATGAACGCGC CCGACAGCTT TGTGCGCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGGCA CGACACTGGT CGCCGGCATA GAcggCCGCC
101 TGCTCGAAGG CGGCACCTTA AATAAGCTCG CCGCCGACAT CGGGCTGTGT
151 TCGCAACTGG GCATCCGACT CGTCCTCATC CACGGCGCGT ACCACTTCCT
201 CGAccgCCTC GCCGCCGCGC AAGgccGCAC GCCGCATTAT TGCCGggggtt
251 tGCGCGTTAC CGACGaAACc tcGctcgGAC AGGCGCAGCA GtttGCCGGC
301 AccgTCCGCA GCCGTTTTGA agcCGCATtG tgcggcagCG tttcaggatt
351 cgcgCGCGCG CCTTCCGTCC CGCTCGTAtc gggcaacttc ctgacCGCCC
401 GTCcgatggg cgtgattgac ggaACCGata tggaatacgc gggggttatc
451 cgcaaaaccg ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGATG CCGCGCTCG GGCATTCTTA CGGCGGCAAA ACCTTCAATC
551 TCGATATGGT GCAGGCCGCC GCTTCCGTCG CCGTCTCGCT TCAGGCCGAA
601 AAATCTGTTT ACCTGACCCT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGCCAGCGA AACCCGACGA CTGATTTCGT CCGCCGTTGC CGCGCTCGAA
751 GCGGGCGTGC ATCGCGTCCA AATCCTCAAC GGGCGCGCCG ACGGCAGCCT
801 GCTGCAAGAA CTCTTACCCC GCAACGGCAT CGGCACGTCC ATTGCCAAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCGACAT CCCGCACATC
901 GCCGCCCTCA TCCGCCCGCT GGAAGAACAG GCGTCCTAT TGCACCGCAG
951 CCGCGAATAC CTCGAAAACC ACATTTCGGA ATTTTCATC CTCGAACACG

```



```

1001 ACGGCGACCT GTACGGCTGT GCCGCACTCA AAACCTTTGC CGAAGCCGAT
1051 TGCGGCGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGg
1101 ctACGGCGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTCGCA CTGTCCACAA ATACCGCGCA ATGGTTTGCC
1201 GAACGGCGCT TTCAGACGGC ATCGGAAGAC GAGCTGCCCC AAACGGGGCG
1251 CAAAGACTAC CGCAGCAACG GACGAAACCC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

g040.pep

```

1 MNAPDSFVAH FREAAPYIRQ MRGTTLVAGI DGRLLGGTL NKLAADIGLL
51 SOLGIRLVLI HGAYHFLDRL AAAQGRTPHY CRGLRVTDET SLGQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPMGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWM PPLGHSYGGK TFNLDMVQAA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLSAQEAQSL AEHAASETRR LISSAVAAL
251 GGVHRVQILN GAADGSLLEQ LFRNGIGTS IAKEAFVSIR QAHSGLDIPHI
301 AALIRPLEEQ GVLLHRSREY LENHISEFSI LEHDGDLGYC AALKTFEAD
351 CGEIACLAVS POAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNRNPIL VRRLLR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

m040.seq

```

1 ATGAGCGCGC CCGACCTCTT TGTCGCCAC TTCCGCGAAG CCGTCCCCTA
51 CATCCGCCAA ATGCGCGGCA AAACGCTGCT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAGCTCG CCGCCGACAT CGGGCTGTGTG
151 TCGCAACTGG GCATCAGGCT CGTCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCCGCTC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TGCGCGTTAC CGACGAAACC TCGCTCGAAC AGGCGCAGCA GTTTGCCGGC
301 ACCGTCGCGA GCCGTTTGA AGCCGCATTG TGCGGCAGCG TTCCGGGTT
351 CGCGCGCGCG CCTTCCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGAATACGC GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCCGCTCG GACATTCCTA CAGCGGCAAG ACCTTCTATC
551 TCGATATGCT TCAAACCGCC GCCTCCGCCG CCGTCTCGCT TCAGGCCGAA
601 AAACCTGTTT ACCTGACCCT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCGGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGGCGGGCA AACCGGACGG CTGATTTCGT CCGCCGAAC CTTCACCGCG
751 AACGGCATCG GCACGTCCAT TGCCAAAGAA GCCTTCGTCT CCATCCGGCA
801 rGCGCAywgG G.CGACATCC CGCACATCGC CGCCCTCATC CGCCCGCTGG
851 AAGAACAGGG CATCTGCTG CACCGCAs.c GCGAATACCT CGAAAACCAC
901 ATTTCCGAAT TTTCCATCCT CGAACACGAC GGCAACCTGT ACGGTTGCGC
951 CGCCCTGAAA ACCTTTGCCG AAGCCGATTG CGGCGAAATC GCCTGCCTTG
1001 CCGTCTCGCC GCag.cACAG GACGGCGGCT ACGGCGAACG CnTGCTTGCC
1051 CACATTATCG ATAAGCGCGC CGGCATAGGC ATAAGCAGGC TGTTCGCACT
1101 GTCCACAAAT ACCGGCGAAT GGTTCGCCGA ACGCGGCTTT CAGACGGCAT
1151 CGGAAGACGA GTTGCCCGAA ACGCGGCGCA AAGACTACCG CAGCAACGGA
1201 CGGAACCTCG ATATTCTGGT ACGTCGCCTG CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

m040.pep

```

1 MSAPDLFVAH FREAVPYIRQ MRGKTLVAGI DDRLLGGDTL NKLAADIGLL
51 SOLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFYLDMLQTA ASAAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLSAQEAQSL AEHAGGQTRR LISSAELFTR
251 NGIGTSIAKE AFSIRQAHX XDIPHIAALI RPLEEQGILL HRXREYLENH
301 ISEFSILEHD GNLYGCAALK TFAEADCGEI ACLAVSPQXQ DGGYGERXLA
351 HIIKARGIG ISRLFALSTN TGEWFAERGF QTASEDELPE TRRKDYRSNG
401 RNSHILVRRLL HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

a040.seq

a040.pap

1	MIVPDLFVAH	FREAAPYIRQ	MRGKTLVAGI	DDRLLGGDTL	NKFAADIGLL
51	<u>SQLGIRLVLI</u>	HGARHFDRH	AAAQGRTPHY	CRGLRVTDET	SLEQAQQFAG
101	TVRSRFEAAL	CGSVSGFARA	PSVPLVSGNF	LTARPIGVID	GTDMEYAGVI
151	RKTDTAALFR	QLDAGNIIVWL	PLGHYSYSGK	TFHLDMLQTA	ASVAVSLQAE
201	KLVYLTLSDG	ISRPDGTILAV	TLSPAQAQSL	AEHAGETERR	LISSAVVALE
251	GGVHRVQILN	GAADGSLLQE	LFTNRNGIGTS	IAKEAFVSIR	QAHSGDIPHI
301	AALIRPLEEQ	GILLHRSREY	LENHISSEFSI	LEHGDNLYGC	AALKTFEADF
351	CGEIACLAVS	PQAQDGGGYE	RLLAHIIDKA	RIGISIRLFA	LSTNTGEWFA
401	ERGFQTASED	ELPETRRKDY	RSNGRNSHIL	VRRRLR*	

	10	20	30	40	50	60
m040.pep	MSAPDLFVAHFREAVPYIROMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI					
	: :					
a040	MIVPDLFVAHFREAAPYIROMRGKTLVAGIDDRLLEGDTLNKFAADIGLLSQLGIRLVLI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m040.pep	HGARHFLLDRHAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
a040	HGARHFLLDRHAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPPLGHSYSGK					
a040	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPPLGHSYSGK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAGGQTRR					
	:					
a040	TFHLDMLQTAASVAVSLQAEKLVYLTLSDGISRPDGTLAVTLSAQEAQSLAEHAGGETRR					

	190	200	210	220	230	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI 					
a040	LISSAVAALGGVHRVQILNGAADGSLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI 250 260 270 280 290 300					
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS 					
a040	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS 310 320 330 340 350 360					
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY 					
a040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY 370 380 390 400 410 420					
m040.pep	RSNGRNSHILVRRRLHRX 					
a040	RSNGRNSHILVRRRLHRX 430					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 040 shows 88.3% identity over a 436 aa overlap with a predicted ORF (ORF 040.ng) from *N. gonorrhoeae*:

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
g040	MNAPDSFVAHFREAAPYIRQMRGTTLVAGIDGRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA	120
g040	HGAYHFLDRLAAAQGRTPHYCRGLRVTDETSLGQAQQFAGTVRSRFEAALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK	180
g040	PSVPLVSGNFLTARPMGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYGGK	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRDPGTLAETLSAQEAQSLAEHAGGQTRR	240
g040	TFNLDMVQAAASVAVSLQAEKLVYLTLSDGISRDPGTLAETLSAQEAQSLAEHAASETRR	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI	276
g040	LISSAVAALGGVHRVQILNGAADGSLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS	336
g040	AALIRPLEEQGVLLHRXREYLENHISEFSILEHDGDLYGCAALKTFAEADCGEIACLAVS	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	396
g040	PQAOQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	420
m040.pep	RSNGRNSHILVRRRLHRX	413
g040	RSNGRNPHILVRRRLHRX	437

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
1  ATGAGTTCGC CCAAACACAT CGGCTTGCAG GCGGCGAGCA ACGGCGGCCT
51  GATTACCGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GGTGCGCTGG
101 TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151 GGTTCAGATT GGACGGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201 CAAACGCCGG CTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCACTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301 CATCCCGCCC ACGCGCTCAA ATTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCAACGCGA ATCCGCCGAC AAACCTGCCT GCGTGTGCT GTTTTGAAG
451 GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
1  MSSPKHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQRESAD KLACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCGAGCA ACGGCGGACT
51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GGCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGACT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCCGC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCAACGCGA ATCCGCCGAC GAACTCGCCT GCGTCTTGCT GTTTTGAAG
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
1  ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCRRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYSPDGGGHT GNGTQRESAD ELACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCGAGCA ACGGCGGACT
51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATA GGCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGACT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CGCAGCGCGA AGCCGCCGAC GAACTCGCCT GCGTGTGCT GTTTTGAAG
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
1  ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCRRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQREAAD ELACVLLFLK
```


151 EFLG*

m041/a041 98.7% identity over a 154 aa overlap

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
a041	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSW					
a041	PQKYEVCKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
a041	LYSPDGGGHTGNGTQREADELACVLLFLKEFLGX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 041 shows 96.8% identity over a 154 aa overlap with a predicted ORF (ORF 041.ng) from *N. gonorrhoeae*:

m041/g041

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	:					
g041	MSSPKHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSW					
g041	PQKYEVCKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
g041	LYSPDGGGHTGNGTQRESADKLACVLLFLKEFLGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 159>:

g041-1.seq

```

1  ATGAAATCCT ACCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGCG CGCGCACTTT CAGACGGCAT TTTGAATCAA
151 ATGCAGGACA CGCGGCAGAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAGAATG CGGAATATCC GAAGGGCGTG TACCGCATGT
251 GTACGGCGGC GACCTACCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTTCGATGA GTTGCTCGGC GACGATGTGT ATTTGGGCGG
351 CGTGTCGCAC TTGGTGGAGC AGCCCAACCG CGCGCTGCTG ACTTTGAACA
401 AATCGGGCGG CGATACGGCG TATACGCTGG AAGTGGATT TCGAAGCAGG
451 GAATTGGTAG AGGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAAG TGTGGCTGGT GGAACGCGGC

```



```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCTG
751 TCCGAAGGCG GGGCGAAACC GTTGAACCTG CCTAATGATT GCGATGTGGT
801 CCGCTATCTG GCGGGACATC TTTTGCTGAC GCTGCGCAAG GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAATGT ACAAGGCCGT CTGAAAGCGT GCGGTTTTCG CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACGTGGTTTA TCTTGCCGCC AGCGATTTCA
1151 CCACGCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAGTACC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGT TCGACGGCA TCGAAGTGGC
1251 GCAGTTTTCG GCGGTGTCGT CCGACGGCGA ACGCATTCC TATTTCACG
1301 TCGGCAAAA CGCGCGCGCC GACACGCCGA CCTTAGTCTA TGCTTACGGA
1351 GGTTCGGCA TTCCTGAATT GCCGATTAT CTGGGCAGCG TCGGCAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTGTATT GGCAACATC CGCGCGGCG
1451 GAGAATTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAACAC
1501 AAAAGCGTTG ATGATTTGTT GGCAGTCGTG CGTGATTTGT CCGAACGCGG
1551 CATGAGTTCG CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGCGCGCC
1601 TGATTACCGC CGCCGCTTC GTGCGGAAC CGCAAAGCAT CGGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGATC CGTTATCCGC TGCTGTCCGC
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGCAGAAA TACGAAGCCT
1751 GCAAACGCGG GCTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCACT CATTACCACC AGCCTCAGCG ACGACCGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CAAACTCGCC TCGGTGTTGC TGTTTTTGAA
2001 AGAATTTTGG GGATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1  MKSYDPYRH FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51  MQDTRQIPFC QEHRARMYHF HQNAEYPRGV YRMCTAATYR SGYPEWKILF
101 SVADFDLELG DDVYLGGVSH LVEQPNRALL TLNKSGGDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 SEGGAKEPLNL PNDCDVVGYL AGHLLTLRK DWHRANQSYF SGALVAVKLN
301 RGELGAAQLL FAPDETOALE SVETTKRFV ASLLENVQGR LKAWRFADSK
351 WQEAELPHLP SGALEMDQP WGGDVVYLA SDFTTPTLTF ALDLNVMELT
401 VMRLQPQFV SDGIEVRQFW AVSSDGERIP YFHVGNKNAAP DPTLVYAYG
451 GFGIPELPHY LGSVGKYWLE EGNFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLAVV RDLSEGMSS PKHIGLQGS NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1  ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGGCG CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGACGCA ATTGCTTGGC GACGATGTGT ATTTGGGCGG
351 CGTGTGCGAC TTGGTGGAAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATTGGGCAG CGATACGGCG TACACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAGTTGGTCG AAGGCGGTTT TCACTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCTGTGTAT CAAATCGCGC AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ATCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AAACCTATTT GCGGGTCTCA

```



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751 GCCGAAGGCG AGGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTGGT
801 CGGCTATCTG GCGGGGCATC TTTTGTCTGAC GCTGCGCAAG GACTGGAACC
851 GCGCGAACCA AAGCTATCCG AGCGGCGCGC TGGTGGCGGT GAAGCTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCGAGCCTGT
1001 TGGAGAACGT ACAAGGCCGT CTGAAAGCAT GGCGGTTTGC CGACGGCAAA
1051 TGGCAGGAAG TCGAATTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCT TGGGGCGGCG ACGTGGTTTA CTTTGCCGCC AGCGATTCA
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAACGTACC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCGAATT GCCGATTAT CTGGGCGAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GCGCAACATC CGCGGCGGCG
1451 GCGAGTTCGG CCCCGCGCTG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTTATT GGCAGTCGTG CGCGATTGT CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCTTC GTGCGCAAC CGCAAAGCAT CGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCCG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGGCT CATACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAACTGCGC GAAACCTCCG
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CGAACTCGCC TCGCTCTTGC TGTTTTGTAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 162; ORF 041-1>:

m041-1.pep

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLENDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKG VYRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSLKLGSDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW NERQLTQSGY PREVWLVERG
201 KSFEESLPVY QIGEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLRVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRKL DWNRRANQSY SGAALVAVKLN
301 RGEELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADGK
351 WQEVLPRLP SGALEMTDQP WGGDVVYLAA SDFTTPLTLF ALDLNVMELT
401 VMRRQPQFDF SDGINVQFVW TTSADGERIP YFHVGNKNAAP DMPTLVYAYG
451 GFGIPPELPHY LGSIGKYWLE EGNAFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLAVV RDLSEGGISS PEHIGLOGGS NGCLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKEYAKLR ETSAQSWLYS PDGGGHTGNG
651 TQRESADELA CVLLFLKEFL G*

```

m041-1/g041-1 94.6% identity in 671 aa overlap

	10	20	30	40	50	60
m041-1.pep	MKSYPDPYRHFENLDSAETQ NFAAEANAET RARFLENDKA RALSDGILAQ LQDTRQIPFC					
g041-1	MKSYPDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKARALSDGILNQMDTRQIPFC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041-1.pep	QEHRARMYHFHQDAEYPKG VYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
g041-1	QEHRARMYHFHQDAEYPKG VYRMCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m041-1.pep	LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHFPAGKNHVSWRDENSVWVCPAW					
g041-1	LVEQPNRALLTLNKSGGDTAYTLEVDLEAGELVEGGFHFPAGKNHVSWRDENSVWVCPAW					
	130	140	150	160	170	180
	190	200	210	220	230	240
m041-1.pep	NERQLTQSGYPREVWLVERGKSFEESLPVYQIGEDGMMVN AWRYLDPQGS PIDLIEASDG					
	: : : : : :					

g041-1	DERQLTESGYPREVVLVERGKSFEESLPAYQIDKGAMMVNAWRYLDPQGSPIDLIEASDG
	190 200 210 220 230 240
m041-1.pep	FYTKTYLRVSAEAGEAKPLNLPNDCDVVGYLAGHLLLTLRKDWNRANQSYPSGALVAVKLN
	250 260 270 280 290 300
g041-1	FYTKTYLQVSSEGGAKPLNLPNDCDVVGYLAGHLLLTLRKDWHRANQSYPSGALVAVKLN
	250 260 270 280 290 300
m041-1.pep	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRLLKAWRFADGKWQEVLPRLP
	310 320 330 340 350 360
g041-1	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRLLKAWRFADSKWQEAELPHLP
	310 320 330 340 350 360
m041-1.pep	SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTVMRRQPQQFSDGINVQQFW
	370 380 390 400 410 420
g041-1	SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTVMRLQPQQFVSDGIEVRQFW
	370 380 390 400 410 420
m041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI
	430 440 450 460 470 480
g041-1	AVSSDGERIPYFHVGNKNAAPDTPTLVYAYGGFGIPELPHYLGSVCKYWLEEGNAFVLANI
	430 440 450 460 470 480
m041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDDLLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF
	490 500 510 520 530 540
g041-1	RGGGEFGPRWHQAAQGISKHKSVDDLLAVVRDLSESGMSSPKHIGLQGGSNGLITAAAF
	490 500 510 520 530 540
m041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCRRRLGELSPYHNLSDG
	550 560 570 580 590 600
g041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEACKRRRLGELSPYHNLSDG
	550 560 570 580 590 600
m041-1.pep	IDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSWLYSPDGGGHTGNGTQRESADELA
	610 620 630 640 650 660
g041-1	IDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADKLA
	610 620 630 640 650 660
m041-1.pep	CVLLFLKEFLGX
	670
g041-1	CVLLFLKEFLGX
	670

m041-1/P55577

sp|P55577|Y4NA_RHISN PROBABLE PEPTIDASE Y4NA >gi|2182536 (AE000086) Y4nA [Rhizobium sp. NGR234] Length = 726

Score = 370 bits (940), Expect = e-101

Identities = 217/682 (31%), Positives = 331/682 (47%), Gaps = 22/682 (3%)

Query: 2 KSYDPYRHFENLDSAEQNFAAEANAETRARFLENDKARALSDGILAQLDTRQIPFCQ 61
K DP + +D + + N T + ++ L LQ T +I

Sbjct: 42 KDASDPRAYLNEIDGDKAMTWVEAHNLSTVDKLSKDPYSEYQADALTILQATDRIASPS 101

Query: 62 EHRARMY-HFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFELLGDDVILGGVSH 120
R M +F QD + +G++R T +YRSG P+W+ + V + G G

Sbjct: 102 FARDGMIDNFWQDGHVQGLWRRTTWESYRSGNPQWRTILDVDALSKAEGKTWVFEGGDC 161

Query: 121 LVEQPNRALLTSLKSGSDTAYTLEVDLEAGELVEGGFHPAGKNHVSWRDENSVMVCPAW 180
L N L+ LS G D E D+ GE V+ GF P GK V+W DEN+++V W

Sbjct: 162 LPPTSNLCLIRLSDDGGKADVVREFDIAKGEFVKEGFVLPEGKQSVTWVDENTIIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNAWRYLDPOGSPI 232
 ++T SGY +V+RG+S +++ ++ E G++ ++ +D +

Sbjct: 222 TPGEVTSYGAYVTKVVRGQSLDQAVEIFRGQKDVSAERGVLRLDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDWNANQS-YPS 291
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFFNTELAFFYPNGH----PDTRKVVLPLTTAVFSGYKQAIYWLKSDWTSAGKTVFHN 337

Query: 292 GALVAVKLNREGELGAAQL----LFAPDETQALESVETTKRFVVASLLENVQGRKAWRFA 347
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAIIAFDLKAALADPARVEPLVLFMPNEHQSVAGTTOTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKQWEVELPRLPSGALEMTDQFWGGDVVYLAASDFTTPTLTLFALDLNVMELTVMRRQPQ 407
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KCGWSSFKLALPENSTLSLTSSDDESQDLFVFESEGFLEPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFSDSDGINVQQFWTTTSADGERIPYFHVGNKAAAP---DMPTLVYAYGGFGIPELPHYLGS 464
 +FD+ G+ QQFW TS DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGTVPYFLVARKDVKLDGNTPTILYAYGGFQIPMQPSYSAVL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSEGGISSPEHI 524
 GK WLE+G A+ LANIRGGGEFGP+WH A ++. + DD AV +DL + ++S H+

Sbjct: 518 GKWLKEGGAYALANIRGGGEFGPKWHDAGLKTNRQVYDDFQAVAQDLIAKVTSTPHL 577

Query: 525 GLQGGSSNGGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPKQYEV 584
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGGSSNGGLLMGVQMIQRPDNLNAVVIQVPLDMVNFTRMSAGASWQAEYGSPPD-PVE 636

Query: 585 KRLRGELSPYHNLSGDIDYPPALITTSLSDDRVPALHAKFYAKLRETSAQSWLYSPDGG 644
 L +SPYHN+ G+ YP TS DDRV P HA K A + + Y G

Sbjct: 637 GAFRLRSISPYHNKAGVAYPEPFFETSTKDDRVGPVHARKMAALFEDMGLPFYYENIEG 696

Query: 645 GHTNGTQRESADELACVLLFL 666
 GH +E A A +++

Sbjct: 697 GHAAAAANLQEHARRYALEIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1  ATGAAATCCT ACCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGCAAAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTC CATCAAGATG CGGAATATCC GAAAGGCGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGACGCA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 CGTGTGCGAC CTGGTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATCGGGCGG CGATACCGCG TACACGCTGG AAGTGGATT TGAAGCAGGG
451 GAGTTGGTAG AAGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCGTGTAC CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 GCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CGGCTATCTG GCCGGACATC TTTTGTGAC CTTGCGTAAA GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGGC GCAGCTTTTG TTTGCGCCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGCTG GCGAGCCTGC
1001 TGGAAAACGT ACAGGTCGT CTGAAAGCGT GCGGTTTAC TGATGGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGEGCGCT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CCTTGGCGCC AGCGATTTC
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAACGTACC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCTT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGCGCA TTCCCGAATT GCCGCATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTGTATT GCGCAACATC CGCGGCGGCG

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1451 GCGAGTTCGG CCCGCCCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
 1501 AAAAGCGTTG ATGATTATT GGCAGTCGTG AGCGATTGT CCGAACGCGG
 1551 TATCAGTTTC CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
 1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
 1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
 1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
 1751 GCAAACGCGG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
 1801 ATCGATTATC CGCCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
 1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
 1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
 1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TGCCTGTTGC TGTTTTTGAA
 2001 AGAGTTTTTG GGCTAA

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

1 MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
 51 LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
 101 SVADFDELLG DDVYLGVS LVEQPNRALL TSKSGGDTA YTLEVDLEAG
 151 ELVEGGFHF AGKNHVS WRD ENSVWVCPAW DERQLTESGY PREVWLVERG
 201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
 251 AEAGEAKPLNL PNDCDVVGYL AGHLLLT LRK DWHRANQSYPS GALVAVKLN
 301 RGELGAAQLL FAPNETQALLESVETTKRFVVASLLENVQGR LKAWRFTDGLP
 351 WQETELPRLP SGALMTDQF WGGDVVYLAA SDFTTPTLTF ALDLNVMELT
 401 VMRRQPPQFD SDGINVQFWS TTSADGERIP YFHVGNKNAAP DMPTLVYAYG
 451 GFGIPELPHY LGSIGKYWLE EGNANFLANI RGGGEFGPRW HQAAQGISKH
 501 KSVDDLAVV SDSLSEGISS PEHIGLQGS NGGLITAAAF VREPQSIGAL
 551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
 601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
 651 TQREAADELA CVLLFLKEFL G*

a041-1/m041-1 97.9% identity in 671 aa overlap

	10	20	30	40	50	60
a041-1.pep	MKSYDPYRHFENLDSAETQ	NFAAEANAET	RARFLNNDKA	RALSDGILAQ	LQDTRQIPFC	
m041-1	MKSYDPYRHFENLDSAETQ	NFAAEANAET	RARFLNNDKA	RALSDGILAQ	LQDTRQIPFC	
	10	20	30	40	50	60
	70	80	90	100	110	120
a041-1.pep	QEHRARMYHFHQDAEYPKGV	YRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGVS	
m041-1	QEHRARMYHFHQDAEYPKGV	YRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGVS	
	70	80	90	100	110	120
	130	140	150	160	170	180
a041-1.pep	LVEQPNRALLTSKSGGDTA	YTLEVDLEAG	ELVEGGFHF	PAGKNHVS	WRDENSVWVCPAW	
m041-1	LVEQPNRALLTSKSGGDTA	YTLEVDLEAG	ELVEGGFHF	PAGKNHVS	WRDENSVWVCPAW	
	130	140	150	160	170	180
	190	200	210	220	230	240
a041-1.pep	DERQLTESGYPREVWLVERG	KSFEESLPVY	QIAEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
m041-1	DERQLTESGYPREVWLVERG	KSFEESLPVY	QIAEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
	190	200	210	220	230	240
	250	260	270	280	290	300
a041-1.pep	FYTKTYLQVSAEAGEAKPLNL	PNDCDVVGYLAGHLLLT	LRKDWHRANQSYPS	GALVAVKLN		
m041-1	FYTKTYLQVSAEAGEAKPLNL	PNDCDVVGYLAGHLLLT	LRKDWHRANQSYPS	GALVAVKLN		
	250	260	270	280	290	300
	310	320	330	340	350	360
a041-1.pep	RGELGAAQLLFAPNETQALLES	SVETTKRFVVASLLENVQGR	LKAWRFTDGLP	WQETELPRLP		
m041-1	RGELGAAQLLFAPNETQALLES	SVETTKRFVVASLLENVQGR	LKAWRFTDGLP	WQETELPRLP		
	310	320	330	340	350	360

a041-1.pep	370	380	390	400	410	420
	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
m041-1	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
a041-1.pep	430	440	450	460	470	480
	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
a041-1.pep	490	500	510	520	530	540
	RGGGEFGPRWHQAAQGISKHKSVDLLAVVSDLSERGISSPEHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSESGIISPEHIGLQGGSNGLITAAAF					
a041-1.pep	550	560	570	580	590	600
	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPKYEVCKRRLGELSPYHNLSDG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPKYEVCKRRLGELSPYHNLSDG					
a041-1.pep	610	620	630	640	650	660
	IDYPPALITTSLSDDRVPALHAKFYAKLRETSFQSWLYSPDGGGHTGNGTQREAADELA					
m041-1	IDYPPALITTSLSDDRVPALHAKFYAKLRETSFQSWLYSPDGGGHTGNGTQRESADELA					
a041-1.pep	670					
	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

g042.seq

1	ATGACGATGA	TTTGCTGCG	CTTCCAagcG	TTCGTGCCGC	ATACCAGCGC
51	GTTATCCAAC	ACTTCCACGG	CAGCCGGCCC	TTCCTGCCCG	ATGGCGGCGG
101	TGCGGTGCGAT	GATGAAATC	CAGCCGGGGT	TTTTCTCTTT	GATGTATTCG
151	AAGGAAACGG	GCTGCCCGTG	CCCTTCGTTG	CGTAAAGATT	CGTCCACGGG
201	CGGCAGGCCG	ATGTCGCCGT	GTATCCAAC	TGCCAACCGC	GATTGCGTGC
251	CGAAGCGCGA	CACCTTGTG	CCTGTAACCG	ACAGCACCAG	CCGCGTCCT
301	TTGCCTTTGG	cggCTTCGCG	CTTTTGGGCG	AACAGCGCGT	CAATCTGCGC
351	ATTCAATTCC	GCCACGCGCG	CTTCCTTACC	GAAATCCGC	GACAGGGTCT
401	CCATCTGCTT	CTCGCCGCTG	GTGCGGATAT	TGCCGTGTGC	CACCGTCAAA
451	TCTATGgtgG	TCGCGTTTTT	CGCCAACTGT	TCATACGCTT	CCGCACCCGG
501	CCCGCCGGTA	ATGACAAACT	GCGGATTGTG	GCGGTGCAGG	GATTGCAAT
551	CGGGCTCAAA	CAGCGTCCCC	ACCGTTGCCG	CCTTGTCAAA	TGCAGGCTGC
601	AAATAG				

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

g042.pep

1	MTMICLRFOA	FVPHTSALS	N TSTAAGPSCP	MAAVRSMKI	QPGFFSLMYS
51	KETGCPGPSL	RKDSSTGGRP	MSPCIQLANR	DCVPKADTLL	PVTDSTSPRP
101	LPLAASRFWA	NSASICAFNS	ATRASLPKIR	DRVSICFSPL	VRILPLSTVK
151	SMVVAFFANC	SYASAPGPPV	MTNCGLWRCR	DSQSGSNSVP	TVAALSNAGC
201	K*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

m042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCTT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGTG GTGCGGATAT TGCCGTGTGC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCCG
501 CCCGCCGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

m042.pep

```

1  MTMICLRFOA FVPRTSALSX TSTAAGXSCP MAAVRSMKI QSGFFSLMYS
51  KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRCR ASXSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

a042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGGCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCTT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGTG GTGCGGATAT TGCCGTGTGC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGT TCATACGCTT CCGCGCCCCG
501 CCCGCCGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

a042.pep

```

1  MTMICLRFOA FVPRTSALSX TSTAAGPSCP MAAVRSMKI QSGFFSLMYS
51  KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAGC
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFOAFVPRTSALSXTSTAAGXSCPMMAVRSMMKIQSGFFSLMYSKETGCPGPSL					
a042	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMMAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTPRPLPLAASRVWANNSASICAENS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTPRPLPLAASRVWANNSASICAENS					
	70	80	90	100	110	120
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
a042	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
	130	140	150	160	170	180


```

a042      |||||
          AARASLPKIRAKVSICFSPVLVRLPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          130      140      150      160      170      180

          190      200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          |||||
a042      ASXSGSNSVPTVAALSNAGCKX
          190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

          10      20      30      40      50      60
m042.pep  MTMICLRFOAFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL
          |||||
g042      MTMICLRFOAFVPHTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPGPSL
          10      20      30      40      50      60

          70      80      90      100     110     120
m042.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDDSTSPRPLPLAASRVWANSASICAFNS
          |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDDSTSPRPLPLAASRFWANSASICAFNS
          70      80      90      100     110     120

          130     140     150     160     170     180
m042.pep  AARASLPKIRAKVSICFSPVLVRLPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          |||||
g042      ATRASLPKIRDRVSICFSPVLVRLPLSTVRSMVVAFFANC SYASAPGPPVMTNCGLRWR
          130     140     150     160     170     180

          190     200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          |||||
g042      DSQSGSNSVPTVAALSNAGCKX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGGCC TTCCTGCCCG ATGGCGGCGG
101 TACGTCGAT  GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCCGT CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCCCTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1  MTMICLRFOA FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDDSTSPR
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPV VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap

240

	10	20	30	40	50	60
m042-1.pep	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
g042	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTSPRPLPLAASRVWANSASICAFNS					
g042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSVMVAFFANCYSYASAPGPPVMTSX					
g042	ATRASLPKIRDRVSICFSPLVRILPLSTVKSVMVAFFANCYSYASAPGPPVMTNCGLRWCR					
	130	140	150	160	170	180
g042	DSQSGSNSVPTVAALSNAAGCKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

```

a042-1.seq
1  ATGACGATGA  TTTGCTTGCG  CTTCCAAGCG  TTCGTGCCGC  GTACCAGCGC
51  GTTATCCAAT  ACTTCGACAG  CCGCCGGCCC  TTCCTGCCCG  ATGGCGGCGG
101 TACGGTCGAT  GATGAAAATC  CAATCGGGGT  TTTTCTCTTT  GATGATTTCG
151 AAGGAAACAG  GCTGCCCGTG  CCCCTCGTTG  CGTAAAGATT  CGTCTACAGG
201 CGGTAGGCCG  ATGTCGCCGT  GTATCCAAC  TGCCAACCGC  GACTGCGTGC
251 CGAAGGCCGA  CACCTTGTG  CCCGTAACCG  ACAGCACCAG  CCCGCGTCCT
301 TTGCCTTTGG  CGGCTTCGCG  CGTTGGGCG  AACAGCGCGT  CAATCTGCGC
351 CTTCAATTCC  GCCGCGCGCG  CTTCTTGCC  GAAATCCGC  GCCAAGGTCT
401 CCATCTGCTT  TTCGCCGCTG  GTGCGGATAT  TGCCGTTGTC  CACCGTCAGA
451 TCTATGGTGG  TCGCGTTTTT  CGCCAACGTG  TCATACGCTT  CCGCGCCCGG
501 CCGCCCGGTA  A

```

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

```

a042-1.pep
1  MTMICLRFQA  FVPRTSALSN  TSTAAGPSCP  MAAVRSMMKI  QSGFFSLMYS
51  KETGCPGPSL  RKDSSTGGRP  MSPCIQLANR  DCPKADTLL  PVTDSSTSPR
101 LPLAASRVWA  NSASICAFNS  AARASLPKIR  AKVSICFSPL  VRILPLSTVR
151 SMVVAFFANC  SYASAPGPPV  MTS*

```

m042-1/a042-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
m042-1.pep	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
a042-1	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTSPRPLPLAASRVWANSASICAFNS					
a042-1	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSVMVAFFANCYSYASAPGPPVMTSX					
a042-1	AARASLPKIRAKVSICFSPLVRILPLSTVRSVMVAFFANCYSYASAPGPPVMTSX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:

g043.seq
 1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GTCGGCCCAT CAGCACTTTT
 51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GCCTGAACGC TTCgttgaAC
 101 CGTCCCGCGT ggcggtagcc gcaAAAGTGC ATcGCGGCTT GGATGGTGCT
 151 GCCCGATTTC ATGAGGGGcga gcGCGTGTTT CAGCCGCAGG CGGCGCAGGC
 201 GTCCGCGGAC GGTTCGCGCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
 251 CATTCTGTTCA GCCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGGCG
 301 GGCGAATTCG CTGTTCAAAA TATCGGCGGC TTCGTCTATG CGCCGGCGGC
 351 GGTAGCCGTT GTCGTGGCGG CGGAAGGTGA AGCGTAA

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

g043.pep
 1 MVVSNQNIYA VGPSALFHIR RQKSVMPPER FVEPSRVAVA AKVHRGLDGA
 51 ARFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQPD AAGDFGDGQRA
 101 GEFVQNIIGG FVYAPAAVAV VVAAEGEA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 177>:

m043.seq
 1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCTT CAGCACTTCT
 51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
 101 CGTCCCGCGT GCGGCTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT
 151 GCCGATTTCG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAGGC
 201 ATCCGCGGAC GGTTCGCGCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
 251 CATTCTGTTCA GTCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
 301 GGCGAATTCG TGTTCAGGA TGTGCGCGC TTCGTCTATG CGCCGACGGC
 351 GGTAAACGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

m043.pep
 1 MVVSNQNIYA AGPSALLHIR RQKSVMPSE FVEPSRVAVA AKVHGGLDGA
 51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
 101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

m043/g043

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	: : : : : : : : : :					
g043	MVVSNQNIYAVGPSALFHIRRQKSVMPSEFVEPSRVAVAAKVHRGLDGAARFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	: : : : : : : : :					
g043	QPQAAQASGDGFAGLRFEIAFQVAFVQPDAGDFGDGQRAFEFVQNIIGGFVYAPAAVAV					
	70	80	90	100	110	120
	130					
m043.pep	VVAAEGEAQX					
g043	VVAAEGEAAX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

a043.seq
 1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCTT CAGCACTTCT
 51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
 101 CGTCCCGCGT GCGGCTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

242

```

151 GCCGGATTCG ATGAGGGCGA GCGCGTGTTC CAGCCGCAGG CGGCGCAGGC
201 ATCCGGCGAC GGTTCGCGG GTTTGCCTT TGAAATAGCG TTTCAGGTAG
251 CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTCAGGA TGTGCGCGC TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
  1 MVVSNQNIYA AGPSALLHIR RQKSVMPSER FVEPSRVAVA AKVHGGLDGA
  51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
 101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
a043	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	10	20	30	40	50	60
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	70	80	90	100	110	120
m043.pep	VVAAEGEAQX					
a043	VVAAEGEAQX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
  1 ATGCTGCCCC ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGCGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTAGCCCC TTCGATAACG GCGGTCAGCT
 201 CCATGCGGTT GTTGGTGGTT TGCGCTTCGC CGCCGAAAAG TTCTTTTTCG
 251 CGGCTGCCGT AGCGCATTA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
  1 MLPDQSVEFL PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
  51 GAAAPERFQP PDNGQLHAV VGGLRFAAEK PFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
  1 ATGCCGTCCG ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTCCA TGCCATTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTAGCTCC TTCGATGACG GCAGTCAGTT
 201 CCATGCGGTT GTTGGTGGTT TGCGCTTCGC CGCCGAAAAG TTCTTTTTCG
 251 TGGTACCGT AGCGCAyTAa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
  1 MPDQXSVEFF PEVVVFDGLF GGGFPAVALP TVYPVFHAI F DVLRVGADDD
  51 GAAAPERFQS FDDGSQFHAV VGGLRFAAEK PFFVATVAH*

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 185>:

```
a044.seq
1  GTGCCGTCGG ACCAGCGCGT CGAGTCTCTT CCACAAGTCG TCGTTTGTGA
51  CGGGCTGTTT GCGGCGCGGT TTCCAGCCGT TCGCCTTCCA ACCGTGTATC
101 CAGTTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTCAGTCC TTCGATGACG GCGGTCAGTT
201 CCATACGGTT GTTGGTGGTT TCGCCTTCGC CGCCGAAAAG TTCTTTTCG
251 TGGCTGCCGT AGCGCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 186; ORF 044.a>:

```
a044.pep
1  VPSDQRVEFF PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
51  GAAAFERFQS FDDGGQFHTV VGGLRFAAEK FFFVAVAH*
```

m044/a044 91.0% identity over a 89 aa overlap

	10	20	30	40	50	60
m044.pep	MPSDXSVEFFPEVVVFDGLFGGGFPVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS					
	: : : : :					
a044	VPSDQRVEFFPQVVVFDGLFGGGFPVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQS					
	10	20	30	40	50	60
	70	80	90			
m044.pep	FDDGSQFHAVVGGLRFAAEKFFVFATVAHX					
	: : :					
a044	FDDGGQFHTVVGGLRFAAEKFFVAAVAHX					
	70	80	90			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 044 shows 86.5% identity over a 89 aa overlap with a predicted ORF (ORF 044.ng) from *N. gonorrhoeae*:

m044/g044

	10	20	30	40	50	60
m044.pep	MPSDXSVEFFPEVVVFDGLFGGGFPVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS					
	: : : :					
g044	MLPDQSVEFLPQVVVFDGLFGGGFPVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQP					
	10	20	30	40	50	60
	70	80	90			
m044.pep	FDDGSQFHAVVGGLRFAAEKFFVFATVAHX					
	: : :					
g044	FDNGGQLHAVVGGLRFAAEKFFFAAAVAHX					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 187>:

```
g046.seq
1  ATGTCGGCAA TGCTGCGTCC GACAAGCAGC CCGCCGCgcc gCGCCTGTAT
51  GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC gaATATGGAA AGGCTGCCgt TTTcGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TtcgctGGAA CGGACGCGCG
251 CGATCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGagaGCGCG AGcagcaagt cggcatcttC
351 CgcgcggcgG Cgttataatg tgAAGGGGGA TGCGccgttg ccgaAAACGG
401 TTTGGacatc gaggcggctg CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAAcg9 TTACGTCGTT GTTGGTGATG GCGGCAAGGT TTTGCGCGAC
```


501 GGTAGAACCT ACCTGCCCCGT TGCCTAAAAT GAGGATTTTC ACGGTATGGG
551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep

1 MSAMLRPTSS PPRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLVM AARFCATVEP TCPLPKMRIF TVWVAG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAaT CCGC.r.sGC gCGcCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CCGCAACTTT GCAGCGGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep

1 MSAMLRPTSX PXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CCGCAACTTT GCAGCGGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep

1 MSAMLRPTSS PPRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTIRTRSSAKRKT CNAPGQSIRP ASCSVTSCSG LMVSVMPNME					
a046	MSAMLRPTSSPPRRACMMTIRTRSSAKRKT CNAPGQSIRP ASCSVTSCSG LMVSVMPNME					

245

	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
a046	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
a046	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXRXRACMMTIRTRSSAKRKTGNAPGQSIRPASC SVTSCSGLMVSVMPNME					
g046	MSAMLRPTSPFRRACMMTIRTRSSAKRKTGNAPGQSIRPASC SVTSCSGLMVSVMPNME					
	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
g046	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
g046	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

1	ATGGTCATCA	TACAGGCGcg	gcGCGGCGGG	CTGCTTGTCG	GACGCAGCAT
51	TGCCGACATC	GCCCAAGATT	TGCCCGACGG	GGCCGACTGC	CAAATCTGCG
101	CCGTTTACCG	CAACAACCGC	CTCATCGTCC	CCGCGCCGCA	AACCGTCATC
151	ATCGAAGGCG	ACGAAATCCT	GTTTGCCGCC	GCCGCCGAAA	ACATCGGGGC
201	GGTCATACCc	gaATTGCGCC	CCAAAGAAAC	CAGCACC CGC	CGCATCATGA
251	TTGCCGCGCG	CGGCAACATc	tgctACCGCC	TCGCCAAGCA	GCTCGAACAC


```

301 GCATAcacG TCAAAATCAT CGAATGCCGG CCGCGCcgTg ccgaATGGAT
351 AGCCGAAAAC ctcgAcaacA CCCTCGTCCT GCAAGGTTCC Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTatg tCCGCCCTTT TGGCGAAAAA
501 CCTcggcgCG AAGCgcgtca tcggCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGCGGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCACG
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAAC GGAGAACTC
901 ATCCAAGTCA AAATGGGCTT TTTCCGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

g047.pep

```

1  MVIIQARRGG LLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51  IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI CYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLLDNE YIDEIDVFCF
151 LTNDDESIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TGSI LAHIR RGDIVAVHPI RRGTAETEV VAHGDKKTS IIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

m047.seq

```

1  ATGGTCATCA TACAGGCGcG C...syGCGGA sTGCTTGTCG GACGCAGCAT
51  TGCCGACATC GCCCAAGATT TGCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT ATTGCGGCC CGCGCCGAAA ACATCGGCGC
201 GGTCAATCCC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCCGGCGGC GGCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTCGAACACG CATAACAGT yAAAATCATC GAATGCCGGC CGCGCCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTCyTG CAAGGTTCCG
401 CAACCGACGA AACCTGCTC GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GCGGAaAAAC CTCGGCGCGA AGCGCGTCAT CGGCATCGTC AACCGCTCAA
551 GCTACGTCGA TTGCTCGAA GGCAACAAAA TCGACATCGT CGTCTCCCCC
601 CACCTCATCA CCATCGGCTC GATACTCGCC CACATCCGGC GCGGCGACAT
651 CGTTGCGGTC CACCCATCC GGCGCGCAC GCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAAA ACTTCCGCCA TCATCGGCAG GCGCATCAGC
751 GGCATCAAAT GGCCGAAGG CTGCCACATT GCCGCCGTCG TCCGCGCCGG
801 AACCAGCGAA ACCATTATGG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCACAT CATCTTTTTC GTCTCGCGCC GCGCATCCT GAACGAACGT
901 GAAAAACTCA TCCAGGTCAA AATGGGCTTT TTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

m047.pep

```

1  MVIIQARXXG XLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51  IEGDEILFAA AAENIGAVIP ELRPKETQRN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLV LQGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAE IEVVAHGDK TSAIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRLINEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

a047.seq

```

1  ATGGTCATCA TACAGGCGCG GCGCGCGGA CTGCTTGTCG GACGCAGCAT

```



```

51  TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGCGC ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGGCGC
201 GGTACATACC GAATTGCGCC CCAAAGAAAC CAGCACCCGC CGCATCATGA
251 TTGCCGGCGG CGGCAACATC GGCTACCGTC TCGCCAAGCA GCTCGAACAC
301 GCATACAACG TCAAAATCAT CGAATGCCGG CCGCGCCGTG CCGAATGGAT
351 AGCCGAAAC CTGACAACA CCCTCGTCCT GCAAGGTTCC GCAACCGACG
401 AAACCTGCT CGACAACGAA TACATCGACG AAATCGACGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTATG TCCGCCCTTT TGGCGAAAAA
501 CCTCGGCGCG AAGCGCGTCA TCGGCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCACACG
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCCAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGCGACCACA
851 TCATCTTTT CGTCTCGCGC CGGCGCATCC TGAACGAACT GAAAAAECT
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 198; ORF 047.a>:

```

a047.pep
1  MVIIQARRGG LLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51  IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI GYRLAKQLEH
101 AYNVKIECR PRRAEWIAEN LDNTLVLQGS ATDETLLDNE YIDEIDVFCA
151 LTNDDESIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS A IIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRIILNELEK
301 IQVKMGFFG*

```

m047/a047 96.5% identity over a 312 aa overlap

```

              10      20      30      40      50      60
m047.pep      MVIIQARXXGXLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
              |||||  | |||||||
a047           MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m047.pep      AAENIGAVIPELRPKETQRNPXXIMIXGGGNIGYRLAKQLEHAYNVKIECRPRRAEWI
              |||||  : |||  |||||
a047           AAENIGAVIPELRPKETSTR---IMIAGGGNIGYRLAKQLEHAYNVKIECRPRRAEWI
              70      80      90      100     110

              130     140     150     160     170     180
m047.pep      AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESIMSALLAKNLGAKRVIGIV
              |||||
a047           AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESIMSALLAKNLGAKRVIGIV
              120     130     140     150     160     170

              190     200     210     220     230     240
m047.pep      NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK
              |||||
a047           NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK
              180     190     200     210     220     230

              250     260     270     280     290     300
m047.pep      TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRIILNEL
              |||||
a047           TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRIILNEL
              240     250     260     270     280     290

              310
m047.pep      EKLIQVKMGFFGX
              |||||

```


a047 EKLIQVKMGFFGX
300 310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGXLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNQPPXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRAEWI	120
g047	AAENIGAVIPELRPKETSTR---IMIAGGGNICYRLAKQLEHAYNVKIIIECRPRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLDDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLDDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	237
m047.pep	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL	300
g047	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL	297
m047.pep	EKLIQVKMGFFGX	313
g047	EKLIQVKMGFFGX	310

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

```

1  ATGCTCGACA AAGGCGAGGA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTc ggcCCcgTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG
101 CAGGTCGAC CACAGCCACC CGCATGGACA AATTACCCG CCAAATGCTC
151 AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201 cacctGCGAA GccatCGCCG ACAACAAGGC CGTGTAACCTC ATGGCAGTCG
251 GCGGCGCGGC ATACCTCGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCCG AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351 TATGCCCGTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451 TGA

```

This corresponds to the amino acid sequence.<SEQ ID 200; ORF 048.ng>:

g048.pep

```

1  MLDKGELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51  KQTGLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAV YEFVKKMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

```

1  ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTC GGCCCCGTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCGG

```


m048.ppt

a048.seq

a048.pcp

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDF	TNRLIYYVGP	VPDVPVGDE	VVGAGPPTTA	TRMDKFTRQ	MLEQTDLLGMIG
	:					
a048	MLDKGEELPVDF	TNRLIYYVGP	VPDVPVGDE	VVGAGPPTTA	TRMDKFTRQ	MLEQTDLLGMIG
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAI	ADNKAVYLM	AVGGAAYLV	AKAIKSSKVL	AFPELGMEAI	YEFVKKDMPV
	:					
a048	KSERGAATCEAI	ADNKAVYLM	AVGGAAYLV	AKAIKSSKVL	AFPELGMEAI	YEFVKKDMPV
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESI	HATAPRKWQ	AKIGIIPVES	X		
				:		
a048	TVAVDSKGESI	HATAPPQWQ	AKIGIIPVKS	X		
	130	140	150			

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:

250

m048/g048

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDFTNRLIYYVGPVDPVGVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIG					
	: :					
g048	MLDKGEELPVDFTNRLIYYVGPVDPVGVGDEVVGPAGPTTATRMDKFTRQMLKQTLGLGMIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAIADNKAVYLMVAVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPV					
	: :					
g048	KSERGAATCEAIADNKAVYLMVAVGGAAYLVAKAIKSSKVLAFPELGMEAVYEFVVKDMPV					
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
g048	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 205>:

g049.seq

```

1   ATGCGGGCGC AGGCGTTTGA TCAACCGTTC GGTCAGCTCC TGTTCCGACA
51  GGCAGAACAC TTCGCGCCCG TTGACGGCTT TCGGGTTCAG GATATTGATT
101 TGGACGGGCA TCAACGCCTC TTCCGCACCG CCTTCGCCGT TTTCGCAAC
151 CCCGTCTGCC GCCGTACCGG ATTCTGCCGC ATCGGCGTTT TCCCGCCCT
201 CAATCTGTGC GGTTCAAAT TCGGCACTGT CTTTTTGGC ATCGAACCGG
251 ATTCTCCGCC GCGATTTCGAT GTGTTTTTCC GAAAccggca tTGCAGGGA
301 AGCCTgcgcg TTGAGCCAGT TTTCCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCgc tGTTGTGTTT TTCCTGCCAT
401 TTCTTCAGAT ACGCCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 206; ORF 049.ng>:

g049.pep

```

1   MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRL FRTAPAVFRN
51  PVCRRITGFCR IGVFPALNLC GFKFGTVFFG IEPDSPPRFD VFFRNRHLQG
101 SLRVEPVFLK DDHRVGDFDL AAIGNGAVVF FLPLQLIRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 207>:

m049.seq (partial)

```

1   ATGCGGGCGC AGGCGTTTGA TCAGCCGTTC GGTCAGCTCC TGTTCCGACA
51  GGCAGAACAC TTCGCGCCCG TTGACGGCTT TCGGGTTCAG GATATTGATT
101 TGGACGGGCA TCAACGTTTC TTCCGCATCG TTTTCCCGGT TTTCGAAAC
151 CGCCGGCTCA TTCGTGCCGG ATTCTGCCTC GTCGGCGTTT TCCCGCTTT
201 CAATCTGTCC GGTTCAAAT TCGACACTGT CTTTTTGGT ATCAAACCGG
251 ATTCTCCGCC GCGATTTCGAT GTGTTTTTCC GAAACCGACA TTGCAGGGA
301 AGCCTGCGCG TTGAGCCAGT TTTCCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTGTGTTT CTCCTGCCAT
401 TTTTTCAGAT ACGCCTT...

```

This corresponds to the amino acid sequence <SEQ ID 208; ORF 049>:

m049.pep (partial)

```

1   MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRF FRIVFPVFRN
51  RRLIRAGFCL VGVFPFNLNLS GFKFDTVFFG IKPDSPPRFD VFFRNRHLQG
101 SLRVEPVFLK DDHRVGDFDL AAIGNGGIVF LLPFLQIRL...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 209>:

a049.seq

a049.pap

m049/a049 90.6% identity over a 139 aa overlap

m049/g049

		10	20	30	40	50	60
m049.pep		MRAQA	FDPQ	PFGQL	LFGQA	EHFAP	VDGFRVQDIDLDGHQRFFRIVFPVFRNRRLIRAGFCL
g049		MRAQA	FDPQ	PFGQL	LFGQA	EHFAP	VDGFRVQDIDLDGHQRLFRRTAFVFRNPFVCRRTGFPCR
		10	20	30	40	50	60
		70	80	90	100	110	120
m049.pep		VGVF	PAPNL	SGFK	FDTV	FFGI	KPKDSPPRFDVFFRNRLQGSLRVEPVFLKDDHRVGFDFL
		:				:	
g049		IGVF	PAPNL	CGFK	FGT	VFFGI	EPEDSPPRFDVFFRNRLQGSLRVEPVFLKDDHRVGFDFL
		70	80	90	100	110	120
		130	139				
m049.pep		AAIGN	G	G	I	V	FLLPFFQIRL
					:		:
g049		AAIGN	G	A	V	V	FFLPFLQIRLX
					:		:
		130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

```
g050.seq
  1 atgggcgCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGg
 51 cacgcccGAA AAAGccgtgt TGATGGcaaa AGAATCCCTG ATGAGCCACA
101 TCGacatCca aGaATTGCAG GAAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGGtcc
351 TGTCGAactc acgccGCcgc gtgtCGAAGA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

```
g050.pep
  1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
 51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPHT AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVED*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

```
m050.seq
  1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGTATCG GCATCGGCGG
 51 C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GgAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA TGGCCCGATT TGA
```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

```
m050.pep
  1 MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
 51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPHT AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDGPI *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

```
a050.seq
  1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
 51 TACGCCCgAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GGAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA CTGGCCC
```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

```
a050.pep
  1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
 51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPHT AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDWP
```

m050/a050 97.7% identity over a 129 aa overlap

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLS	MSHIDIQELQEKAASGAELSTTEALRLELF				
a050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLS	MSHIDIQELQEKAASGAELSTTEALRLELF				

253

	10	20	30	40	50	60
m050.pep	70	80	90	100	110	120
	EKNVALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
a050	EKNVALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMHSIDIQELQEKAASGAELSTTEALRLLELF					
g050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMHSIDIQELQEKAASGAELSTTEALRLLELF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKNVALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
g050	EKNVALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```

1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACAAACGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCGGA CATGAGCGTG GAAAAGATGG TTAACGAAGG CGTACGCCGC
301 GCCTACACTT GGGAAAGCAA CACCCTGCGC GCTTCGGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCACA
401 TGAGCATCGT GCGGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAAATC CAAACTCGCT ATGCTCAACC CTTCGGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACGATGGGC GCGGGCTGGT
551 GTCTCCCGG CATCTTGGGC ATCGGCATCG GCGGCACgC. CGAAAAAGCC
601 GTGTTGATGG cgaAAGAATC CCTGATGAGC CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAGA GTCAACGCGC TGGGCATCGG CGCGCAAGGC
751 TTGGGCGGTG TGACCACCGT GTTGGACGTG AAAATCCTCG ATTACCGGAC
801 CCATGCCGCC TCCAAACCGA TTGCCATGAT TCCCAACTGT GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GTCCTGTCGA ACTCAGCCG
901 CCGCGCGTCG AAGACTGACC CGATCTGACT TACAGCCCGC ACAACGGCAA
951 ACGCGTCGAT GTCGATAAGC TGACCAAAGA AGAAGTGCCA AGCTGGAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCGG CCGCGATGCC
1051 GCGCACAAAC GCCTCGTCAA TATGCTCGAC AAAGGCGAGG AGTTGCCCGT
1101 CGATTTCACC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCG
1151 GCGATGAAGT CGTCGGTCCC GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTTACCC GCCAAATGCT CAAACAAACC GGCCTCTTGG GCATGATCGG

```



```

1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGTACCT CATGGCAGTC GCGGCGCGCG CATACCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCG GAATTGGGTA TGGAAAGCCGT
1401 TTACGAATTT GAAGTCAAAG ATATGCCCGT AACCGTCGCC GTGGACAGCA
1451 AAGGGGAATC CATCCACGCC ACCGCCCGCG GCAATGGCA GGCAGAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYVHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVGM DVQWDADMSV EKMVNEGVR
101 AYTWEGNTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSENSKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQQ
251 LGGLTTLVDV KILDYPTTHA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVED*PDLT YSPDNKGRVD VDKLTKEEVA SWKTGVDLLL NGKILTRDA
351 AHKRLVNMLD KGEELPVDFE NRLIYVGPV DPVGDEVVGP AGPTTATRMD
401 KFTRQMLKQT GLLGMIGKSE RGAATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAVYEF EVKDMPTVTA VDSKGESIHA TAPRKWQAKI
501 GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir||B44511 fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11  QSIDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAENNRPICQDTG 70
          Q+ DA + H K L+ E + K Q L NS + A+ P CQDTG
Sbjct: 53  QAFHDASFMLRPAHQKQVAAIILHDPEASEND---KYVALQFLRNSEIAAKGVLPCTCQDTG 109

```

```

Query: 71  IATVFLKVGM DVQWDADMSVEKMVNEGVRRAITWEGNTLRASVLADPAGKRQNTKDNTPA 130
          A + K G V W E+ +++GV Y E N + A K NT N PA
Sbjct: 110 TAIIVGKGRQV-WTGGGD-EETLSKGVYNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131  VIHMSIVPGGKVEVTCAAKGGGSENSKSL-----AMLNPSDNIVDWVLKTIPTMGAGWCP 185
          I + V G + + C AKGGGS NK+ L A+L P + +++++ + T+G CP
Sbjct: 167 QIDLYAVDGDGEYKFLCVARGGGSANKTYLYQETKALLTPG-KLKNFLVEKMRTLGTAAACP 225

```

```

Query: 186  PXXXXXXXXXTPKAVLMAKESLSHIDIQELQEKAAASGAELSTTEALRLELFEKVNXXX 245
          P T + L + +H EL + + L EL E+
Sbjct: 226 PYHIAFVIGGTSATNLKTVKLASAHY-YDELPTGNEHGQAFRDVQLEQELLEEAQKLG 284

```

```

Query: 246  XXXXXXXXXXXTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGS-----PVELTPP 301
          D++++ P H AS P+ M +C+A R+++ +++ G +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSCSADRNIKAKINREGIWIEKLEHNP 343

```

```

Query: 302  RVEDXPDLTYSPDNKGRVDVDKLTKE---EVASWKTGVDLLLNGKILTRDAAHKRLVNM 358
          + +VD+++ KE +++ + L L G I+ GRD AH +L +
Sbjct: 344 QYIPOELRQAGEGEAVKVDLNRPMKEILAQLSQYPVSTRLSLTGTIIVGRDIAHAKLKE 403

```

```

Query: 359  LDKGEELPVDFTNRLIYXXXXXXXXTTATRMDKFTQMLKQTGLLGMIGK 418
          +D G+ELP + IYY TTA RMD + + G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPYIYAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGSMIMLAK 463

```

```

Query: 419  SERGAATCEAIADNKAVYLMVGG-AAYLVAKAIKSSKVLAFPELGMEAVYEFVVDMPV 477
          R +A + YL ++GG AA L ++IK + +A+PELGMEA+++ EV+D P
Sbjct: 464 GNRSQVTDACHKHGGFYLGSIIGGPAVLAQOSIKHLECVAYPELGMEAIWKIEVEDFPA 523

```

```

Query: 478  TVAVDSKG 485
          + VD KG
Sbjct: 524 FILVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATT TCGATGCCTT
51  CCAATTCTATC AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCTGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGTGCA ACAGCCGTAT GTGTGCGGAA AACAAACGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCTCAA AGTCGGTATG AACGTCCAAT
251 GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCGC

```



```
301 GCCTACACTT GGAAGGCAA TACGCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCATA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAAATC CAAACTCGCC ATGCTCAATC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACCATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTTGGGT ATCGGCATCG GCGGCACGCC CGAAAAAGCC
601 GTGCTGATGG CAAAAGAGTC CCTGATGAGC CACATCGACA TTCAAGAATT
651 GCAGGAAAAG GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAATC CTTGAAAAA GTCAACGCGC TGGGCATCGG CGCACAAGGC
751 TTGGGCGGAC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTATCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCGGAATGCG GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTCGA ACTCAGCCCG
901 CCGCGCGTCG AAGACTGGCC CGATTGACT TACAGCCCGC ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAGA AGAAGTGCCA AGCTGGAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CCGCATGCCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCAAC AAAGGCGAAG AATTGCCCGT
1101 CGATTTCACC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCG
1151 GCGATGAAGT CGTCGGTCCG GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGTGG CCACCTCGGA AGCCATCGCC GACAACAAAG
1301 CCGTGACCT CATGGCAGTC GCGGCGCGCG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGCTTCCCC GAATTGGGCA TGGAGCCAT
1401 TTACGAATT GAAGTCAAAG ACATGCCCGT AACCGTCGCG GTAGATAGCA
1451 AAGGCGAATC CATCCAGGCC ACCGCCCGCG GCAATGGCA GCGGAAAATC
1501 GGCATCATCC CCGTCGAATC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pep

```
1  MTVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVM NVQWDADMSV EEMVNEGVR
101 AYTWEQNTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSEKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGGTPEKA
201 VLMAKESIMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQG
251 LGGLTTVLVDV KILDYPTHA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVEDWPDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLL NGKILTGRDA
351 AHKRLVDMLN KGEELPVDFE NRIYYVGPV DPVGDVVGVP AGPTTATRMD
401 KFTRQMLEQT DLLGMIGKSE RGVATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKDMPTVTA VDSKGESHA TAPRKWQAKI
501 GIIPVES*
```

m050-1/g050-1 98.2% identity in 507 aa overlap

m050-1.pep	10	20	30	40	50	60
m050-1.pep	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
g050-1	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
m050-1.pep	70	80	90	100	110	120
m050-1.pep	NNRPICQDTGIATVFLKVMNVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK					
g050-1	NNRPICQDTGIATVFLKVMNVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK					
	70	80	90	100	110	120
m050-1.pep	130	140	150	160	170	180
m050-1.pep	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGSEKSKLAMLNPSDNIVDWVLKTIPTMG					
g050-1	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGSEKSKLAMLNPSDNIVDWVLKTIPTMG					
	130	140	150	160	170	180
m050-1.pep	190	200	210	220	230	240
m050-1.pep	AGWCPPGILGIGIGTPEKAVLMAKESIMSHIDIQELQEKAASGAELSTTEALRLELFEK					
g050-1	AGWCPPGILGIGIGTPEKAVLMAKESIMSHIDIQELQEKAASGAELSTTEALRLELFEK					
	190	200	210	220	230	240
m050-1.pep	250	260	270	280	290	300
m050-1.pep	VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSVPVELTP					
g050-1	VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSVPVELTP					
	250	260	270	280	290	300

256

	310	320	330	340	350	360
m050-1.pep	PRVEDWPDLT	YSPDNGKRV	VDKLTKEE	VASWKTGD	VLLNGKIL	TGRDAAHKRLV
g050-1	PRVEDXPDLT	YSPDNGKRV	VDKLTKEE	VASWKTGD	VLLNGKIL	TGRDAAHKRLV
	370	380	390	400	410	420
m050-1.pep	KGEELPVDF	TNRLIYYV	GPVDPVG	DEVVGPAG	PTTATRMD	KFTRQMLEQT
g050-1	KGEELPVDF	TNRLIYYV	GPVDPVG	DEVVGPAG	PTTATRMD	KFTRQMLEQT
	430	440	450	460	470	480
m050-1.pep	RGVATCEAI	ADNKAVYLM	AVGGAAYL	VAKAIKSS	SKVLAFPE	LGMEAIYEF
g050-1	RGVATCEAI	ADNKAVYLM	AVGGAAYL	VAKAIKSS	SKVLAFPE	LGMEAIYEF
	490	500				
m050-1.pep	VDSKGESIH	ATAPRKWQ	AKIGIIPV	ESX		
g050-1	VDSKGESIH	ATAPRKWQ	AKIGIIPV	ESX		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

a050-1.seq

1	ATGACCGTCA	TCAAACAGGA	AGACTTTATC	CAAAGCATT	TTCGATGCTT
51	CCAATTCATC	AGCTACTACC	ATCCCAAAGA	CTACATCGAC	GCGCTTTATA
101	AGGCGTGGCA	GAAGGAAGAA	AACCCCGCCG	CCAAAGACGC	GATGACGCAG
151	ATTTTGGTCA	ACAGCCGCAT	GTGTGCCGAA	AACAACCGCC	CCATCTGCCA
201	AGATAACCGT	ATCGCGACCG	TGTTTTTGAA	AGTCGGTATG	GATGTGCAAT
251	GGGATGCAGA	CATGAGCGTC	GAAGAGATGG	TTAACGAAGG	CGTGCGCCGC
301	GCCTACACTT	GGGAAGGCAA	TACGCTGCGC	GCTTCCGTTT	TCGCCGACCC
351	CGCCGGCAAA	CGCCAAAATA	CCAAAGACAA	CACGCCCGCC	GTCATCCATA
401	TGAGCATCGT	GCCGGGCGAC	AAAGTCGAAG	TAACCTGCGC	GGCAAAAGGC
451	GGCGGTTCTG	AAAACAAATC	CAAACCTGCG	ATGCTCAACC	CTTCCGACAA
501	CATCGTCCAT	TGGGTATTGA	AAACCATTC	GACCATGGGC	GCGGGCTGGT
551	GTCCTCCGGG	CATCTTGGGC	ATCGGCATCG	GCGGTACGCC	CGAAAAAGCC
601	GTGTTGATGG	CGAAAGAATC	CCTGATGAGC	CACATCGACA	TCCAAAGAAT
651	CCACGCAAAA	GCCGCGTCCG	GCGCGGAATT	GTCCACCACC	GAAGCCCTGC
701	GCCTCGAACT	CTTTGAAAAA	GTCAACGCGC	TAGGCATCGG	CGCGCAAGGC
751	TTGGGCGGTC	TGACCACCGT	GTTGGACGTG	AAATCCTCG	ATTACCCGAC
801	CCACGCGGCC	TCCAAACCGA	TTGCCATGAT	TCCGAACATG	GCCGCCACCC
851	GCCACGTCGA	ATTTGAATTG	GACGGCTCAG	GCCCTGTGCA	ACTCAGCCCG
901	CCGCGCTCGC	AAGACTGGCC	CGATTGACT	TACAGCCCGC	ACAACGGCAA
951	ACGCGTCCAT	GTCGACAAGC	TGACCAAGA	AGAAGTGGCA	AGCTGAAAAA
1001	CCGCGGACGT	ATTGCTGTTG	AACGGCAAAA	TCCTACCCGG	CCGCGATGCC
1051	GCACACAAC	GCCTCGTCGA	TATGCTCGAC	AAAGCGGAAG	AATTGCCCGT
1101	CGATTTCACC	AACCGCCTGA	TTTACTACGT	CGGCCCGGTC	GATCCGGTCG
1151	GCGACGAAAT	CGTCGGCCCA	GCAGGTCCGA	CCACCGCCAC	CCGCATGGAC
1201	AAATTCACCC	GCCAAATGCT	CGRACAAACC	GACCTCTTGG	GCATGATCGG
1251	CAATCCGAG	CGCGGCGCGG	CCACCTGCGA	AGCCATCGCC	GACAACAAAG
1301	CCGTGTACCT	CATGGCAGTC	GCGGCGCGG	CGTATCTCGT	GGCAAAAGCC
1351	ATCAAACTCT	CCAAAGTCTT	GGCGTTCGCC	GAATTGGGCA	TGGAAGCCAT
1401	TTACGAATTT	GAAGTCAAA	ACATGCCCGT	AACCGTCCGC	GTAGACAGCA
1451	AAGCGGAATC	CATCCACGCC	ACCGCCCGC	CCCAATGGCA	GGCGAAAAAT
1501	GGCATCATCC	CCGTCAAATC	TTGA		

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

a050-1.pep

1	MTVIKQEDFI	QSICDAFQFI	SYHPKDYID	ALYKAWQKEE	NPAAKDAMTQ
51	ILVNSRMCAE	NNRPICQDTG	IATVFLKVGM	DVQWDADMSV	EEMVNEGVRR
101	AYTWEGNTLR	ASVLADPAGK	RQNTKDNTPA	VIHMSIVPGD	KVEVTCAAKG
151	GGSENKSKLA	MLNPSDNIVD	WVLKTIPTMG	AGWCPPGILG	IGIGGTPEKA
201	VLMAKESLMS	HIDIQELQEK	AASGAELSTT	EALRLELFEK	VNALGIGAQQ
251	LGGTLTVLDV	KILDYPHAA	SKPIAMIPNC	AATRHVEFEL	DGSGPVELTP
301	PRVEDWPDLT	YSPDNGKRV	VDKLTKEEVA	SWKTGDVLLL	NGKILTGRDA
351	AHKRLVMDLD	KGEELPVDF	NRLIYYVGPV	DPVGDEIVGP	AGPTTATRMD
401	KFTRQMLEQT	DLGGMIGKSE	RGAAATCEAIA	DNKAVYLMVAV	GGAAYLVAKA
451	IKSSKVLAF	ELGMEAIYEF	EVKDMPVTVA	VDSKGESIHA	TAPPQWQAKI
501	GIIPVKS*				

a050-1/m050-1 98.4% identity in 507 aa overlap

a050-1.pep	10	20	30	40	50	60
	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
m050-1	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
a050-1.pep	70	80	90	100	110	120
	NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK					
m050-1	NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK					
	70	80	90	100	110	120
a050-1.pep	130	140	150	160	170	180
	RQNTKDNTPAVIHMSIVPGDKVEVTC AAKGGGSENKSKLAMLNPSDNIVDWLKTIPMTG					
m050-1	RQNTKDNTPAVIHMSIVPGDKVEVTC AAKGGGSENKSKLAMLNPSDNIVDWLKTIPMTG					
	130	140	150	160	170	180
a050-1.pep	190	200	210	220	230	240
	AGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLLEFEK					
m050-1	AGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLLEFEK					
	190	200	210	220	230	240
a050-1.pep	250	260	270	280	290	300
	VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP					
m050-1	VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP					
	250	260	270	280	290	300
a050-1.pep	310	320	330	340	350	360
	PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLD					
m050-1	PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN					
	310	320	330	340	350	360
a050-1.pep	370	380	390	400	410	420
	KGEELPVDFTNRLIYYVGPVDPVGVDEIVGPAGPTTATRMDFTRQMLEQTDLLGMIGKSE					
m050-1	KGEELPVDFTNRLIYYVGPVDPVGVDEVVGPAGPTTATRMDFTRQMLEQTDLLGMIGKSE					
	370	380	390	400	410	420
a050-1.pep	430	440	450	460	470	480
	RGAAATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA					
m050-1	RGVATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA					
	430	440	450	460	470	480
a050-1.pep	490	500				
	VDSKGESIHATAPQWQAKIGIIPVKSX					
m050-1	VDSKGESIHATAPRKWQAKIGIIPVESX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

g052.seq

```

1  ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
51  CTGCGAGCCG ACGGCGGACA GCAGGCTGTT GTCCACCAACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCGGA
251 TGCCGAATTT GGTACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 224; ORF 052.ng>:

g052.pep


```

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
101 RLRLETTWSP ACRKVKNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

```

m052.seq
1 ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCATTTA TATCAGTCGG CGACACGGG CTCACTCCGA
251 TGCCGAATTT GGTAAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCG GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

```

m052.pep
1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
101 RLRLETTWSP ACRKVKNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

```

a052.seq
1 ATGGCTTTGG TCGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC
151 AAGGGATTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCGTTTA TATCAGTCGG CGACACGTGA CTCACTTCGA
251 TGCCGAATTT GGTAAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCG GCCTGCAAAA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

```

a052.pep
1 MALVAEETEI SAPCFKG*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP
51 KGLDGVSKNS SLVLALTAAF HSFISVGD* LTSMPLVTM LLIKPTVVPN
101 RLRLEITWSP ACKKVKNAA*

```

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
a052	MALVAEETEI SAPCFKGXCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m052.pep	SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLLETTWSPACRKVKNAAX					
a052	SLVLALTAAFHSFISVGDXTLTPMPNLVTMLLIKPTVVPNRLRLLEITWSPACKKVKNAAAX					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

m052/g052

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					


```

g052      MALVAETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANSASAKSKSATSPKGLDGVSKNS
           10      20      30      40      50      60
           70      80      90      100     110     120
m052.pep  SLVLALTAAFHSFISVGDTWLTSMPNLATMLLIKPTVVPNRLRLEITWSPACKVKVNAAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g052      SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX
           70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073.seq
1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
51  TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AGTCCGGGGC GGataccGGC GCGGAGTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAAAAGAGT TCCACGACTT TCCACGCGGC TGCTTGGTCG
301 GCGACTTCAA AACCGATGAC GATGCCGCCG CCGTTTGTCT GTTTGCGGAT
351 AAGCTCCGCC TCGGATGGT CGGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073.pep
1  MCMPIAIRVS DGICRIFFPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
51  SPGRIPAAFS SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAAWS.
101 ATSKPMTMPP PFCCLRISSA CWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073.seq
1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
51  GCCGTCTGAA ACACGCAATC AGCGTGCGAG TGCCTGTTTC AAATCGTCAA
101 TCAAATCGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151 CGGATGTTGG CCGCGAGTTT TTCTTCGGGC TGCATCCTGC CGTGCGTGGT
201 TGTCCACGGG TGGTAATGG TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251 GGGAAAAGAG TTCCACGCCG TCCACAACTT TCCACGCCGC TTCTTGATCG
301 GCAACTTCAA AGCCGATGAC GATGCCGCCG CCGTTTGTCT GTTTGCGGAT
351 AAGCGCCGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073.pep
1  MCMPIKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
51  RMLAASFSSG CILPCVVH WVMVERTSPR LAVREKSSTP STTFHAASXS
101 ATSKPMTMPP PFCCLRISSA XGWSNPNV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073.seq
1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
51  TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AATCCGGGGC GGATGTTGGC GCGGAGTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301 GCTTGGTCGG CGACTTCAA GCGGATGACG ATGCCGCCGC CGTTTGTCTG
351 TTTGCGGATA AGCTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073.pep
1  TCMSYKIRVS DGICGVFFPM PSEXRNQRAS ACFKSSIKSP TYSKPTDRRT
51  NPGRMLAASF SSGCILPCVV VHGWVMVERT SPRLAVREKS STPSTTFHAA
101 AWSATSKPMT MPPPFCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

260

	10	20	30	40	50
m073.pep	MCMPYKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVHGWVVERTSPRLAVREKSSTPTTFHAASXSATSKPMTMPPPFCLLRI				
a073	SSGCILPCVVHGWVVERTSPRLAVREKSSTPTTFHAAAWSATSKPMTMPPPFCLLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSGNPVX				
a073	SSAXGWSGNPVX				
		130			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPYKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
g073	MCMPYAIRVSDGICRIFPPMPSETRNQRASACFKSSIKSPTYSKPTDRRTSPGRIPAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVHGWVVERTSPRLAVREKSSTPTTFHAASXSATSKPMTMPPPFCLLRI				
g073	SSGCILPCVVHGLVMVERTSPRLAVREKSST---TFHAAAWSATSKPMTMPPPFCLLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSGNPVX				
g073	SSACGWSGNPVX				
		120			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCCTT ACTTCATCAC CCTCTTAACG ATGGAATA CAAAAAGCGC
51  GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTT GCGTTTCGG GCAACGCTGC GTTGCCTGT
151  GCCGCCAAAG CCAGCGGGGC GGCTGTACA ACAGCCAGTT TTGCGCCGTA
201  TTTACGGCAG GTGTTAATAA ATTTATGAT ATTTTCCTTT ACGAAATTTT
251  TAAAAAATG TGTTCGGGG CTTGTGAAG GTTTAGAGA CCGCTGCCG
301  GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAAA ATTACAAATT
351  CCCCCTAT CTCTTCAAT GCCGAGCTAA AAGCGTCTC ATAGCTGTCA
401  TATTACCGG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFILLT MENTKSAKT PTTIQASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAATV TASFAPYLRL VLI NFMI FSF TKFLKKVCG LCEGFRDLRLP
101 GLLNLIFFFV ESENYKFPAY LFQCRKSVF IAVIFTG*

```


1	ATGCCGTCTT	ACTTCATCAC	TCTCTTAACG	ATGGAAAATA	CAAAAAGCGC
51	GGCGAAAATG	CCCACTACAA	TCCAACCGGC	TTCCATACCG	TCCGCTTTTG
101	CGGCTTCCAA	AGCGTTTTTT	GCCGTATCGG	GCAACGTTGC	ATTTGCGATGT
151	GCGGCCAAAG	CCAGGGGAGC	AGCTGTTACA	ACAGCCAGTT	TTGCGCCGTA
201	TTTACGGCAG	GTGTTAATAA	ATTTTCATGAT	ATTTTCCTTC	AAAAAGTGTT
251	TGGCGGTAAT	GGATGGAGCG	TTTTTCAGAC	GACCGCCGAA	CATCCGAAAA
301	TCAGTCTTTC	AAAAATCCGA	ATACGACAAA	TTCGTATTGG	TTGCCGATTT
351	CTTCCAAACC	TGCGTTAATC	GCTTCTTCGA	AGTCGTAGAA	ATAATCGGCA
401	TTGGTGATTA	A			

1 MPSYFITLLI MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51 AAKARGAAVT TASFAPYLRL VLINFMISF KKCLAVMDGA FRRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVEE IIGIGD*

m075/g075

```

      10      20      30      40      50      60
m075.pep  MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAGAAVT
          |||||||||||||||||||||||||||||||:|||||
g075      MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAGAAVT
          10      20      30      40      50      60

      70      80      90      100     110
m075.pep  TASFAPYLQVLINFMIFSF---KKCLAVMDGAFFRPPNIRKSVFQKSEYDKFVLVAD
          ||||||||||||||||| |||: : :| |::: :| |::: :|
g075      TASFAPYLQVLINFMIFSFTKFLKKVCVGLCEGFRDRLPGLNLNLIFFVFESENYKFPAY
          70      80      90      100     110     120

      120     130
m075.pep  FFQTCVNRFFEVEIIGIGDX
          :|| :: | : |
g075      LFQCRASVFIIVFTGX
          130

```

1	ATGCCGCTCTT	ACTTCATCAC	TCTCTTAACG	ATGGAAAAGA	CAAAAAGCGC
51	GGCGAAAACG	CCCCTACAA	TCCAACCGGC	TTCCATACCG	TCCGCTTTTG
101	CGCGCTCCAA	AGCGTTTTTT	GCTGTATCGC	GCAACGTTCG	ATTTGCATGT
151	CGCGGCCAA	ACAGGGGAGC	AGCTGTTACA	ACAGCCAGTT	TGGCCCGGTA
201	TTTACGGCAG	GTGTTAATAA	ATTTCATGAT	ATTTTCCTTC	AAAAAGTGT
251	TGGCGGTAAT	GGATGGAGCG	TTTTTCAGAC	GACCGCCGAA	CATCCGAAAA
301	TCAGTCTTT	AAAATCCGA	ATACGACAAA	TTCGTATTGG	TGCGCGATTT
351	CTTCCAAACC	TGCGTTAATC	GCTTCTTCGA	AGTCGTAGAA	ATAATCGGCA
401	TTGGTGATTA	A			

1 MPSYFITLLT MEKTKSAAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51 AAKARGAAVT TASFAPYLRL VLINEMIFSF KKCLAVMDGA FFRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVVE IIGIGD*

m075/a075 98.5% identity over a 136 aa overlap

	10	20	30	40	50	60
m075.pep	MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
a075	MPSYFITLLTMEKTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m075.pep	TASFAPYLRLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLRLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
	130					
m075.pep	CVNRFFEVEIIGIGDX					
a075	CVNRFFEVEIIGIGDX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

```

g080.seq
1  ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAAGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA TACGGTTGAG
301 GTCGTCCTGA CCGAGCGCAA GCCGTTGCGA CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAA TGTCGTTTTG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACgAGA TGAAACGCCT CCgGCTTTTT
601 ACcgaAGCGT GGCAGCATCT gttgcGTAAG AATAAAAAAT GGTTATCCTA
651 TGTGGATATG Aggtataagg acggatttTC agtcccccat gctCCCGACG
701 GTTTACCCGA AAAAGAATcc gAAGAAATatt gggaaacaggt ttgggacata
751 ttacggcctg gcgtcggaaa cggttcgacg caaatatcaa tcagttatAA
801 GGGCAGacga acaatggaac AGcagtaa
  
```

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

```

g080.pep
1  MWDNARAMER LTRWLLVMM MLLAASGLVW FYN SNHLPVK QVSLKGNLVY
51  SDKKALGSLA KEYIHGNILR TDINGAQEAY RRY PWIASVM VRRRFPD TVE
101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RGPMPVFRGA EG TSAEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARSAWNVL DNGITVRLGR ENEMKRLRLF
201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVPH APDGLPEKES EEYWEQVWDI
251 LRPGVGNGST QISISYKGRR TMEQQ*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

```

m080.seq
1  ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGACATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
301 GTCGTCCTGA CCGAGCGCAA GCCGTTGCGG CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTTG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
  
```


601 ACCGAAGCGT GGCAGCATCT GTTTCGTAAA AATAAAAATC GGTTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTTCCGACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep
 1 MWDNAEAMER LTRWLLVMMA MLLAASGLVW FYNSNHLVPK QVSLKGNLVY
 51 SDKKTGLSLA KEYIHGNILR TDINGAQEAY RRPWIASVM VRRRFPDTVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES EE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng) from *N. gonorrhoeae*:

m080/g080

	10	20	30	40	50	60
m080.pep	MWDNAEAMERLTRWLLVMMA MLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKTGLSLA					
080	MWDNAEAMERLTRWLLVMMA MLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKTGLSLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m080.pep	KEYIHGNILRTDINGAQEAYRRPWIASVMVRRRFPDTVEVVLTERKPVARWGDHALVDG					
080	KEYIHGNILRTDINGAQEAYRRPWIASVMVRRRFPDTVEVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m080.pep	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m080.pep	DNGITVRLGRENEMKRLRLFTEAWQHLLRK NKNRLSYVDMRYKDGFSVRYASDGLPEKES					
080	DNGITVRLGRENEMKRLRLFTEAWQHLLRK NKNRLSYVDMRYKDGFSVRYASDGLPEKES					
	190	200	210	220	230	240
m080.pep	EE*					
080	EEYWEQVWDILRPGVNGSTQISISYKGRRTMEQXX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq
 1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
 51 CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
 101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTAGTTTAT
 151 TCCGATAAGA AAGCATTGGG CAGTTGGCG AAAGAATACA TCCATGGGAA
 201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
 251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
 301 GTCCTCTGA CCGAGCGCAA GCCGTCGCG CGTTGGGGCG ACCATGCCTT
 351 GGTGGACGGC GAAGCAATG TTTTGAAGC CCGTTGGAC AGACCCGGAA
 401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCGT
 451 TATGACGAAT TTTGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTGCTTTT GACAACGGCA

551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
 601 ACCGAAGCGT GGCAACATCT GTTGCCTAAA AATAAAATC GGTATACCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTC AGTCCGCTAT GCTCCCACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep

1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNSNHLPVK QVSLKGNLVY
 51 SDKKALGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE
 101 VVLTERRKPA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAQHLLRK NKNRLSYVDM RYKDGFSVRY APDGLPEKES EE*

m080/a080 99.2% identity over a 242 aa overlap

m080.pep	10	20	30	40	50	60
	MWDNAEAMERL LTRWLLVMMAMLLAASGLVWFYNSNHLPVKQVSLKGNLVYSDKKTLGSLA					
a080	MWDNAEAMERL LTRWLLVMMAMLLAASGLVWFYNSNHLPVKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
m080.pep	70	80	90	100	110	120
	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDVEVVLTERRKPVARWGDHALVDG					
a080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDVEVVLTERRKPVARWGDHALVDG					
	70	80	90	100	110	120
m080.pep	130	140	150	160	170	180
	EGNVFEARLD RPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
a080	EGNVFEARLD RPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
	130	140	150	160	170	180
m080.pep	190	200	210	220	230	240
	DNGITVRLGRENMKRLRLFTEAQHLLRK NKNRLSYVDMRYKDGFSVRYASDGLPEKES					
a080	DNGITVRLGRENMKRLRLFTEAQHLLRK NKNRLSYVDMRYKDGFSVRYAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
 51 GCCGTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA
 101 TTCGGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG
 151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GGCGCGGGCG CGGTTGTGGT
 201 TTCGCGCGAA GATTGCGCGG CTTTGGGCGG CGCGTTGAAA GTCGATGACA
 251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC
 301 CCGTTTGTGT TCGGCATTAC CGGTTCCGGC GGCAAGACGA CGGTGAAGGA
 351 GATGCTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATGAT GCCGTTTCGG
 401 CGACGGCAGG CAACTTCAAC AACCACAtcg gaTTGCCGCT GACTTTATTG
 451 AAATtaaaAcg aAAAAACCCG CTATGCCGTG ATTGAAATGG GCATGAACCA
 501 TTTTGGcgaa ctggcggtTt taacgcaaaT CGCCAAACCC GATGCCGCTT
 551 TGGtcaACAA CGCCCTGCGC GCCCATGTCG GATGCGGTTt cgacggagtg
 601 GGCGATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTcAGA
 651 CGGCATGGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
 701 CCGCAACGTT TAATTTGAAT ACGTGCACTT TCGGCGTCGA TAGCGGCGAT
 751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTTGATT


```

801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAATCCC GACAGTATGA AAGCCCGCGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG CATTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagtcgGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTGAGCC ACGATTGGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGAtggaAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

g081.pep

```

1 MKPLDLNFIC QALKLPMPSE NKPVSRIVD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNALR AHVCGGFDGV
201 GDIKAKSEI YAGLCSDGMA LIPQEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFDLVCG DERTAVVLPV PGRHNHVNAA AAAALALAAG
301 LSLNDVAEGL QGFSNIKGR LNVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMGELGED EAAAMHAEVG AYARDQIEA AYFVGDNSVE
401 AAEKFGADGL WFAAKDPLIQ VLSHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

m081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCT GGTGCGGCGG CGGTGTGTTG
201 TTCGCGCGAA GATTGTGCTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGGCAAAGG CGTGGCGTGA AAATGTGAAT
301 CGTTTGTGTG TCGGCATTAC CGGTTCCGGC GGCAAGACGA CGGTGAAGGA
351 AATGTGGCTG GCGGTATTGC GCCGCCGTTT CGGCGATGAT GCCGTGTTGG
401 GACGCGCAGG CAACTTCAAC AACCATATCG GATTGCCGCT GACTTTGTTG
451 AAGTTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTCGCGGAA CTGGCGGTTT TAACGCAmAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCT GCTGCGGTTT CGACGGAGTG
601 GCGGATATTG CCAAAGCGAA AAGCGAGATT TACCAAGGTT TATGTTTCAA
651 CCGCATGCA CTGATTCTCT AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTTCACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTGATTT
801 GGTGTGCGGC GATGAGCGCG CCGCCGTGGT GCTGCCTGTT CCCGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAAGTG GCGGAGGACG AAGCCGCCGC TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCC CGACCAAGGC ATCGAAGCGG CTATTTTGTG CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGGCGCG GACGGTTTGT GGTTCCGCCG
1251 CAAAGACCCG TTGATTCAAG TGTGCGCCA CGATTGCCCC GAACGCGCCA
1301 CCGTGTGGT GAAAGGTTCT CGCTTTATGC AGATGGAAGA AGTGGTCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

m081.pep

```

1 MKPLDLNFIC QALKLPMPSE SKPVSRIVD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLAA GAAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTXIAKP NAALVNNAMR AHVCGGFDGV

```


201 GDIKAKSEI YQGLCSDGIA LIQEDANMA VFKTATLNLN TRTFGIDSGD
 251 VHAENIVLKP LSCEFDLVCG DERAADVLPV PGRHNVHNA AAAALALAAG
 301 LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAIDVL
 351 ARMPAPRIFV MGD MGELGEL GEDEAAAAMHA EVGAYARDQG IEAAYFVGDN
 401 SVEAAEKFGA DGLWFAAKDP LIQVLRHDL PERATVLVKGS RFMQMEEVVE
 451 ALEDK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 081 shows 94.1% identity over a 455 aa overlap with a predicted ORF (ORF 081.ng)
 from *N. gonorrhoeae*:

m081/g081

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLPMPSESKPVSRIVTDSDIRAGDVFFALAGERFDAHDFVEDVLAA					
g081	MKPLDLNFICQALKLPMPSENKPVSRIVTDSDIREGDFVFFALAGGRFDAHDFVGGVLSA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
g081	GAAAVVVSREDCAALGGALKVDDTLAALQTLAKAWRDNVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNKHYAVIEMGMNHFGE LAVLTXIAKP					
g081	AVLRRRFGDDAVSATAGNFNNHIGLPLTLLKLNKHYAVIEMGMNHFGE LAVLTQIAKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAHRAHVCGFDGVDIAKAKSEIYQGLCSDGIALIPQEDANMAVFKTATLNLN					
g081	DAALVNNAHRAHVCGFDGVDIAKAKSEIYAGLCSDGMALIPQEDANMAVFKTATFNLN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKLPSCEFDLVCGDERAAVLPVPGRHNVHNA AAAALALAAG					
g081	TCTFGVDSGDVRAENIVLKLPSCEFDLVCGDERTAVVLPVPGRHNVHNA AAAALALAAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFSNIKGR LNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
g081	LSLNDVAEGLQGFSNIKGR LNVKAGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
g081	MGDMGELGE--DEAAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGS RFMQMEEVVEALEDKX					
g081	LIQVLSHDLPERATVLVKGS RFMQMEEVVEALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

a081.seq

```

1   ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGGCG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGTTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTGG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GCGGATATTG CCAAGCGCAA AAGCGAGATT TATCAAGGCT TATGTTTCAA
651 CGGCATGGCG CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCCACGCGG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC AACGAGTGCG CAGCGTGGT TCTGCCCGTT CCCGCGCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTAAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCGC CCATGCACGC CGAAGTCGGC GCGTACGCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGCGCC ACGATTGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAGGTTT CCGCTTTATG CAGATGGAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

a081.pep

```

1   MKPLDLNFIC QALKLMPSE SKPVSRIVTD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLAA GAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNFN NHIGLPLTLL
151 KLNKHHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNAMR AHVCGGFDGV
201 GDIKAKSEI YQGLCSDGMA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFDLVCG NECAAVVLPV PGRHNVHNA A A A A A S L A A G
301 LSLNDVAEGL KGFSNIKGRL NVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMGELGED EAAAMHAEVG AYARDQIEA AYFVGDN SVE
401 AAEKFGADGL WFAAKDPLIQ VLRHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

m081/a081 96.7% identity over a 455 aa overlap

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLMPSESKPVSRIVTDSDIRAGDVFFALAGERFDAHDFVEDVLAA					
a081	MKPLDLNFICQALKLMPSESKPVSRIVTDSDIRAGDVFFALAGGRFDAHDFVEDVLAA					
	10	20	30	40	50	60
m081.pep	GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAVVVSREDCAAMDGALKVDDTLTALQMLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAVVVSREDCAAMDGALKVDDTLTALQMLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNKHHRYAVIEMGMNHFGE LAVLTQIAKP					
a081	AVLRRRFGDNAV LATAGNFNNHIGLPLTLLKLNKHHRYAVIEMGMNHFGE LAVLTQIAKP					
	130	140	150	160	170	180

268

	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVGCDFGVGDIKAKSEIYQGLCSGIALIPQEDANMAVFKTATLNLN					
a081	: : : : : :					
	190	200	210	220	230	240
	DAALVNNAMRAHVGCDFGVGDIKAKSEIYQGLCSGDMALIPQEDANMAVFKTATLNLN					
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFIDLVCGERAAVVLVPGRHNVHNAAAAALALAAG					
a081	: : : : :					
	250	260	270	280	290	300
	TRTFGIDSGDVHAENIVLKPLSCEFIDLVCNECAAVVLVPGRHNVHNAAAAALSLAAG					
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFNSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
a081	: : : : :					
	310	320	330	340	350	360
	LSLNDVAEGLKGFNSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHAEVGAAYARDQGIEAAYFVGDNVSVEAAEKFGADGLWFAAKDP					
a081	: : : : :					
	370	380	390	400	410	
	MGDMGELGE---DEAAAMHAEVGAAYARDQGIEAAYFVGDNVSVEAAEKFGADGLWFAAKDP					
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGSRFQMEEVVEALEDKX					
a081	: : : : :					
	420	430	440	450		
	LIQVLRHDLPERATVLVKGSRFQMEEVVEALEDKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

```

g082.seq
1  aTGTGTTGT  TGAAGTTGCC  TGCCGTCGCC  GAAACGGCAT  CATCGCCGAA
51  ACGGCGGCGC  AATACCGCAG  CCAGCATCTC  CTTACCCGTC  GTCTTGCCGC
101 CCGAACCAGT  AATGCCGAAC  ACAACGGGT  TCACATTATC  GCGCCACGCC
151 TTCGCCAAGC  TTTGCAACGC  GGCAAGCGTG  TCATCGACTT  TCAACGCGCC
201 GCCCAAAGCC  GCGCAATCTT  CGCGCGAAAC  CACAACCGCC  GCGCGCCCG
251 CAGACAATAC  GCCTCCAACA  AAATCATGCG  CGTCAAACCG  CCCGCCCGCC
301 AATGCGAAAA  ACACATCGCC  TTCCCGAATA  TCGCGGCTGT  CGGTTACGAT
351 GCGCGACACG  GGTGTTGTTT  CAGACGGCAT  CGGAAGCTTG  AGGGCTTGGC
401 AGATGAAATT  TAGGTCCAGT  GGTTTCATAT  TTGCTTTCGT  TAATATTCGG
451 GCGGCGGACA  CATCGGTAGC  GGCTGATTTT  TTTATCGCCT  GTTTTGTCTG
501 GGTAAACAC  AGATTATTTT  CCCATTCTCA  TTCGGCATT  TTTCTGTACG
551 TATCATTTT  TAGACGTATT  TTTAGCCGAT  TTGCCTTTTC  CCGCATACCA
601 CGGCGCGGG  TCGTCGGACT  GTCTGTCGAT  AAAGGCAAG  TTATTGCCTT
651 CGCCCGGCAC  ATCGGGGACA  TTCCCCAAA  AATCATAGCC  GTCATCGGGC
701 AAGTCGTCG  TTTGATACC  CGTCCAAC  CCGAATCCGC  GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

```

g082.pep
1  MWLLKLPAVA  ETASSPKRRR  NTAASISFTV  VLPPEPVMPN  TNGFTLSRHA
51  FANVCNAAVS  SSTFNAPPKA  AQSSRETTTA  AAPADNTPPT  KSCASNRPPA
101 NAKNTSPSRI  SRLSVTMRDT  GLFSDGIGSL  RAWQMKFRSS  GFIFAFVNIR
151 AADTSVAADF  FIACFAVVKH  RLFSHSHSAF  FLYVSFFRRI  FSRFAFSRIP
201 RRGVGLSVD  KGKVIAFARH  IGDIPPKIIA  VIGQLVGFD  RPTAESA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

```

m082.seq
1  ATGnnGTTGT  TGAAGTTGCC  TGCCGTCGCC  AACACGGCAT  CATCGCCGAA
51  ACGGCGGCGC  AATACCGCAG  CCAGCATTTT  CTTACCCGTC  GTCTTGCCGC
101 CCGAACCAGT  AATGCCGAAC  ACAACGGAT  TCACATTTTC  ACGCCACGCC
151 TTTGCCAGCG  TTTGCAATGC  GGCAAGCGTG  TCATCGACTT  TCAACGCGCC

```



```

201 ATCCATTGCA GCACAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCAG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CGTCAAACCG CTCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTTGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAAACAC AGATTATTTT CCCATTCTCA TTCGGsATTT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 256; ORF 082>:

```

m082.pep
  1 MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTFSRHA
  51 FASVCNAASV SSTFNAPSIA AQSSRETTA AAPAANTSST KSCASNRSPA
 101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
 151 AADTSVAADF FIACFAVVKH RLFSHSHSXF FLYVSFFRRI FSRFAFSRIP
 201 RRGVVQSVD KGKVIAFALH IGNIPPKIIA VIGQLVGFD TPTAESAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 082 shows 92.7% identity over a 247 aa overlap with a predicted ORF (ORF 082.ng) from *N. gonorrhoeae*:

m082/g082

	10	20	30	40	50	60
m082.pep	MXLLKLPAVANTASSPKRRRNTAASISFTVVLPPEPVMPNTNGFTFSRHAFASVCNAASV					
g082	MWLLKLPAVAETASSPKRRRNTAASISFTVVLPPEPVMPNTNGFTLSRHAFANVCNAASV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m082.pep	SSTFNAPSIAAQSSRETTTAAAPANTSSTKSCASNRSPANAKNTSPARMSRLSVTMRDT					
g082	SSTFNAPPKAAQSSRETTTAAAPADNTPPTKSCASNRPPANAKNTSPSRISRLSVTMRDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m082.pep	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF					
g082	GLFSDGIGSLRAWQMKFRSSGFIFAFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m082.pep	FLYVSFFRRIFSRFAFSRIPRRGVVQSVDKGKVIAFALHIGNIPPKIIAVIGQLVGFD					
g082	FLYVSFFRRIFSRFAFSRIPRRGVVGLSVDKGKVIAFARHIGDIPPKIIAVIGQLVGFD					
	190	200	210	220	230	240
m082.pep	RPTAESAX					
g082	RPTAESAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 257>:

a082.seq

```

  1 ATGTGGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA
 51 ACGGCGGCGC AATACCGCAG CCAACATTC CTTCACCGTC GTCTTGCCGC

```


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```

101 CCGAGCCGGT AATACCGAAC ACAAACGGGT TCACATTCTC GCGCCACGCC
151 TTCGCCAACA TTTGCAACGC GGTAAAGCGTG TCATCGACTT TCAACGCGCC
201 ATCCATTGCA ACGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCCG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CATCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTACGAT
351 GCGCGACACG GGTTCGCTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTCATAT TACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTT TTTATCGCT GTTTGCTGT
501 GGTAAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTT TAGACGTATT TTTAGTCGAT TTGCCTTTT CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCGTCGAT AAAGGCAAG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTCGATACC CGTCCAACG CCGAATCCG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

a082.pep

```

1 MWLLKLPAVA KTALSPKRRR NTAANISFTV VLPPEPVIPN TNGFTFSRHA
51 FANICNAVSV SSTFNAPSIA TQSSRETTA AAPAANTSST KSCASNRPFA
101 NAKNTSPARM SRLSVTMRDT GLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSSHSAF FLYVSFFRRI FSRAFSRIP
201 RRGVVGQSV DKGKVI AFALH IGNIPPKIIA VIGQLVGFD T RPTAESAX

```

m082/a082 95.5% identity over a 247 aa overlap

	10	20	30	40	50	60
m082.pep	MXLLKLPAVANTASSPKRRRNTAASISFTVVLPEPVIPNTNGFTFSRHAFASVCNAASV					
a082	MWLLKLPAVAKTALSPKRRRNTAANISFTVVLPEPVIPNTNGFTFSRHAFANICNAVSV					
	10	20	30	40	50	60
m082.pep	70	80	90	100	110	120
a082	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRPANAKNTSPARMSRLSVTMRDT					
	70	80	90	100	110	120
m082.pep	130	140	150	160	170	180
a082	GLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF					
	130	140	150	160	170	180
m082.pep	190	200	210	220	230	240
a082	FLYVSFFRRIFSRAFSRIPRRGVVGQSV DKGKVI AFALHIGNIPPKIIAVIGQLVGFD					
	190	200	210	220	230	240
m082.pep	RPTAESAX					
a082	RPTAESAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

g084.seq

```

1 ATGAAacaAT CCGcccgaaT aAAAAATATG GATCAGACAT TAAAAAATAC
51 attgggcatt tGCGCGcttt tagcctTTTG TTTTggcgCG gccATCGCAT
101 CAGGTTATCA CTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGC
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GCTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCCTT CTTATCAGAT AGTCGGTTCC
301 ATATTGGAAG GCAATCCTGC CGAGGCGCGT GAATTTGTCT GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTTATTTT GGCTTGACAG

```


g084.pcp

```

1  MKQSARIKNM DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51  ALASVVELLL LARGFPRVSS VVLLIYVGTI ALYLPVGGWLY GAPSQIVIGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTWKVCVS VGVFADVKNY
151 KRRSKIWLTI LHTLSSCAV MEKTAGDKDW REPDAAGLLN IFDLYYDLAF
201 RAGTICRQAR PHFGSSKKSX NMAYPPTCAQ V*

```

m084.seq

1	ATGAAACAAT	CCGCCCGAAT	AAAa .ATATG	AATCAGACAT	TACTTTTATAC
51	ATTGGGCATT	TGCGCGCTTT	TAACTTTTnn	nnnnnnnnnn	nnnnnnnnnn
101	nnnnnnTATCA	CCnGGAATAT	GAATACGGCT	ACCGTTATTC	TGCCGTGGGT
151	gctttTGCTT	CGGTGTATAT	TTTATTATTA	TGGCAGCCGG	GTTTCCCGCG
201	CGTTTCTTCA	GTTGTTTTAC	TGATTTACGT	CGGCACAAAC	GGCCTATTAT
251	TGCCGGTTCGG	CTGGCTGTAT	GGTGCGCCGT	CTATCAGAT	AGTCGGTTCG
301	ATATTGCGAAA	GCAATCCTGC	CGAGGCGCCT	GAATTTTGTC	GCAATCTTCC
351	CGGGTCGCTT	TATTTTGTGC	AGGCATGATT	TTTCATTTTT	GGCTTGACAG
401	TTTGGAAATA	TTGTGTATCG	GGGGGGTAT	TGCTGACGT	AAAAAATAT
451	AAACGCCGCA	GCAAAATATG	GCTGACTATA	TTATTGACTT	TGATTTTGTC
501	CTGCGCGGTG	ATGGATAAAA	TCCGCCAGCGA	TAAAGATTG	CGAGAACCTG
551	ATGCGCGCCT	GTTGTTGAAT	ATTTTCGAC	TGTATTACGA	TTTGGCT .TC
601	CGCGCGCGCA	CAATATGCCG	CCAAGCGGCG	CCACATTTTG	GAAGCAGCAA
651	AAAAAGCGTC	AACATGGCAT	ATCCGTCATG	TGCGCCCAA	GTATAA

m084 . pep

```

1  MKQSARIKXN  NQTLIYTLGI  CALLTFXXXX  XXXXXYHPEY  EYGYRYSAVG
51  ALASVVFLLI  LARGPVRVS  VVLLIYVGT  ALYLPVGNLY  GAPSQIVGS
101  ILESNPAEAR  EFVGNLPGSL  YFVQALFFIF  GLTVWKYCVS  GGVFADVKNY
151  KRRSKLWLT  LLTLLISCAV  MDKIASDKDL  REPDAGLLLN  IFDLYYDLAX
201  RAGTICRQAR  PHFGSSKKS  VMAYPSCCAQ  V*

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/g084

```

      10      20      30      40      50
m084.pep  MKQSARIKXMNQITLLYTLGLTFCALLTF-----YHPEYEGYGRYSAVGALASVVFLLL
          ||||| : ||| ||||| : ||||| ||||| ||||| ||||| |||||
g084      MKQSARIKNMDQTLKNTLGLTALLAFCFGAASGYHLEYEGYGRYSAVGALASVVFLLL
          10      20      30      40      50      60

          60      70      80      90      100     110
m084.pep  LARGFPRVSSVLLIYVGTITALYLPVGWLYGAPSYQIVGSILESNPAEAREFVGNLPGSL
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g084      LARGFPRVSSVLLIYVGTITALYLPVGWLYGAPSYQIVGSILESNPAEAREFVGNLPGSL
          70      80      90      100     110     120

          120     130     140     150     160     170
m084.pep  YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLITILLTLILSCAVMDKIASDKDL
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g084      YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLITILLTLILSCAVMEKIAGDKDW
          130     140     150     160     170     180

```


	180	190	200	210	220
m084 . pep	REPDAGLLLNIFDLYDLAXRAGTICRQARPHFGSSSKSVNMAYPSCCAQVX				
g084	REPDAGLLLNIFDLYDLAFRAGTICRQARPHFGSSSKSVNMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

a084 . seq

```

1  ATGAAACAAT CCGCCGAAT AAAAAATATG GATCAGACAT TAAAAATAC
51  ATTGGGCATT TGC GCGCTTT TAGCCTTTT TTTTGGCGCG GCCATCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCGT CTTATCAGAT AGTCGGTTCG
301 ATATTGAAA GCAATCCTGC CGAGGCGCGT GAATTGTGCG GCAATCTTCC
351 CGGGTCGCTT TATTTGTGC AGGCATTATT TTTCAATTTT GGCTTGACAG
401 TTTGAGATA TTGTGTATCG GGGGGGTAT TTGCTGACGT AAAAACTAT
451 AAACGCCGCA GCAAATATG GCTGACTATA TTATTGACTT TGATTTGTC
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCTTCC
601 .GCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTT GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

a084 . pep

```

1  MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51  ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWRYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYDLAS
201 XAGTICRQAR PHEGSSKSV NMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKMNQTLTYTLGICALLTFXXXXXXHYHPEYGYRYSAVGALASVVFLLL					
	: :					
a084	MKQSARIKMNQTLKNTLIGICALLAFCFGA AIASGYHLEYEYGYRYSAVGALASVVFLLL					
	10	20	30	40	50	60
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGLY GAPS YQIVGS ILESNPAEAREFVGNLPGSL					
a084	LARGFPRVSSVLLIYVGTALYLPVGLY GAPS YQIVGS ILESNPAEAREFVGNLPGSL					
	70	80	90	100	110	120
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGLY GAPS YQIVGS ILESNPAEAREFVGNLPGSL					
a084	LARGFPRVSSVLLIYVGTALYLPVGLY GAPS YQIVGS ILESNPAEAREFVGNLPGSL					
	70	80	90	100	110	120
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
m084 . pep	REPDAGLLLNIFDLYDLAXRAGTICRQARPHFGSSSKSVNMAYPSCCAQVX					
a084	REPDAGLLLNIFDLYDLASXAGTICRQARPHFGSSSKSVNMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCAGCGCGT TGAAAGATAA

```



```

51  GGCAAAAGGC GTGTTCTGA TCGGCGTCGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151 GCGGTTTACA GGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201 CAGCCCCGCC TCGCGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTt tatCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

g085.pep

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGL NLTDVTLLE
51 AVQTAYAQA EAGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

m085.seq

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCCTG CGCGATGCAC TGGTAGGCAA
51 GGCAAAAGGC GTGTTCTTGA TTGGTGTGCA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151 GCCGTTTACA GGCATATGC CCAAGCCGAA GCAGGCGATA TTGTGTTGCT
201 CAGCCCCGCC TCGCGAGCT TTGATATGTT CAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTt TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

m085.pep

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGL NMTDCATLGE
51 AVQTAYAQA EAGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

m085/g085

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGLNMTDCATLGEAVQTAYAQA E					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGLNLTDCVTLEEA VQTAYAQA E					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

a085.seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCCTG CGCGACGCGC TTGCCGGCAA
51 GGCAAAAGGC GTGTTCTGA TCGGTGTGCA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151 GCGGTTTACA AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTGCTGCT
201 CAGCCCCGCC TCGCGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTt TATCGGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

a085.pep

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATLEE
51 AVQKAYAQA EAGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

m085/a085 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGLNMTDCATLGEAVQTAYAQA E					


```

|||||
a085  MGKGQDFTPLRDALAGKAKGVFLIGVDAPQIRRDLDGCDLNMTCATLEEA VQKAYAQA E
      10      20      30      40      50      60
      70      80      90
m085.ppe AGDIVLLSPACASFD MFKGYAHRSEVFIEAFKALX
      |||||
a085  AGDIVLLSPACASFD MFKGYAHRSEVFIEAFKALX
      70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 271>:

g086.seq

```

1  ATGGTGGTGC TGATGACGGC GTTCGGCCTG CTGATGATTT ATTCCGGCTTC
51  TGTGTATTTG GCATCGAAGG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GGCAGGCGGG GTTCGTCGTT GCCGGCCTTA TAGCGAGCGG TTTTATTATGG
151 TTCTTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CTTATCCGGC CTGTTGCTGG TAGCCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTC AAGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAG TTTGGGTTGG CAGTCGATTT
401 GCGGGGGGAC GGCCAACCTG ATTATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAAACAT TAGAAATGTA CGGCGGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTCTGAT AATGGTACAG CCGGATTTTCG
551 GTTCGTTTGT CGTCATTACC GTCATTACCG TTGGAATGCT GTTCTGGCA
601 GGATTGCCGT GAAATATTT TTTGTCTCTG GTAGGCAGCG TCTTGGGTGG
651 GATGGTCTCG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTGGGA CCCGTGGAAA GACCCGCGAG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TGCGAGTTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCTGAA GAATTCGGCT TCTTCGGGAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGGCG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGtttgA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGctgCcg tTGATGTCCT ATGGcggTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATCGATT
1151 ATGAAAACCG CCAGAAATG CCGGTTTACC GGGTGGAGTA AA

```

This corresponds to the amino acid sequence <SEQ ID 272; ORF 086.ng>:

g086.pep

```

1  MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGFLW
51  FLCRMRTWRR LVPWIFALSG LLLVAVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTRREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILLPIMLV AFGLVLIMVQ PDFGSFVVIT VITVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDLPWK DPQGAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIAB EFGFFGMCVL
301 IFCYGWLVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGVNIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLLL RIDYENRQKM RGYRVE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 273>:

m086.seq

```

1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCCGGCTTC
51  TGTGTATTTG GCATCAAAAG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATGG
151 TCTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CTTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTC AAGCTGGCGG CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAG TTTGGGTTGG CAGTCGATTT
401 GCGGGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGrCACGT
451 CGTGaaACAT TAGAAATGTA CCGCGGTwTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTCTGAT AATGGTACAG CCGGATTTTCG

```



```

551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCGTCCTG GTAGGCAGCG TCTTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTGGGA CCCGTGGAAA GACCCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TGCAGATTTG AGCAAACGCG GCTTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTGCGTT TCTTCGGTAT GTGCGTGCCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTGGAT CGGkrTCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA mCAAAGyCT GACGCGGCCG Tg.AtGTCCw ATGGCGGTTT
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTkG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGGTTATC GGGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 274; ORF 086>:

m086.pep

```

1  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTREE VLRSMESLGW QSIWRGTANL IMSATNPQXR
151 RETLEMYGRX RAILLPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK DPQAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGLVVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGXQ SFFNIGVNI
351 ALPKKGLTXP XMSXGSSVF FMLISMMLLX RIDYENRRKM RGYRVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 086 shows 96.7% identity over a 396 aa overlap with a predicted ORF (ORF 086.ng) from *N. gonorrhoeae*:

m086/g086

	10	20	30	40	50	60
m086.pep	MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW FLCRMRTWRR					
g086	MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW FLCRMRTWRR					
	10	20	30	40	50	60
m086.pep	LVPWIFALSGL LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTREE					
g086	LVPWIFALSGL LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTREE					
	70	80	90	100	110	120
m086.pep	LVPWIFALSGL LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTREE					
g086	LVPWIFALSGL LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTREE					
	70	80	90	100	110	120
m086.pep	VLRSMESLGW QSIWRGTANL IMSATNPQXR RETLEMYGRX RAILLPIMLV AFGLVLIMVQ					
g086	VLRSMESLGW QSIWRGTANL IMSATNPQXR RETLEMYGRX RAILLPIMLV AFGLVLIMVQ					
	130	140	150	160	170	180
m086.pep	VLRSMESLGW QSIWRGTANL IMSATNPQXR RETLEMYGRX RAILLPIMLV AFGLVLIMVQ					
g086	VLRSMESLGW QSIWRGTANL IMSATNPQXR RETLEMYGRX RAILLPIMLV AFGLVLIMVQ					
	130	140	150	160	170	180
m086.pep	PDFGSFVVIT VIAVGMLFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK					
g086	PDFGSFVVIT VIAVGMLFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK					
	190	200	210	220	230	240
m086.pep	PDFGSFVVIT VIAVGMLFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK					
g086	PDFGSFVVIT VIAVGMLFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK					
	190	200	210	220	230	240
m086.pep	DPQAGYQLTH SLMIAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL					
g086	DPQAGYQLTH SLMIAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL					
	250	260	270	280	290	300
m086.pep	DPQAGYQLTH SLMIAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL					
g086	DPQAGYQLTH SLMIAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360

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```

m086.pep  IFCYGLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFFNIGVNIGALPXXGLTXP
|||||
g086      IFCYGLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFFNIGVNIGALPTKGLTLP
          310      320      330      340      350      360

          370      380      390
m086.pep  XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX
|||
g086      LMSYGGSSVFFMLISMMLLLRIDYENRQKMRGYRVEX
          370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 275>:

```

a086.seq
1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATT ATTCCGGCTTC
51  TGTGTATTTG GCATCAAAAG AAGGCGGCGA TCAGTTTTTC TATTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTGC
201 CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCGGT CATCCTTTAT TTGGCAAGCC TGTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAG TTTGGGTTGG CAGTCGATT
401 GGCGGGGAC GGCCTACTG ATCATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAACAT TAGAATGTA CGGCCGTTT CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGT TGGTGCTGAT AATGGTACAG CCGGATTTCG
551 GTTCGTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCGTCCTG GTAGGCAGCG TCTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTGGGA CCCGTGGAAA GACCCGAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTGGG
801 TGCGAGTTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTCGGT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGGG GCGTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CCGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGCTGCCG TTGATGTCTT ATGGCGGTTT
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATAGATT
1151 ATGAAAACCG CCGGAAATG CGCGTTACC GGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 276; ORF 086.a>:

```

a086.pep
1  MVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTTRREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFLEPWK DPQAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGLVVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGVNIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLLL RIDYENRRKM RGYRVE*

```

m086/a086 98.0% identity over a 396 aa overlap

```

          10      20      30      40      50      60
m086.pep  MVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR
|||||
a086      MVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR
          10      20      30      40      50      60

          70      80      90      100     110     120
m086.pep  LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYLASLFTTRREE
|||||
a086      LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYLASLFTTRREE

```


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	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESLQWQSIWRGTANLIMSATNPQXRRETLEMYGRXRAILPIMLVAFGLVLIMVQ					
a086	VLRSMESLQWQSIWRGTANLIMSATNPQARRETLEMYGRFRAILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
a086	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m086.pep	DPQAGYQLTHSLMAIGRGWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
a086	DPQAGYQLTHSLMAIGRGWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m086.pep	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFNIGVNIGALPKKGLTXP					
a086	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFNIGVNIGALPTKGLTLP					
	310	320	330	340	350	360
	370	380	390			
m086.pep	XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGVRVEX					
a086	LMSYGGSSVFFMLISMMLLLRIDYENRRKMRGVRVEX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

g087.seq

```

1  ATGGGCGGTA  AAACCTTTAT  GCTGATGGCG  GCGGGAACGG  GCGGACACAT
51  TTTCCAGCT  CTGGCTGTGG  CGGATTCATT  GCGCGTCCGC  GGTGCATCATG
101 TAATTTGGCT  GGGCAGCAAG  GATTTCGATG  AAGAGCGCAT  CGTGCCGCAA
151 TACGGCATA  GCTTGAAAC  GCTGGCGATT  AAAGGAATAC  GCGGCAACGG
201 CATCAAACGC  AAGCTGATGC  TTCCGTTTAC  TCTGTACAAA  ACCGTCCGCG
251 AAGCGCAGCG  GATTATCCGC  AAACACCGTG  TCGAGTGGT  CATCGGCTTC
301 GGCGGTTTTG  TTACCTTTCC  CGGCGGTCTG  GCGGCGAAAC  TCTTGGGCGT
351 GCCGATTGTG  ATTACAGAGC  AAAACGCCGT  GGCAGGCTTG  TCCAACCGCC
401 AccTGTCCG  ctGGGCGAAA  CGGGTGTGT  ACGCTTTTCC  GAAAGCGTTC
451 AGCCACGAAG  GCGGTTTGGT  CGGCAACCCC  GTCGCGCCGC  ATATTAGCAA
501 CCTGCCCGTG  CCTGCCGAAC  GCTTCCAAGG  GCGCGAAGGC  CGTCTGAAAA
551 TTTTGGTGGT  CGGCGGCAGT  TTGGGTGCGG  ACGTTTTGAA  CAAAACCGTA
601 CCGCAGGCGT  TGGCACTGCT  GCCTGAAGAG  GTGCGCCCGC  AGATGTACCA
651 CCAGTCGGGG  CGTAACAAGC  TGGGCAATCT  TCAGGCGGAT  TATGACGCGT
701 TGGGCGTGAA  AGCGGAATGC  GTGGAATTTA  TTACCGACAT  GGTGTCCGCC
751 TACCGTGATG  CCGATTGGT  GATTGCGCGT  GCCGCGCGCG  TGACGATTGC
801 CGAGTTGACG  GCGGCGGGG  TGGGCGCGTT  GTTAGTGCCG  TATCCTCAGC
851 CCGTTGATGA  CCATCAAACC  GCCAACGCGC  GTTTCATGGT  GCAGGCAGAA
901 GCGGGGCTGC  TGTTGCCGCA  AACCAGTTG  ACGGCGGAAA  AACTCGCCGA
951 AATCCTCGGC  AGCCTCAACC  GCGAAAAATG  CCTCAAATGG  GCGGAAAAACG
1001 CCGGTACGTT  GGCATTGCCG  CACAGCGCGG  ATGACGTTGC  CGAAGCCGCG
1051 ATTGCGTGTG  CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

g087.pep

```

1  MGGKTFMLMA  GGTGGHIFPA  LAVADSLRVR  GHVIVLGSK  DSMEERIVPQ
51  YGIRLET Lai  KGIRNGIKR  KLMLPFTLYK  TVREAQRIIR  KHRVECVIGF
101 GGFVTFPGL  AAKLLGVPIV  IHEQNAVAGL  SNRHLSRWAK  RVLVYAFPAF
151 SHEGGLVGNP  VRADISNLPV  PAERFQREG  RLKILVVGS  LGADVLNKTV

```


201 PQALALLPEE VRPQMYHQSG RNKLGNLQAD YDALGVKAEC VEFITDMVSA
251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
301 AGLLLPQTQL TAEKLAELG SLNREKCLKW AENARTLALP HSADDDVAAA
351 IACAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

```
m087.seq
1  ATGGGCGGTA  AAACCTTTAT  GCTGAwkkCG  GCGGAACGG  GCGGACATAT
51  TTCCCCGCG  CTGGCGGTGG  CGGATTCATT  GCGCGCGCG  GGCCATCATG
101 TGATTGGCT  GGGCAGCAAG  GATTTCGATG  AAGAGCGTAT  CGTGCCGCAA
151 TACGCATAC  GCTTGGAAAC  GCTGGCGATT  AAGGCGCTGC  GCGGCAACGG
201 CATCAAACGC  AAACCTGATG  TGCCGGTTAC  TTTGTATCAA  ACCGTCCGCG
251 AAGCGCAGCG  GATTATCCGC  AAACACCGTG  TCGAGTGCCT  CATCGGCTTC
301 GGCGGCTTCG  TTACCTTCCC  CGGCGGTTTG  GCGGCGAAGC  TATTArCGT
351 GCCGATTGTG  ATTCACGAGC  AAAACGCCGT  GGCAGGTTTG  TCCAACCGCC
401 ACCTGTCCGC  CTGGGCGAAG  CGGGTGTTGT  ACGCTTTTTC  GAAAGCGTTC
451 AGCCACGAAG  CGGGCTTGGT  CGGCACCCCG  GTCGCGCGCG  ATATTAGCAA
501 CCTGCCCGTG  CCTGCCGAAC  GCTTCCAAGG  CGCTGAAGGC  CGTCTGAAAA
551 TTTTGGTGGT  CGGCGGCAGT  TTGGGCGCGG  ACGTTTTGAA  CAAAACCGTA
601 CCGCATGCAT  TGGCTTTGCT  GCCCGACAAT  GCGCGTCCGC  ATATGTACCA
651 CCAATCGGGA  CGGGGCAAGC  TGGGCATCTT  GCAGCGGnnn  nnnnnnnnnn
701 nnnnnnnnnn  nnnnnnnnnn  nnnnnnnnnn  nnnnnnnnnn  nnnnnnnnnn
751 nnnCGGGAT  TGGGTGCGTT  GTTAGTGCGG  TATCTCAGC  CGGTTGACGA
801 TCACCAAACC  GCCAACGCGC  GTTTTATGTT  GCAGGCGGAG  GCGGGATTGC
851 TGTTGCCGCA  AACCCAGTTG  ACGGCGGAAA  AACTCGCCGA  GATTCTCGGC
901 GGCTTAAACC  GCGAAAAATG  CCTCAAATGG  GCAGAAAACG  CCCGTACGTT
951 GCGACTGCCG  CACAGTGCGG  ACGAGTGGGC  GGAAGCCGCG  ATTGCGTGTG
1001 CGGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

```
m087.pep
1  MGGKTFMLXX  GGTGGHIFPA  LAVADSLRAR  GHVIVWLGSK  DSMEERIVPQ
51  YGIRLETLAI  KGVRNGNIKR  KLMPLVTLQY  TVREAQRIIR  KHRVECVIGF
101 GGFVTFPGGL  AAKLLXVPIV  IHEQNAVAGL  SNRHLSRWAK  RVLYAFPKAF
151 SHEGGLVGNP  VRADISNLPV  PAERFQGREG  RLKILVVGGS  LGADVLNKTV
201 PHALALLPDN  ARPMMYHQSG  RGKLGILQAE  XXXXXXXXXX  XXXXXXXXXXX
251 XAGLGALLVP  YPHAVDDHQT  ANARFMVQAE  AGLLLPQTQL  TAEKLAETLG
301 GLNREKCLVK  AENARTLALP  HSADDVAEAA  IACAA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/q087

	10	20	30	40	50	60
m087.pep	MGGKT	FMLXXGGTGGHIFPALAVADSLRARGHHV	IWLGSKDSMEERIV	PQYGR	LET	LAI
g087	MGGKT	FMLMAGGTGGHIFPALAVADSLRVRGHHV	IWLGSKDSMEERIV	PQYGR	LET	LAI
	10	20	30	40	50	60
	70	80	90	100	110	120
m087.pep	KGVRGNGIKRKLMLPVT	LYQTVREAQRIIRK	HRVECVIGFGGFVTF	PGGLAAKLLXV	P	IV
g087	KGIRGNGIKRKLMLPFT	LYKTVREAQRIIRK	HRVECVIGFGGFVTF	PGGLAAKLLGV	P	IV
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAF	PKAFSHEGGLVGNPVRADISNL	PVPAERFQ	REG		
g087	IHEQNAVAGLSNRHLSRWAKRVLYAF	PKAFSHEGGLVGNPVRADISNL	PVPAERFQ	REG		
	130	140	150	160	170	180

279

	190	200	210	220	229
m087 . pep	RLKILVVGGS LGADVLNKTVP HALALLPDNARPHMYHQS GRGKLGLQA-----				
	: : : :				
g087	RLKILVVGGS LGADVLNKTVP QALALLPEEVRPQMYHQS GRNKLGNLQADYDALGVKAEC				
	190	200	210	220	230 240
	230 240 250				
m087 . pep	-----AGLGALLVPYPH AVDDHQTANARFMVQAE				
g087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPH AVDDHQTANARFMVQAE				
	250	260	270	280	290 300
	260 270 280 290 300 310				
m087 . pep	AGLLLPQTQLTAEKLA EILGSLNREKCLKWAENARTLALPHSADDVAEAAIACAAX				
g087	AGLLLPQTQLTAEKLA EILGSLNREKCLKWAENARTLALPHSADDVAEAAIACAAX				
	310 320 330 340 350				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087 . seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGGAACGG GCGGACATAT
51  TTTCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG
101 TAATTGGCT GGGCAGCAAG GATTCGATGG AAGAGCGCAT CGTGCCGCAA
151 TACGACATCC TGCTCGAAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TGCCGTTTAC TTTGTATCAA ACTGTCCGCG
251 AAGCGCAGCA GATTATCCGC AAACACCGTG TCGAGTGCGT CATCGGCTTC
301 GCGCGCTTCG TTACCTTTCC CGGCGGTTTG GCGGCGAAGT TATTAGGCGT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC
401 ACCTGTCGCG CTGGGCGAAG CGGGTGTGT ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGCGAGT TTGGGCGCGG ACGTTTGTAA CAAAACCGTA
601 CCGCAGGCAT TGGCTTTGCT GCCCGACAAT GCGCGTCCGC AGATGTACCA
651 CCAATCGGGA CGGGGCAAGC TGGGCAGCTT GCAGGCGGAT TACGACGCGC
701 TGGGCGTGCA AGCGGAATGC GTGGAATTTA TTACCGATAT GGTGTCCGCC
751 TACCGCGATG CCGATTGGT GATTTGCCGT GCCGCGCGCG TGACGATTGC
801 CGAGTTGACG GCGGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCAGC
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG
901 GCGGGATTGC TGTTGCCGCA AACCAGTTG ACGGCGGAAA AACTCGCCGA
951 GATTCTCGGC GGCTTAAACC GCGAAAATG CCTCAAATGG GCAGAAAACG
1001 CCCGTACGTT GGCAGTCCG CACAGTCCG ACGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087 . pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRAR GHHVIWLGSK DSMEERIVPQ
51  YDILLETLA I KGVNRNGIKR KLMLPFTLYQ TVREAQIIR KHRVECVIGF
101 GGFVTFPGL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTVP
201 PQALALLPDN ARPQMYHQS RGLGSLQAD YDALGVQAE VEFITDMVSA
251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
301 AGLLLPQTQL TAEKLA EILG SLNREKCLKW AENARTLALP HSADDVAEAA
351 IACAA*

```

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087 . pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVIWLGSKDSMEERIVPQYIGIRLET LAI					
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVIWLGSKDSMEERIVPQYDILLET LAI					
	10	20	30	40	50	60

280

	70	80	90	100	110	120
m087.pep	KGVVRNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
a087	KGVVRNGIKRKLMLPFTLYQTVREAQQIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m087.pep	RLKILVVGGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQAXXXXXXXXXXX					
a087	RLKILVVGGSLGADVLNKTVPQALALLPDNARPMYHQSGRGKLGSLQADYDALGVQAEC					
	190	200	210	220	230	240
	250	260	270	280	290	300
m087.pep	XX-----XXXXXXXXXAGLGALLVPYPHAVDDHQTANARFMVQAE					
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
	290	300	310	320	330	
m087.pep	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDDVAEAAIACAAX					
a087	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

g088.seq

```

1  ATGTTTITAT  GGCTCGCACA  TTTCAGCAAC  TGGTTAACCG  GTCTGAATAT
51  TTTTCAATAC  ACCACATTCC  GCGCCGTAT  GGCGGCGTTG  ACCGCCTTGG
101 CGTTTTCCTT  GATGTTTCGG  CCGTGGACGA  TACGCAGGCT  GACCGCGCTC
151 AAATGCGGGC  AGGCAGTGGC  TACCGACGGC  CCGCAAACCC  ACCTCGTCAA
201 AAACGGCAGC  CCGACGATGG  GCGGTTTCGT  GATTCTGACC  GCCATTACCG
251 TGTCCACCCT  GTTGTGGGGC  AACTGGGCGA  ACCCGTATAT  CTGGATTCTC
301 TTGGGCGTAC  TGCTTGCCAC  CGGTGCGCTC  GGTTTTTACG  ACGACTGGCG
351 CAAAGTCGTT  TATAAAGACC  CCAACGCGGT  GTCCGCCAAA  TTCAAAATGG
401 TGTGGCAGTC  AAGCGTTGCC  GTTatcgCG  GTttggcaTT  GTTTTACctt
451 gCcgCAATT  CCGCCAACAA  TATTTTGATT  GTCCCGtttt  TCAAACAAAT
501 CGCCCTGCCG  CTGGGCGTGG  TCGGCTtttt  gGtggtgTCT  TACCTGACCA
551 TCGTCGGCAC  ATCCAACGCC  GTCAACCTCA  CcgaCGGCTT  GGACGGCCTT
601 GCCGCcttcc  cgttcgtcct  cgttgccgcC  GGGCTCGCCA  ttttcgccTA
651 CGTCAGCGGA  CACTACCAAT  TTTCCCAATA  CCTCCAGCTT  CCCTATGTCT
701 CCGGCGCGAA  CGAAGTCGCT  ATATTCTGCA  CCGCCATGTG  CGGCGCGTGC
751 CTCGGATTTT  TGTGGTTCAA  CGCCTATCCC  GCGCAAGTCT  TTATGGGCGA
801 TGTGCGCGCG  CTGGCATTGG  GTGCCGCGCT  CGGTaccGtt  gCCGTcaTcg
851 tCCGCCAAGA  ATTTGTcctc  gtcattaTGG  GCGGTCTGTT  cgtcgtagaa
901 gccgtgTCCG  TTATGCTTCa  tgtcggCTGG  TACAAGAAAA  Ccaaaaaacg
951 CATCTTcCTg  acgGcaccga  ttcataacca  ttaCCaactt  cgatgCTGGa
1001 aagaaaacgca  agtcgtcgtc  CGTtTcTGGA  TTAtTaccat  cgtcgtgggt
1051 tTgatagggt  tGagtaccct  caAAattcgc  ggaaactatg  ccgTCCGAAC
1101 ACCTTTCAGA  CGGCATTGA  ACGCGCAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

g088.pep

```

1  MFLWLAHFSN  WLTGLNIFQY  TTFRAVMAAL  TALAFSLMFG  PWTIRRLTAL
51  KCGQAVRTDG  PQTHLVKNGT  PTMGGSLLLT  AITVSTLLWG  NWANPYIWIL
101 LGVLLATGAL  GFYDDWRKVV  YKDPNGVSAK  FKMVWQSSVA  VIAGLALFYI
151 AANSANNILI  VPFFKQIALP  LGVVGFVLVS  YLTIVGTSNA  VNLTGDLGDL

```


201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
 301 AVSVMLHVGW YKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 285>:

m088.seq

```

1  ATGTTTTTAT GGCTCGCACA TTTCAGCAnC TGGTTAACCG GTCTGAATnn
51  nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
101 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
151 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
201 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
251 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
301 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
351 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
401 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
451 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn
501 nnnnnnnnnnn nnnGGCGTGG TCGGCTTTT GGTGTTGTCT TACCTGACCA
551 TCGTCGGCAC ATCCAATGCC GTCAACCTCA CCGACGGCTT GGACGGCCTT
601 GCGACCTTCC CCGTCGTCCT CGTTGCCGCC GGCCTCGCCA TCTTCGCCTA
651 TGCCAGCGGC CACTCACAAT TTGCCCAATA CCTGCAATTA CCTTACGTTG
701 CCGGCGCAAA CGAAGTGGTG ATTTTCTGTA CCGCCATGTG CGGCGCGTGC
751 CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
801 TGTCGGTGCA TTGGCATTGG GTGCCGCGCT CGGTACCGTC GCCGTTATCG
851 TCCGCCAAGA GTTTGTCCTC GTCATTATGG GCGGATTATT TGTCGTAGAA
901 GCCGTATCCG TTATGCTTCA GGTGGCTGG TATAAGAAAA CCAAAAAACG
951 CATCTTCCTG ATGGCGCCCA TCCATCACCA CTACGAACAA AAAGGCTGGA
1001 AAGAAACCCA AGTCGTCGTC CGCTTTTGA TTATTACCAT CGTCTTGGTG
1051 TTGATCGGTT TGAGTACCCT CAAAATCCGC TGAACCTATG CCGTCTGAAC
1101 ATCTTTCAGA CGGCATTGTA ACGCGCAATA A

```

```

1  MFLWLAHFSN WLTGLNIFOY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSILIT AITVSTLLWG NWANPYIWIL
101 LGVLLATGAL GFYDDWRKVY YKDPNGVSAK FKMVWQSSVA VIAGLALFYL
151 AANSANNILI VPFFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTDGLDGL
201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
301 AVSVMLHVGW YKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

```

This corresponds to the amino acid sequence <SEQ ID 286; ORF 088>:

m088.pep

```

1  MFLWLAHFSX WLTGLNXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
51  XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
101 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XGVVGFLVLS YLTIVGTSNA VNLTDGLDGL
201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEV IFCTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
301 AVSVMLQVGW YKTKKRIFL MAPIHHHYEQ KGWKETQVVV RFWIITIVLV
351 LIGLSTLKIR XTYAVXTSFR RHLNAQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 088 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 088.ng)

from *N. gonorrhoeae*:

m088/g088

```

m088.pep                                10      20      30
                                         GVVVGFLVLSYLTIVGTSNAVNLTGDLGLA
g088      IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTGDLGLA
                                         |||
                                         150      160      170      180      190      200

```



```

                                40      50      60      70      80      90
m088.pep  TFPVVLVAAGLAIFAYASGHSQPAQYLQLPYVAGANEVVI FCTAMCGACLGFLWFNAYPA
           :|| ||||| ||||| :|| :|| ||||| ||||| :|| ||||| ||||| |||||
g088       AFFFVLVAAGLAIFAYVSGHYQFSQYLQLPYVAGANEVAIFCTAMCGACLGFLWFNAYPA
           210      220      230      240      250      260

                                100     110     120     130     140     150
m088.pep  QVFMGDDVGALALGAALGTVAVIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM
           ||||| ||||| ||||| ||||| ||||| :|| ||||| ||||| |||||
g088       QVFMGDDVGALALGAALGTVAVIVRQEFVLVIMGGLFVVEAVSVMLHVGWYKTKKRIFLT
           270      280      290      300      310      320

                                160     170     180     190     200
m088.pep  APIHHHYEQKGWKETQVVVRFWIIITIVLVLIGLSTLTKIRXTYAVXTSFRRHNAQX
           ||||| :|| :|| ||||| ||||| ||||| ||||| :|| ||||| |||||
g088       APIHHHYQLRCWKETQVVVRFWIIITIVVVLIGLSTLTKIRGNYAVRTPFRRHNAQX
           330      340      350      360      370

```

a088.seq

This corresponds to the amino acid sequence <SEQ ID 288; ORF 088.a>:

a088.pap

m088/a088 99.5% identity over a 205 aa overlap

```

                150      160      170      180      190      200
m088.pep  XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGVVGFVLVLSYLTIVGTSNAVNLTGDLGDLA
                                     |||||
a088      TAGLALFYLAANSANNILIVPFFKQIALPLGVVGFVLVLSYLTIVGTSNAVNLTGDLGDLA

```


283

	150	160	170	180	190	200
	210	220	230	240	250	260
m088.pep	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGLWFNAYPA					
a088	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGLWFNAYPA					
	210	220	230	240	250	260
	270	280	290	300	310	320
m088.pep	QVFMGDVGAALGAALGTVAIVRQEFVLVIMGGLFVVEAVSVMLQVQWYKTKKRIFLM					
a088	QVFMGDVGAALGAALGTVAIVRQEFVLVIMGGLFVVEAVSVMLQVQWYKTKKRIFLM					
	270	280	290	300	310	320
	330	340	350	360	370	
m088.pep	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTPFRRLNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

```

g089.seq
1  ATGCCGCCCA  AAATCACGAA  GAGCGGGTTT  TGCAAACCGG  CAATCGCGGC
51  GGCGGTCGCG  CCGACATTCT  TGCCTTTGCT  GTCGTCGATG  AATACCACGC
101 CGTTTTTCTC  GCCGATTTT  TCCACACGGT  GCGGCAAGCC  TTGGAAGGTT
151 TTGACGTGTT  CCAGCAATGC  TTCGCGCGGC  AAACCGACGG  CCTCGCACAA
201 AGCCACGGCA  GCCATAACGT  TGGCGGCGTT  GTGCAAACCT  TGCAGCGGGA
251 TGTCTTGCGT  AGAAATCAAA  TCTTCATTGC  CTTGTTTTAA  ACAGCCCGTC
301 CCGCGTTCCA  ACCAAAAATC  GGCTTCGTGT  TCCAAGGAAA  ACCGTTTCAC
351 TTCACGCCCT  GCCCGTTTCA  TGGCGCGGCA  GAACACGTCG  TCCGCATTCA
401 AAACCTGCAC  TCCATCGCCA  CGGAAAATCT  CGGCTTTGGT  ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

```

g089.pep
1  MPPKITKSGF  CKPAIAAAVA  PTFVPLLSSM  NTTPFFSPIF  STRCGKPWKV
51  LTCSSNASRG  KPTASHKATA  AITLAALCKP  CSGMSCVEIK  SSLPCFKQPV
101 PRSNQKSASC  SKENRFTSRP  ARFMARQNTS  SAFKTCTPSP  RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

```

m089.seq
1  ATGCCGCCCA  AAATCACKAw  GAGCGGATTT  TGCAAACCGG  CAATCGCGGC
51  GGCAGTCGCG  CCGACATTCT  TGCCTTTGCT  GTCGTCGATA  AACACCACGC
101 CGTTTTTCTC  GCCGATTTT  TCCACGCGGT  GCGGCAGGCC  TTGGAAGGTT
151 TTGACGTGTT  CGAGCAATGC  TTCGCGCGAC  AAACCGATGG  CCTCACACAA
201 AGCCACKGCA  GCCATGACGT  TAGCGGCGTT  GTGCAKACCT  TGCAACGGwA
251 TGTCTTGCGT  GACAAATCAA  TCTTCATTGC  CTTGTTTCAG  GCGGCCTGTC
301 TCGCGTTCCA  ACCAGAAATC  AGCTTCGTGT  TCCAACGAAA  ACCATTTTAC
351 CTCGCGCCCG  GCACGCTTCA  TCGCGCGGCA  GAACGCATCG  TCCGCATTCA
401 AAACCTGCAC  GCCGTCGCCA  CGGAAAATCT  TGGCTTTGGT  ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

```

m089.pep
1  MPPKITXSGF  CKPAIAAAVA  PTFVPLLSSI  NTTPFFSPIF  STRCGRPWKV
51  LTCSSNASRD  KPMASHKATA  AMTLAALCXP  CNMGSCVTIK  SSLPCFRRPV
101 SRSNQKSASC  SNENHFTSRP  ARFIARQNAS  SAFKTCTPSP  RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng) from *N. gonorrhoeae*:

m089/g089

284

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRPWKVLTCSSNASRD					
	: : : : :					
g089	MPPKITXSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGRPWKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	: : : : : :					
g089	KPTASHKATAAITLAALCKPCSGMSCVEIKSSLPCFKQPVFRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTC TSPSPRKILALVCAX					
	: : : :					
g089	ARFMARQNTSSAFKTC TSPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

a089.seq

```

1   ATGCCGCCTA AAATCACGAA GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GCGGTCGCA CCGACGTTTC TGCCTTTGCT GTCGTCGATG AACACCACGC
101 CATTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGAAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGGC AAACCGACGG CTTGCGACAA
201 GGCAACGGCA GCCATCACGT TAGTGCGGTT GTGCAAGCCT TGCAGCGGAA
251 TATCTTGCGT GGCAATCAAA TCTTCATTGC CTTGTTTCAG GCGACCTGTC
301 TCACGTTCAC ACCAAAAATC GGCTTCGTAT TCCAACGAAA ACCATTTCAC
351 CTCGCGCCCG GCGCGCTTCA TCGCACGACA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC ACCGTCGCCA CGGAAATCT TGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

a089.pep

```

1   MPPKITXSGF CKPAIAAAVA PTFVPLLSSM NTPFFSPIF STRCGRP*KV
51  LTCSSNASRG KPTASHKATA AITLVALCKP CSGISCVAIK SSLPCFRRPV
101 SRSNQKSASY SNENHFTSRP ARFIARQNAS SAFKTC TSPSP RKILALVCA*

```

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRPWKVLTCSSNASRD					
	: : : : :					
a089	MPPKITXSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGRPWKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	: : : : : :					
a089	KPTASHKATAAITLVALCKPCSGISCVAIKSSLPCFRRPVSRSNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTC TSPSPRKILALVCAX					
	: : : :					
a089	ARFIARQNASSAFKTC TSPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

g090.seq

```

1   ATGCGCGTAG TCGAGCAAAT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA

```


g090 . pep

m090.seq

m090.pgp

m090/g090

a090.seq

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

a090.pep

1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA
 51 LQFRLQNRRA DIARDNGIQP TLDAEIADQA RYRGFAVAAG NRNLVAAAV
 101 HNVRRQFDVA QHAXRRFA*

m09/a090 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAFG	VFQLEAGKLQ	HPHVRLFAFAL	PFRLQNRRA
	:					
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAFG	VFQLETGKLQ	HPHVRLFAFAL	QFRLQNRRA
	10	20	30	40	50	60

	70	80	90	100	110	119
m090.pep	DIARDNGIQPALDTEIADQ	ARYRGFAVAAGNRNYLVV	PAVHNVRRQ	QFDVAQHAXRRFAX		
a090	DIARDNGIQPTLDAEIADQ	ARYRGFAVAAGNRNLVAAAV	HNVRRQ	QFDVAQHAXRRFAX		
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence < ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:

m090-1.seq

1 ATGACGCGCT TTGCATTCA GACGGCATCA CAAAGCCTTA AACGCTTCGA
 51 TAAACACTTC CGAACGGTGC GCGTAGCCTT TGAACATATC AAAGCTCGCG
 101 CAGGCGGGG TGAGCAACAC AATATCGCCT GCTTCGGCTT GGGCATATGC
 151 CGTCTGAACG GCTTCTCCCA AAGTGGCGCA GTCGGTCATA TTCAAGCCGC
 201 AGCCGTCCAA ATCGCGGCGG ATTTGCGGCG CATCGACACC AATCAAGAAC
 251 ACGCCTTTTG CCTTGCCTAC CAGTGACATCG CGCAGGGGCG TGAAGTCCTG
 301 CCCTTTACCC ATGCCGCCCA AAATCACGAA GAGCGGATTT TGCAAAACCGG
 351 CAATCGCGCG GGCAGTCGCG CCGACATTCG TGCCCTTGCT GTCGTCGATA
 401 AACACACGCG CGTTTTCTC GCCGATTTT TCCACGCGGT GCGGACGGCC
 451 TTGGAAGGTT TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG
 501 CCTCACACAA AGCCACGGCA GCCATGACGT TAGCGGCGGT GTGCAGACCT
 551 TGCAACGGAA TGTCTTGCGT GACAATCAAA TCTTCATTGC CTTGTTTCAG
 601 GCGGCTGTGC TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA
 651 ACCATTTTAC CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG
 701 TCCGCATTCA AAACCTGCAC GCCGTGCGCA CGGAAATCT TGGCTTTGGT
 751 ATGCGCATAG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA
 801 TGTTACAGCA CGTCGCGGCA GTCGGACGCA GGCTTTCGGT GTTTTCCAGT
 851 TGGAAAGCTGG AAAGCTCAA CACCCACACG TCCGCTTTT TGCTTCGCG
 901 CTGCCATTCC GCCTCCAAA CCGGCGTGCC GATATTGCCC GCGATAACGG
 951 TATCCAGCCC GCACTTGATA CAGAGATAGC CGACCAGGCT CGTTACCGTG
 1001 GTTTTGCCGT TGCTGCCGGT AATCGCAATT ACCTTGTCGT CCCGGCGGTT
 1051 CACAATGTCC GCCAGCAATT CGATGTGCGC CAACACGCGT CCGCCGTTTT
 1101 GCTTGAACGC CTCAATATCC GGCTGCCGCT CGCTGATGCC GGGACTGAGA
 1151 GCCAGAAATAT CGAAACCGTT GTCCAGCGCA TCTTTCAGAC GGCCCGTGTA
 1201 AAACACCAAC CCGTCAAACA TCTTACCGAT TTGCGACACG CGTTCGGCT
 1251 TCAGCTCCGC ATCATACGCA GCAACCTCCG CGCCGTTTTT GCGCAGGTAG
 1301 GCAATCATGG AAATACCCGT ACCGCGGAGT CCGGCGACGA GGATTTTTTT
 1351 GTTTTGAAAA GTCATTTGG TTTGTCTTAA

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

m090-1.pep

1 MTAFATQAS QSLKRFDKHF RTVRVAFEDI KARAGGAEQH NIACFGLGIC
 51 RLNGFSQSGA VGHIAAAVQ IAADLRIDT NQEHAFCLAY QCIAQGREVL
 101 PFTHAQNHE ERLQTDGNGR GSRADIRAF VVDKHHAVFL ADFHFAVRQA
 151 LEGFDVFEQC FARQTDGLTQ SHGSHDVSGV VQTLQRNVLR DNQIFIALFQ
 201 AACLAQPEI SFVFRKPFY LAPGTLHRAA ERIVRIQNLH AVATENLGFG
 251 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
 301 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNYLVVPAV
 351 HNVRRQFDVA QHASAVLLER LNIRLPLADA GTESQNIETV VORIFQTVARV
 401 KHQPVKHLTD LRHAFRLQLR IIRSNLRAVF AQVGNHGNTR TAESGDEDFD
 451 VLKSHFGLS*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 303>:

g091.seq

```

1  ATGGAAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTGTTTGA
51  AAGTCATTTT GGTTTTGTCC TAAAACAAAT CATATTGGGC AGGAGACGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCCG ATTAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTGCGAGCT GTTTTGGTCT CCGTTTTGAC
201 AAGCCTTGCC AAGCCATTGT TGAGCGAGCG CAAGGTCTTG GCGCACGCCG
251 CGTCCATCGT AATACATCAA GCCCAAATTG TATTGGGCTT GGGCATCCCC
301 TTGTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 304; ORF 091.ng>:

g091.pep

```

1  MEIPVPPSPA TRIFLFESHF GFVLKQIILG RRRPPLPKPL SDGIASRLIT
51  RLQALVIVAA VLVSVLTSLA KPLLSEKVL AHAASIVIHQ AQIVLGLGIP
101 LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 305>:

m091.seq

```

1  ATGGAAATAC CCGTACCGCC GAGTCCGGCG ACGAGGATTT TTTGTTTGA
51  AAAGTCATTT TGGTTTGTCC TAAAACAAAT CATATTGAGC AGGAGATGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTGCGAGCC GTCTTGGTCT CCGTTTTGAC
201 AAGCCTTGCC AAACCATCTT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCCG CATACATCAC GCCCAAATTG TTTTGGGCTT GGGCTACCCC
301 CTGCGC...

```

This corresponds to the amino acid sequence <SEQ ID 306; ORF 091>:

m091.pep

```

1  MEIPVPPSPA TRIFLFEKSF WFVLKQIILS RRCPPPLPKPL SDGIASCSIT
51  RLQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLGLGYP
101 LR.

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 091 shows 84.2% identity over a 101 aa overlap with a predicted ORF (ORF 091.ng) from *N. gonorrhoeae*:

m091/g091

	10	20	30	40	50	60
m091.pep	MEIPVPPSPATRIFLFEKSFWFVLKQIILSRRCPPLPKPLSDGIASCSITRLQALVIVAA					
	: : : : :					
g091	MEIPVPPSPATRIFLFESHFGFVLKQIILGRRRPPLPKPLSDGIASRLITRLQALVIVAA					
	10	20	30	40	50	60
	70	80	90	100		
m091.pep	VLVSVLTSIAKPFLCKGAVLAHAASFGIHHQAQIVLGLGYPLR					
	: : : : :					
g091	VLVSVLTSIAKPLLSEKVLHAASIVIHQAQIVLGLGIPLFX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 307>:

a091.seq

```

1  ATGGAAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTGTTTGA
51  GAAATCATTT TGGTTTGTCC TAAAACAAAT CATATTGAGC AGGGGATGTC
101 TGATCCTGCT CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCTTTCAGG CGTTGGTCAT TGTGCGAGCT GTCTTGGTAT CCGTTTTGAC
201 AAGCCTTGCC AAGCCATTCT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCCG CATACATCAC GCCCAAATTG TTTTGGGC

```


This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

a091.pep

```

1  MEIPVPPSPA TRIFLFWKSF WFLVKQIILS RGCLILLKPL SDGIASCSIT
51  RFQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLG

```

m091/a091 93.8% identity over a 96 aa overlap

```

              10      20      30      40      50      60
m091.pep      MEIPVPPSPATRIFLFEKSFWEVLKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA
              |||||
a091           MEIPVPPSPATRIFLFEKSFWEVLKQIILSRGCLILLKPLSDGIASCSITRFQALVIVAA
              10      20      30      40      50      60

              70      80      90      100
m091.pep      VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQIVLGLGYPLR
              |||||
a091           VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQIVLG
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

g092.seq

```

1  ATGTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTGCGC
51  AACCGGTCAG ACCTTTAAAA TAACGCCTTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTTGTGCGT
151 ATCGGCGGCG TCGGCATGAG CGGTATCGCC GAAGTCTTGC ACAATTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTCGT TGCCTCTACC GCCGTCAAGA AAGAAaatcc
351 CGAAGTtgtc gcTGCgTTGg AGCGGCAAAAT TCCCGTTATT CCGCGCGCCT
401 TGATGCTGGC AGAGCTGATG CGCTTCCGTG ACGgcatcgc cattgcccgt
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAAAC TACGCGCAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTTCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTGTTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGG CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCGAAA TGAATTAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CCGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGc gtggcGCTgg
1001 aagtcGgCGC ATcggttgAA GCGatcCAAA AaggCTTGCT CCGCTTTGAA
1051 GCGTCGGGCC GCCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgctGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgctGCA CGCGGCGCGT ATCCGAAAA acgtTTGGTG
1201 CtcgCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTACTCAATA CCGTTGatgc GCTGGTACTG ACCGAAGTTT
1301 AtgccgccgG CGAAGAGCCG GTTGCCGCCG CCGactcCCG CGCCTTGGCG
1351 CGTGCTATCC GCGTATTGGG CAAACTTGAG CCGATTTACT GCGAAAatgt
1401 cgccgACCTG CCGCAAATGC TGATGAATGT TTTACAGGAT Ggcgatggtg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgtcccttc cgcgctggtg
1501 gaattgtcga AACAGAttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

g092.pep

```

1  MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHFVG
51  IGGVMSGIA EVLHNLGPKV SGSDQARNAA TEHLSSLGIQ VYPGHTAEHV
101 NGADVIVAST AVKKNPEVV AALERQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```



```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

```

m092.seq
1 ATGTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGGTCAG CCCTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTGTCCGGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCGAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGGTGCAG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAATC AACGCCGCAG
551 GCACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTGTG GTATTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GGCGCGCAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GCGTCGGGCC GCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCGACCCT TGCCGCGGCA CGCGGCGCGT ATCTGGAAAA ACGTTTGGTA
1201 CTCGCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAA GTCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCGCG TGAAGAGCCG ATTGCCGCGC CGGATTCCCG CGCTCTTGCC
1351 CGCGCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTTGACAGGAC GGCGACATCG
1451 TGTGAATAT GGGCGCGGGA AGCATCAACC GCGTCCCGC CGCGCTGCTG
1501 GCATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

```

m092.pep
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVGMGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIATAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng) from *N. gonorrhoeae*:

m092/g092

```

10      20      30      40      50      60
m092.pep  MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVGMGIA

```


a092.seq

1	ATGTTTTTTA	TTTCAATCCG	CTATATATTT	GTCAGAAAAA	TATGGCGCGC
51	AAACGGTCAG	CCCTTTAAAA	TAACGCCTTT	ACGCATCGAA	AATCCACCGG
101	AACGCACATC	TATGATGAAA	AATCGAGTGA	CCAACATCCA	TTTTGTCTGGT
151	ATCCGCGCGC	TCCGGCATGAG	CGGTATCGCC	GAAGTCTTGC	ACAATTTGGG
201	TTTTAAAGTT	TCCGGTTCGG	ATCAGCGCGC	AAATGCCCTG	ACCGAGCATT
251	TGGGCAGCCT	GGGCATTCAA	GTTTATCCCG	GCCATACCGC	AGAACAGCTT


```

301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACCT AACGCCGCGC
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT T GCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAA TGAATTAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CCGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGGCG ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGAACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGCGCACCTT TCCGCGCGCA CGCGCGCGCT ATCCGAAAA ACCTTTGGTA
1201 CTGCGCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAA GTCCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CTGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTTGCAGGAC GGCGACATCG
1451 TGTGTAATAT GGTGCGGGA AGCATCAACC GCGTCCCCGC CGCGTGCTG
1501 GAATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

a092.pep

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFVG
51 IGGVGMGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKTIVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAIG VALEVGASVE AIQKLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRLA
451 RAIRVLGKLE PIYCENVADL PEMLLNLVD GDIVLNMGAG SINRVPAALL
501 ELSKQI*

```

m092/a092 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092.pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMGIA					
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMGIA					
	10	20	30	40	50	60
m092.pep	EVLHNLGFKVSGSDQARNAAEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
	70	80	90	100	110	120
m092.pep	EVLHNLGFKVSGSDQARNAAEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
	130	140	150	160	170	180
m092.pep	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTSLTASILGAAGLDPTFVIGGKL					
a092	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTSLTASILGAAGLDPTFVIGGKL					
	190	200	210	220	230	240
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					

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	190	200	210	220	230	240
m092.pep	250	260	270	280	290	300
a092	FIHRMPFYGKAFLCIDSEHVR	AILPKVSKPYATYGLDDTADI	YATDIENVGAQMKETVHV			
	250	260	270	280	290	300
m092.pep	310	320	330	340	350	360
a092	QMKGHEQGSFEVVLNMPGRH	NVLNALAAIGVALEV GASVE	AIQKLLGFEGVGRRFQKYG			
	310	320	330	340	350	360
m092.pep	370	380	390	400	410	420
a092	DIKLPNGGTALLVDDYGHHP	VEMAATLAAARGAYLEKRL	VLAFQPHRYTRTRDLFED	FTK		
	370	380	390	400	410	420
m092.pep	430	440	450	460	470	480
a092	VLNTVDALVLTVEVYAAGEE	PIAAADSRALARAIRVLGK	LEPIYCENVADLPEMLLN	VLQD		
	430	440	450	460	470	480
m092.pep	490	500				
a092	GDIVLNMGAGSINRVPAALL	LALSQIX				
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

```

g093.seq
1  aTGCAGAAAtt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgctTGGACA GCgGTACCGC CATTTTGAAC GCCTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTTATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGCGGAA GACGGGGCTG TTCAGGGTGC ATTGGAAC TG TGGGCATT C
251 CCTATACCGG CAGCGGTGTC GCCGCCTCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTTCGCA GGCATTGGGA TTACCCGPTC CCGAGTTCGC
351 CGTACTGTAC GATGATACCG ATTTCCGATG CGTCGAAGAA AAATTGGGTC
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggt a
451 aAAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAAaCA
501 CCTTcagggg cgaAAtcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaacCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGGG CGCACAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCTT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

```

g093.pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTIGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPPEFAVLY DDTDFDAVEE KLGLPMFVKP AAEGSSVGUV
151 KVKEKGRLKS VYEELKHLQG RNHCRTFYRR RRIFLPRPER QRAARHTHP
201 RNRVLRRLRSQ VQPRRHLSM SFGRFRDSRR KPDARTGGSR RTGNRCGLRL
251 ARRFPQRYRR QTLVGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

```

m093.seq

```



```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCrAA GACGGGGCGG TTCAGGGTGC ATTGGAAC TGGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTTCGATG CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CCTTCAGGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACCGC GACGACACCA
651 TTTATCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTGCGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACGAGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

m093.pep

```

1  MQNFGKQAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGLSSVGVV
151 KVKGKGRLLS VYEELKHLQX RNHCRTFYRR RRIFLPRPER QRAARHTHS
201 RNRVLRRLRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGSR RAGNRCGRLR
251 ARRFQRYRR QTLVGNQHP ARYDEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

m093/g093

	10	20	30	40	50	60
m093.pep	MQNFGKQAVLMGGFSSEREISLDSGTAILNALKSKGIDAYAFDPKETPLSELKAQGFQTA					
g093	MQNFGKQAVLMGGFSSEREISLDSGTAILNALKSKGIDAYAFDPKETPLSELKERGFQTA					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m093.pep	FNILHGTYGXDGA VQGALELLGI PYTGSGVAASAIGMDKYRCKLIWQALGPLVPEFAVLH					
g093	FNILHGTYGEDGA VQGALELLGI PYTGSGVAASAIGMDKYRCKLIWQALGPLVPEFAVLH					
	70	80	90	100	110	120
	130 140 150 160 170 180					
m093.pep	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVVVKVGKGRLLSVYEELKHLQXRNHCRTFYRR					
g093	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVVVKVGKGRLLSVYEELKHLQGRNHCRTFYRR					
	130	140	150	160	170	180
	190 200 210 220 230 240					
m093.pep	RRIFLPRPERQRAARHTHSRNRVLRRLRSQVQPRRHLSMSFGRFDRSRRKPDARTGGSR					
g093	RRIFLPRPERQRAARHTHPRNRVLRRLRSQVQPRRHLSMSFGRFDRSRRKPDARTGGSR					
	190	200	210	220	230	240
	250 260 270					
m093.pep	RAGNRCGRLRARRFPQRYRRQTLVGNQHPARYDEPX					
	:					
g093	RTGNRCGRLRARRFPQRYRRQTLVGNQHPARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

a093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAATG TTGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTCGATG CGTCGAAGAA AAATGGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTACGAAG AATGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCTG TGTGAACGG CAAAGGCCTG CCCGGCATAC ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAG
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

a093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLG LPMFVKP AEGSSVGVV
151 KVKGKGR LKS VYEELKHFXQ RNHCRTVYRR RRIFLPCVER QRPARTHHP
201 RDRVL* LRSQ VQQRHLSM SFRSDRSRR KPDARTGGS RAGNRCGRLR
251 ARRFQRYRR QTLVGNQHP ARYDRP*

```

m093/a093 95.7% identity over a 276 aa overlap

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS ELKAQGFQTA					
a093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS ELKAQGFQTA					
	10	20	30	40	50	60
m093.pep	70	80	90	100	110	120
a093	70	80	90	100	110	120
	130	140	150	160	170	180
m093.pep	DDTDFDAVEE KLG LPMFVKP AEGSSVGVV KVKGKGR LKS VYEELKHL QXRNHCRT FYRR					
a093	DDTDFDAVEE KLG LPMFVKP AEGSSVGVV KVKGKGR LKS VYEELKHFXQ RNHCRTVYRR					
	130	140	150	160	170	180
m093.pep	190	200	210	220	230	240
a093	190	200	210	220	230	240
	250	260	270			
m093.pep	RAGNRCGRLR ARRFQRYRR QTLVGNQHP ARYDEPX					
a093	RAGNRCGRLR ARRFQRYRR QTLVGNQHP ARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 321>:

```
g094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTGG GGTGAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTGCCGT GCGTAccggc aatggcgatg
151 cCGTCACGGA AGCGCATCAG CTCTGCCAGC ATCAAGGCGC GCGGAATAAC
201 GGGAAATTGC CGCTCCAACG CAgcgacaAC TTCGGgattT TCTTTCTTGA
251 CGGCGGTAGA GGCAACGACG ACATccgcAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

```
g094.pep
1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRISSAS IKARGITGIC RSNAATTSGF SFLTAVEATT TSAPLTCSAV
101 WPG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 323>:

```
m094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTA GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTCG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTGCCGT GCGTGCCGGC AATGGCGATG
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCGGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

```
m094.pep
1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 094 shows 95.1% identity over a 103 aa overlap with a predicted ORF (ORF 094.ng) from *N. gonorrhoeae*:

```
m094/g094

      10      20      30      40      50      60
m094.pep  MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRINSAN
          |||
g094      MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRISSAS
          |||

      70      80      90     100
m094.pep  IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
          |:|||||
g094      IKARGITGICRSNAATTSGFSFLTAVEATTTSAPLTCSAVWPGX
          |||
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 325>:

```
a094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTGG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTGCCGT GCGTGCCGGC AATGGCGATG
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 326; ORF 094.a>:

a094.pep

1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
 51 PSRKINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
 101 WPG*

m094/a094 100.0% identity over a 103 aa overlap

	10	20	30	40	50	60
m094.pep	MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKINSAN					
a094	MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKINSAN					
	10	20	30	40	50	60
	70	80	90	100		
m094.pep	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX					
a094	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 327>:

g095.seq

1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
 51 TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
 151 AACACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
 251 TCCTCGTCTGA TATTGGTAAC GACGGACATA ATCGGGGTCA GTGTAGGAAA
 301 GAGGCATCGG ATCGTCGGCT TCGGCAACGA TGTATTCGCC TTGCCCCAAG
 351 CGGGCGTTGG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 328; ORF 095.ng>:

g095.pep

1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK
 101 EASDRRLRQR CIRLCPGRW CLRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 329>:

m095.seq

1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
 51 TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
 151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
 251 TCCTCGTCTGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
 301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTGCCCCAAG
 351 CGGGCGTTAG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 330; ORF 095>:

m095.pep

1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK
 101 DASDRRLRQR CIRLCPGRX CLRR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 095 shows 97.6% identity over a 124 aa overlap with a predicted ORF (ORF 095.ng) from *N. gonorrhoeae*:

m095/g095

	10	20	30	40	50	60
m095.pep	MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG					

297

```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRQCQRKDASDRRLRQRCIRLCPSGRX
           |||||
g095      HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRGQCRKEASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
  1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTGTC GCGCCGACGT
 51  TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101  GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
151  AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201  TAAACGCCTG ATGCAGCTTC TCAACACTGT GCCCGTAGGT ATCCATATGG
251  TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301  GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351  CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
  1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
 51  NTQKGFAVEG HTVDEIDKRL MQLLNTVPVG IHMFVDIGN DGHNRCQCRK
101  DASDRRLRQR CIRLCPSGRW CLRR*

```

m095/a095 96.0% identity in 124 aa overlap

```

           10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           |||||
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRQCQRKDASDRRLRQRCIRLCPSGRX
           |||||
a095      HTVDEIDKRLMQLLNTVPVGIHMFVDIGNDGHNRQCQRKDASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
  1  ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
 51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101  GCCTGTGCGC CGCAACCGC CAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151  GGTCAAATCT TCCGAAGGAC ATTGataaat ggtgTCGTCT CGGttgtaCt

```


298

```

201  tggcttcgta gTCGTAAAC TCGGTTGCGG GGATGATGTG TATGCCGGGC
251  AGCCCTTTGC CGTTCAGGAC GGGGCAGGAA TATTCGCCGC CGCCGATAAA
301  AcgtTcgga atgaTTcgc ccctgAAGGT GttTCAattc ttcgtaAACG
351  CTTTTCAGAC ggccttTTTC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 334; ORF 096.ng>:

g096.pep

```

1  MAGHTGQVD FQIEFAVGI FEEIDAHA AFRTDCLCAANR QFAHQAFFGF
51  GQIFRRTLIN GVVSVLGFV VVKLGCGDDV YAGQPFVQD GAGIFAAADK
101 TFGNDFAPEG VSILKRFS DGLFL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 335>:

m096.seq

```

1  ATGGCTCGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTCG CGGTTGTACT
201 TGGCTTCGTA GTCGTAAAC TCGGTTGCGG GAATGATGTG TATGCCGGGC
251 AGCCCTTTGC CGTTCAGGAC GGGGCAGGAA TATTCGCCGC CGCCGATAAA
301 ACGTTCGGCA ATGATTTCGC CC.TGAAGGT GTTTC AATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 336; ORF 096>:

m096.pep

```

1  MARHTGQVD FQIEFAVGI FEEIDAHA AFRTDCLRAANR QFAHQAFFGF
51  GQIFRRTLIN GVVA VVLGFV VVKLGCGNDV YAGQPFVQD GAGIFAAADK
101 TFGNDFAXEG VSILKRFS DGLFL*

```

m096/g096 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQVDF	FQIEFAVGI	FEEIDAHA	AFRTDCLRAANR	QFAHQAFFG	FGQIFRRTLIN
g096	MAGHTGQVDF	FQIEFAVGI	FEEIDAHA	AFRTDCLCAANR	QFAHQAFFG	FGQIFRRTLIN
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVA VVLGFV	VVKLGCGNDV	YAGQPFVQD	GAGIFAAADK	TFGNDFAXEG	VSILKRFS D
g096	GVVS VVLGFV	VVKLGCGDDV	YAGQPFVQD	GAGIFAAADK	TFGNDFAPEG	VSILKRFS D
	70	80	90	100	110	120
m096.pep	GLFLX					
g096	GLFLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 337>:

a096.seq

```

1  ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTTG CGGTTGTACT
201 TGGCTTCGTA GTCATAAAC TCGGTCGCGG GGATGATGTG TATGCCGGGC
251 AGGCCTTTGC CGTTCAACAC AGGCAGGAA TATTCGCCGC CGCCGATAAA
301 CCGTTCGGCA ATGATTTCGC CCT.GAAAGT GTTTC AATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 338; ORF 096.ng>:

a096.pep

```

1  MAGHTGQVD FQIEFAVGI FEEIDAHA AFRTDCLRAANR QFAHQAFFGF

```


51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK
 101 PFGNDFAXES VSILRKRFSD GLFL*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHAAFRDCLRAANRQFAHQAFFGFGQIFRRTLIN					
a096	MAGHTGQGVDFQQIEFAVGIFEEIDAHAAFRDCLRAANRQFAHQAFFGFGQIFRRTLIN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDVYAGQPFQVQDGAGIFAAADKTFGNDFAHEGVVSILRKRFSD					
a096	GVVAVVLGFVVVKLGCGNDVYAGQAFVQHRAGIFAAADKPFNDFAHESVSILRKRFSD					
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

1	ATGGATATTT	CAAAACAAAC	ATTGCTGGAT	AGGGTTTTTA	ACCTGAAGGC
51	AAACGGTACG	ACGGTACGTA	CCGAGTTGAT	GGCGGGTTTG	ACGACCTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAATC	CCCTGATTTT	GGGCGAGACC
151	GGAAATGGATA	TGGGGGCGGT	ATTCGTGCT	ACCTGTATCG	CATCCGCCAT
201	CGGCTGTTTT	GTCATGGGTT	TTATCGGCAA	CTATCCGATT	GCGCTTGCCC
251	CGGGGATGGG	GCTGAATGCC	TATTTACCT	TTGCCGTCGT	TAAGGGTATG
301	GGCGTGCCCT	GGCAGGTGGC	GTTGGGTGCG	GTGTTCAATT	CCGGTCTGAT
351	TTTCATCCTG	TTCAGCTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCCTATGGG	TTTGAATG	TCGATTGCCG	CCGGTATCGG	TTTGTTTTGT
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTTGCCA	ATCCGGCAAC
501	CTTGGTCCGC	TTGGGCGATA	TTCATCAGCC	CAGCGCACTG	TTGGCATTGT
551	TCGGTTTTGT	CATGGTGGTC	GTATTGGGGT	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATCTGAC	GATTACCGTC	ATTGCCAGCC	TGATGGGTTT
651	GAACGAGTTT	CACGGCGTGG	TCGGCGAAGT	ACCGGGCATT	GCGCCGACCT
701	TTATGCAGAT	GGATTTTAAA	GGTCTGTTTA	CCGTCAGCAT	GGTCAGCGTG
751	ATTTTCGTCT	TCTTCTTGGT	CGATTGTTC	GACAGTACCG	GAACGCTGGT
801	CGGCGTATCC	CACCGTGCCG	GACTGCTGGT	GGACGGTAAG	CTGCCCCGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CCATGTGGC	AGGTGCGGCT
901	TTGGGTACTT	CTTCAACCAC	GCCTTATGTG	GAAAGCGCGG	CGGGCGTATC
951	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC
1001	TGGCGTGTCT	GATGTCTCTC	CCATTGGCGA	AAAGTGTTCC	GGTATTTGCC
1051	ACCGCGCCCG	CACTGCTTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCGAG
1101	GGACATTGAT	TGGGACGATA	TGACTGAAGC	CGCGCCCGCG	TTCTTGACCA
1151	TTGTCTTCAT	GCCGTTTACC	TATTCGATTG	CAGACGGCAT	CGCCTTCGGC
1201	TTATCAGCT	ATGCCGTGGT	CAAACCTTTG	TGTCGCCGGA	CTGGGGACGT
1251	GCCGCCATG	GTATGGGTTG	TTGCCGTATT	GTGGGCATTG	AAATTCTGGT
1301	ATTGGGCTG	A			

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

1	MDISKQTLTD	RVFNLKANGT	TVRTELMAGL	TTFLTMCYIV	IVNPLILGET
51	GMDMGAVFVA	TCIASAIGCF	VMGFIGNYPI	ALAPGMGLNA	YFTFAVVKGM
101	GVPWQVALGA	VFISGLIFIL	FSFFKVREML	VNALPMLKLM	SIAAGIGLFL
151	ALISLKGAGI	IVANPATLVG	LGDIHQPSAL	LALFGFVMV	VLGYFRVQGA
201	IIITILTITV	IASLMGLNEF	HGVVGEVPGI	APTFMQMDFK	GLFTVSMVSV
251	IFVFFLVDLF	DSTGTLVGVS	HRAGLLVDGK	LPRLKRALLA	DSTAIVAGAA
301	LGTSSSTPYV	ESAAGVSAGG	RTGLTAVTVG	VLMLACLMPF	PLAKSVPVFA
351	TAPALLYVGT	QMLRSARDID	WDDMTAAPA	FLTIVFMPFT	YSIADGIAFG

m097.pep	FSFFKVR	EMLVN	ALP	MGLK	MSIA	AGIGL	FLAL	ISL	KGAG	IIVAN	PATL	VGL	GDI	HQ	PS	AL
g097	FSFFKVR	EMLVN	ALP	MGLK	MSIA	AGIGL	FLAL	ISL	KGAG	IIVAN	PATL	VGL	GDI	HQ	PS	AL
		130		140		150		160		170		180				
m097.pep	LALFGF	AMVV	LGH	FRV	QGA	IIIT	ILTIT	VIAS	LMGL	NEFH	GI	GEV	PSI	APT	FM	QMD
g097	LALFGF	AMVV	LGH	FRV	QGA	IIIT	ILTIT	VIAS	LMGL	NEFH	GI	GEV	PSI	APT	FM	QMD
		190		200		210		220		230		240				
m097.pep	GLFTV	SMV	SIV	FV	FFL	VDL	FD	STG	TLV	GV	SHR	AGL	LV	DG	KLP	R
g097	GLFTV	SMV	SIV	FV	FFL	VDL	FD	STG	TLV	GV	SHR	AGL	LV	DG	KLP	R
		250		260		270		280		290		300				
m097.pep	LGTSS	TPY	VESA	AGV	SAG	GRT	GLT	AVT	VG	VL	ML	ACL	MF	SPL	AKS	V
g097	LGTSS	TPY	VESA	AGV	SAG	GRT	GLT	AVT	VG	VL	ML	ACL	MF	SPL	AKS	V
		310		320		330		340		350		360				
m097.pep	QMLRS	ARD	ID	W	DD	MTE	AP	FL	TIV	F	MP	P	TYS	IAD	G	I
g097	QMLRS	ARD	ID	W	DD	MTE	AP	FL	TIV	F	MP	P	TYS	IAD	G	I
		370		380		390		400		410		420				
m097.pep	VWIV	AVL	W	ALK	FW	YL	LG	X								
g097	VWIV	AVL	W	ALK	FW	YL	LG	X								
		430														

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097.seq

```

1  ATGGACACTT  CAAAACAAAC  ACTGTTGGAC  GGGATTTTTA  AGCTGAAGGC
51  AAACGGTACG  ACGGTGCGTA  CCGAGTTGAT  GCGCGGTTTG  ACAACTTTTT
101 TGACGATGTG  CTACATCGTT  ATCGTCAACC  CTCTGATTTT  GGGCGAGACC
151 GGCATGGATA  TGGGGGCGGT  ATTCGTCGCT  ACCTGTATCG  CGTCTGCCAT
201 CGGCTGTTTT  GTTATGGGTT  TTGTCGGCAA  CTATCCGATT  GCACTCGCAC
251 CGGGGATGGG  GCTGAATGCC  TATTTCACCT  TTGCCGTCGT  TAAGGGTATG
301 GCGGTGCCCT  GGCAGGTTGC  GTTGGGTGCG  GTGTTTCATC  CCGGTCTGAT
351 TTTCATCCTG  TTCAGCTTTT  TTAAAGTCAG  GGAAATGCTG  GTCAACGCAC
401 TGCCTATGGG  TTTGAAAATG  TCGATTGCTG  CCGGTATCGG  TTTGTTTTTG
451 GCACTGATTT  CCTGAAAAG  CGCAGGCATT  ATCGTTGCCA  ATCCGGCAAC
501 CTTGGTCGGC  TTGGGCGATA  TTCATCAGCC  GTCCGCGTTG  TTGGCACTGT
551 TCGGTTTTGC  CATGGTGGTC  GTATTGGGAC  ATTTCCGCGT  TCAAGGCGCA
601 ATCATCATCA  CCATTTTGAC  GATTACCGTC  ATTGCCAGCC  TGATGGGTTT
651 GAACGAATTT  CACGGCATCA  TCGGCGAAGT  GCCGAGCATT  GCGCCGACTT
701 TTATGCAGAT  GGATTTTAAA  GGGTTGTTTA  CCGTCAGCAT  GGTCAAGCGT
751 ATTTTCGTCT  TTTTCCTAGT  CGATCTGTTC  GACAGTACCG  GAACACTGGT
801 CCGTGTATCG  CATCGTGCCG  GACTGCTGGT  GGACGGTAAG  CTGCCCCGCC
851 TGAAACGCGC  ACTGCTTGCA  GACTCTACCG  CTATTGTGGC  AGGTGCGGCT
901 TTGGGTACTT  CTTCAACCAC  GCCTTATGTG  GAAAGTGCGG  CGGGCGTATC
951 GGCAGGCGGG  CGGACAGGTC  TGACGGCGGT  TACCGTCGGC  GTATTGATGC
1001 TCGCCTGCCT  GATGTTTTCA  CCTTGGCGA  AAAGTGTTCC  CGCTTTTGCC
1051 ACCGCGCCCG  CCCTGCTTTA  TGTCGGCAG  CAGATGCTCC  GCAGTGCGAG
1101 GGACATCGAT  TGGGACGATA  TGACGGAAG  CGCACC CGCA  TTCCTGACCA
1151 TTGCTTCAT  GCCGTTTACC  TATTCGATT  CAGACGGCAT  CGCTTTCGGC
1201 TTCATCAGTT  ATGCCGTGGT  TAAACTTTTA  TGCCGCGCGA  CCAAAGACGT
1251 TCCGCTATG  GTATGGATTG  TTGCCGTATT  GTGGGCACTG  AAATTCGGT

```


1301 ATTTGGGCTG A

This corresponds to the amino acid sequence <SEQ ID 344; ORF 097.a>:

a097.pep

```
1  MDTSKQTLDD GIFKLKANGT TVRTELMAGL TTFLTMCYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGICLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPM VWIVAVLWAL KFWYLG*
```

m097/a097 99.3% identity in 436 aa overlap

m097.pep	10	20	30	40	50	60
	MDTSKQTLDDGIFKLKANGTTVRTELMAGLTTFLTMCYIVIVNPNILGETGMDMGAVFVA					
a097	MDTSKQTLDDGIFKLKANGTTVRTELMAGLTTFLTMCYIVIVNPNILGETGMDMGAVFVA					
	10	20	30	40	50	60
m097.pep	70	80	90	100	110	120
	TCIASAIGCFVMGFVGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
a097	TCIASAIGCFVMGFVGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
m097.pep	130	140	150	160	170	180
	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
a097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
	130	140	150	160	170	180
m097.pep	190	200	210	220	230	240
	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGIIGEVPSIAPTTFMQMDFE					
a097	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGIIGEVPSIAPTTFMQMDFK					
	190	200	210	220	230	240
m097.pep	250	260	270	280	290	300
	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA					
a097	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA					
	250	260	270	280	290	300
m097.pep	310	320	330	340	350	360
	LGTSSTTPYVESAAAGVSAGGRTGLTAVTVGVLMACLMSPLAKSVPAFATAPALLYVGT					
a097	LGTSSTTPYVESAAAGVSAGGRTGLTAVTVGVLMACLMSPLAKSVPAFATAPALLYVGT					
	310	320	330	340	350	360
m097.pep	370	380	390	400	410	420
	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
a097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
	370	380	390	400	410	420
m097.pep	430					
	VWIVAVLWALKFWYLGX					
a097	VWIVAVLWALKFWYLGX					
	430					

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

a098.seq

```
1 ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
51 TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCGAG GCTGGCGATC
```


304

```

101 AGTTTGTCCG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTC
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GCGACTTCT TCAAACTCGC
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

```

1 MTADGLEVAF NLNAFAVVR LIPVQEDAAE AGDQFVG DVA RFTRMAFTF
51 RMNAAQHGYA GTHYVHRMG CRQAFQNFH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFKLAFLC QIRMS*

```

m098/a098 100.0% identity in 125 aa overlap

```

              10      20      30      40      50      60
m098.pep    MTADGLEVAFNLNAFAVVRILIPVQEDAAEAGDQFVG DVARFTFRMAFTFRMNAQHGYA
              |||||
a098         MTADGLEVAFNLNAFAVVRILIPVQEDAAEAGDQFVG DVARFTFRMAFTFRMNAQHGYA
              10      20      30      40      50      60

              70      80      90     100     110     120
m098.pep    GTHYVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV GDFKLAFLC
              |||||
a098         GTHYVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV GDFKLAFLC
              70      80      90     100     110     120

m098.pep    QIRMSX
              |||||
a098         QIRMSX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTGGA
51 GCTGACGGGC AAACGGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGTTG
101 CACTGACCGA ATTCTTGCGT AAAGAGCGCG TGGTCGGGGC GTTTGTGCGAA
151 TTTTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCGGAGT TCGGCGCGAC TGCCGCCATG TTCGCCATCG
251 ACGCGCAAAC TATTGATTAT TTGAACTGA CCGGACGTGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAACC GCAGGCTTAT GGGCAGGTGG
351 CTTGAAACC GCCGTTTATC CGCGGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
451 GCGGATTTGG CGGCGAAAGG GCTGGCGAAG CTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCGTGTA
551 CCAATACTTC CAACCGCGC AACGTTGTCT CCGCCGCACT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GAAACGCAA CTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGGAATCTA TTTGAAAGAA GCAGGCTTGT
701 TGCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAgcg CGCGCTcga CCGAAAATCC AACAAAGAAAT
801 CATCGACCGC GAtttgtacg cCACCGCCGT ATTTTCAGGC AACCGCAACT
851 TCGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCCT
901 CCTTTGGTCG TTGCCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCCG CGAAATCCGC CTGAAAGATA
1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAACAAT TCCGCGACAT TTATATCCG ATGTCCGACA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGACCGATG TCCACCTACA
1151 TCCGCCGTCC GCCCTATTGG GAAGGCGCAC TGGCAGGGGA ACGTACATTA
1201 AGAGGTATGC GTCCGCCGCG GATTTTGCCC GACAACATCA CCACCGACCA
1251 CATCTCgcca tCCAATGCGA TTTTGGCCGG cagTGCgca ggtgaATATT

```



```

1301 TGGCGAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451 tggcacgcgT tgaacCAGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC GCGGAAGGGC GTGCGGCTGG
1601 CGGGTGTGGA AGCCATCGCC GCCGAAGGT TCGAGCGCAT CCACCGCACC
1651 AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGGC CTGACCCTCG TGATTACCG TAAAAACGGA
1801 GAAACCGTCG AAGTTCCGGT TACCTGCCGC CCCGATACCG CAGAAGAAGC
1851 ATTGGTATAT GAAGCCGCGC GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1 MLGRASMMRL PDIVGVELTG KRQAGITATD IVLALTEFLR KERVVGAFVB
51 FPEGARSLS IGDRTISMN TPEFGATAAM FAIDAQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEPPSDGQM PDGAVI IAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWVKSSFAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFACF
251 TCNMSGALD PKIQBEIIDR DLYATAVLGS NRNFDRGRIH YAKQAFASP
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAIEYVK
351 PQQFRDIYIP MSDTGTAQKA PSPLYDWRPM STYIRPPYVW EGALAGERTL
401 RGMRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNRRQPL IIIAGADYGO GSSRDWAAGK VRLAGVEAIA ABGFERIHRT
551 NLIGMGVLP L QFKPGTNRHT LQLDGTETYD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAERLALVY EAGGVLRFA QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51 GCTGAACGGC AAACGGCAGG CGGGCATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGGC GTTTGTCGAA
151 TCTTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAAACC GCCGTTTATC CTCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCGACC
451 CCGCATTTGG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCGGA
501 CGGCCAAATG CCCGACGGCT CGGTCATCAT CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCACGC
601 AATGCCAACC GTCTCGGCTT GAAACGCAA CTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCGGGCCTGT
701 TGCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CGCGCTGGAT CCGAAAATCC AGAAAGAAAT
801 CATCGACCGC GATTTGTACG CCACCGCCGT ATTATCAGGC AACC GCAACT
851 TCGACGGCCG TATCCACCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCTT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTCCGAC CCGGCACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCGCTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCGA TTTTGCCCGT CAGTGCCGCA GGCGAGTATT
1301 TGGCGAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTCCGC CAAGGCTCGT
1451 TCGCCGCGCT CGAACCAGAA GGCGAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

```



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1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTACCG TAAAAACGGC
1801 GAAACCGTTG AAGTTCCCGT TACCTGCTGC CTCGATACTG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGGCG GCGTGTGCA ACGGTTTGCA CAGGATTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
  1 MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
 51 FFGEGARSLS IGDRTISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEPPSDGQM PDGSVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWVKSSFAPG SKVAEIIYLKE AGLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFLAS
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
351 PQQFRDVVYP MFDTGTAQKA PSPLYDWRPM STYIRPPYW EGALAGERTL
401 RGMRLAILP DNITDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVKNEDGSVR QGSFARVEPE GETMRMWEAI
501 ETYMRKQPL IIIAGADYQG GSSRDWAAKG VRLAGVEAIV AEGFERIHRT
551 NLIGMGVLP QFKPDTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPVTC LDTAEVLVY EAGGVLQRF QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng)

from *N. gonorrhoeae*:

m099/g099

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
m099.pep	70	80	90	100	110	120
	IGDRATISNMTPEFGATAAMFAIDEQTIDYKLKTGRDDAQVKLVETYAKTAGLWADALKT					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDYKLKTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
m099.pep	130	140	150	160	170	180
	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEPPSDGQMPDGSVIIAAI					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEPPSDGQMPDGAVIIAAI					
	130	140	150	160	170	180
m099.pep	190	200	210	220	230	240
	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWVKSSFAPGSKVAEIIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWVKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
m099.pep	250	260	270	280	290	300
	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFLAS					
g099	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFLAS					
	250	260	270	280	290	300
	310	320	330	340	350	360

307

m099 . pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIPADEEIDAVVAEYVKPQQFRDVIYP
g099	PLVVAYALAGSIRFDIENDVLGVADGREIRLKDIPADEEIDAIVA EYVKPQQFRDIYIP
	310 320 330 340 350 360
m099 . pep	MFDTGTAQKAPSPLYDWRPMSITYIRRPYWEALAGERTLRGMRLAILPDNITTDHLS
g099	MSDTGTAQKAPSPLYDWRPMSITYIRRPYWEALAGERTLRGMRLAILPDNITTDHISP
	370 380 390 400 410 420
m099 . pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR
	430 440 450 460 470 480
m099 . pep	QGSFARVEPEGETMRMWEAIETYMNKQPLIIAGADYQGSSRDWAAGVRLAGVEAIV
g099	QGSLARVEPEGQTMRMWEAIETYMNKQPLIIAGADYQGSSRDWAAGVRLAGVEAIA
	490 500 510 520 530 540
m099 . pep	AEGFERIHRTNLIGMGVLPLOFKPDNTRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG
g099	AEGFERIHRTNLIGMGVLPLOFKPDNTRHTLQLDGTETYDVVGERTPRCGLTLVIHRKNG
	550 560 570 580 590 600
m099 . pep	ETVEVPVTCCLDTAEVLVYAGGVLRFAQDFLEGNAAX
g099	ETVEVPVTCRPTDAEALVYAGGVLRFAQDFLEGNAAX
	610 620 630 640

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099 . seq

```

1  ATGCTGGGAC  GCGCGTCCAT  GATGCGCCTG  CCCGATATTG  TCGGCGTTGA
51  GCTGAACGGC  AAACGGAAGG  CGGGCATTAC  GCGCAGCGAT  ATTGTGTTGG
101 CACTGACCGA  GTTCTGCGC  AAAGAACGCG  TGGTCGGGGC  GTTGTGCGAA
151 TTCTTCGGCG  AGGGCGCGAG  AAGCCTGTCT  ATCGGCGACC  GCGCGACCAT
201 TTCCAACATG  ACGCCGGAGT  TCGGCGCGAC  TGCCGCGATG  TTCGCTATTG
251 ATGAGCAAAC  CATTGATTAT  TTGAACTGA  CCGGACGCGA  CGACGCGCAG
301 GTGAAATTGG  TGGAAACCTA  CGCCAAAACC  GCAGGCTTGT  GGGCAGATGC
351 CTTGAAAACC  GCCGTTATC  CGCGCGTTTT  GAAATTGAT  TTGAGCAGCG
401 TAACGCGCAA  TATGCGAGGC  CCGAGCAACC  CGCAGCGCG  TTTTGCGACC
451 GCCGATTGG  CCGGCAAAGG  CTTGGCTAAA  CCTTACGAAG  AGCCTTCAGA
501 CGGCCAAATG  CCTGACGGTG  CAGTGATTAT  TGCCGCGATT  ACTTCCTGTA
551 CCAATACTTC  CAATCCGCGC  AACGTTGTCG  CCGCCGCGCT  GTTGGCACGC
601 AATGCCAACC  GCCTCGGCTT  GCAACGCAAA  CCTTGGGTGA  AATCTTCGTT
651 TGCCCCGGGT  TCAAAAGTAG  CCGAAATCTA  TTTGAAAGAA  GCAGATCTGC
701 TGCCCGAAAT  GGAAAACTC  GGCTTCGGTA  TCGTTGCCTT  CGCATGTACC
751 ACCTGTAACG  GCATGAGCGG  CGCGCTGGAT  CCGAAATCC  AGAAAGAAAT
801 CATCGACCGC  GATTGTACG  CCACGCGCGT  ATTGTCAGGC  AACCAGCACT
851 TTGACGGCCG  TATCCATCCG  TATGCGAAAC  AGGCTTTCCT  CGCTTCGCCT
901 CCGTTGGTCG  TTGCCTACGC  GCTGGCAGGC  AGCATCCGTT  TCGATATTGA
951 AAACGACGTA  CTCGCGCTTG  CAGACGGCAA  AGAAATCCGC  CTGAAAGACA
1001 TTTGGCCTAC  CGATGAAGAA  ATCGATGCCA  TCGTTGCCGA  ATATGTGAAA
1051 CCGCAGCAAT  TTCGCGACGT  TTATATCCCG  ATGTTGACAA  CCGGCACAGC
1101 GCAAAAAGCA  CCAAGCCCGC  TGTACGACTG  GCGTCCAATG  TCTACCTATA
1151 TCCGCCGCC  ACCTTACTGG  GAAGCGCAC  TGGCAGGGGA  ACGCACATTA
1201 AGCGGTATGC  GTCCGCTGGC  GATTTTGCCC  GACAACATCA  CCACCGACCA

```



```
1251 TCTCTCGCCA TCCAATGCGA TTTTGGCAAG CAGTGCCGCA GCGGAATATT
1301 TGGCAAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTTCGC
1451 TGGCAGCGCT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTTG TGATTACCG TAAAAACGGC
1801 GAGACCGTCG AAGTCCCAT TACCTGCCG CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTT
1901 TGGAAGGGAA CCGGCTTAG
```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```
1  MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51  FEGEGARSLS IGDRTISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAGKGLAK PYEESDQGM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK PWVKSSFAPG SKVAEIYLKE ADLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQKEIIDR DLYATAVLGS NRNFDGRIHP YAKQAFILAS
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDVYIP MFDTGTAQKA PSPLYDWRPM STYIRRPYVW EGALAGERTL
401 SGMRLAILLP DNITDHLSP SNAILASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNRRKQPL IIAAGADYGO GSSRDWAAGK VRLAGVEAIV AEGFERIHRF
551 NLIGMGVLPL QFKPGTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEVLVY EAGGVLQREA QDFLEGNA*
```

m099/a099 97.5% identity in 639 aa overlap

m099.pep	10	20	30	40	50	60
a099	10	20	30	40	50	60
m099.pep	70	80	90	100	110	120
a099	70	80	90	100	110	120
m099.pep	130	140	150	160	170	180
a099	130	140	150	160	170	180
m099.pep	190	200	210	220	230	240
a099	190	200	210	220	230	240
m099.pep	250	260	270	280	290	300
a099	250	260	270	280	290	300
m099.pep	310	320	330	340	350	360
a099	310	320	330	340	350	360

a099						
	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDWPDEEIDAIVA EYVKPQQFRDVYIP					
	310	320	330	340	350	360
m099.pep	370	380	390	400	410	420
	MFDTGTAQKAPSPLYDWRPMSTYIRRPYEWEGALAGERTLRGMRPLAILPDNITTDHLS					
a099						
	MFDTGTAQKAPSPLYDWRPMSTYIRRPYEWEGALAGERTLSGMRPLAILPDNITTDHLS					
	370	380	390	400	410	420
m099.pep	430	440	450	460	470	480
	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR					
a099						
	SNAILASSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR					
	430	440	450	460	470	480
m099.pep	490	500	510	520	530	540
	QGSFARVEPEGETMRMWEAIETYMNRKQPLIIAGADYGQSSRDWAAGKGVRLAGVEAIV					
a099						
	QGSFARVEPEGETMRMWEAIETYMNRKQPLIIAGADYGQSSRDWAAGKGVRLAGVEAIV					
	490	500	510	520	530	540
m099.pep	550	560	570	580	590	600
	AEGFERIHRTNLIGMGVLPQFKPDNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG					
a099						
	AEGFERIHRTNLIGMGVLPQFKPDNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG					
	550	560	570	580	590	600
m099.pep	610	620	630	640		
	ETVEVPVTCCLDTAEVLVYEAGGVLRFAQDFLEGNAAX					
a099						
	ETVEVPITCRDLTAEVLVYEAGGVLRFAQDFLEGNAAX					
	610	620	630	640		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 357>:

g102.seq

```

1   AtgtCCGCCA AAactccgtc gctcttcggc ggcgcgatga Ttattcgccg
51  gaaggttatt ggcgcAGgta tgttcccaa cccacccgcc aacttggggg
101 acgggttaat aggtctcgctg attgtgctgc tgtacacctg gtttccattc
151 tcctccggcg ccctcatgat tttggaagtc aacaccata acCCcgagg
201 ggcaAGtttt gacaccATGg tcAAagacct gctcgGACGc ggctggaaca
251 tcatcaacgg catcgccgtc gctttgTCC tatacggctc gacctacggc
301 tacattttag tcggcggtga cctGACGCC AAAGGCatcg GCAGCGCAGT
351 AGGCGGCAAA ATTCGctca CCGTCGGACA actcgtcttc TTCGGCATCC
401 TCGCCTTTTG CGTATGGGCA TCCGCACGCT TGGTCGACCG CTTTACCGGC
451 GTCCTCATCG GCGGCATGGT ATTAACCTTT ATTGGGCAA CCGGCGGCCT
501 GGTTGCCGAT GCCAAACCGT CCGTCCTCTT CGACACCCAA GCCCCGTCG
551 GCACCGGCTA CTGGATTAC GCGGCCACCG CCCTGCCCGT CTGCCTCGCT
601 TCCTTCGGCT TCCACGGCAA CGTTTCCAGC CTGCTCAAAT ACTTTAAAGG
651 CGACGcgCc aaagtGgCGA aATCcatctg gGcaggtaca ttggTTGCCT
701 tggtaattta cgtccTCTgg caaacgcga tCcaaagcaa cCTGCGcggc
751 aacgagttcg cCCCcgtgat tgccgccgag aggcactCT CCGTCTgaa
801 tgaaccccTG tccaaattcg cccaaaccgg cgatatggat aAaatattgt
851 ccctatttcc ctacatggca atcgccacct cctttttagg cgTAACctta
901 ggctgtgttg acaacatcgc cgacatcttc aaatggaacg acagtatgtc
951 cgggcggggc accaaaaccg tcgcgctgaa ctctctgccg CCCctgattt
1001 cctggctgct cctccccacc ggcttcttta ccgccattgg tgcgtccggc
1051 ctggcgga cgtctggga ccaagGcatc atccccgcca tgctgtcta
1101 cgtttcccc caaaaaattG gcGcaggcaa gacttataAa gtttaCGGCG
1151 gcttgtgct gatgttagtc ttccctttcg gcatcgccaa catcgccga
1201 CAGGTATTGA GccaAatGga ActcgtCccc GTATTAAAG GATAA

```

This corresponds to the amino acid sequence <SEQ ID 358; ORF 102.ng>:

g102.pep


```

1  MSAKTPSLFG  GAMIAGKVI  GAGMFPNPTA  NLGDGLIGSL  IVLLYTWFPF
51  SSGALMILEV  NTHNPRGASF  DTMVKDLLGR  GWNIINGIAV  ALVLYGSTYA
101 YILVGGDLTA  KGIGSAVGGK  ISLTVGQLVF  FGILAFVCWA  SARLVDRETF
151 VLIGGMVLTF  IWATGGLVAD  AKPSVLFDTQ  APVGTGYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWAGT  LVALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  RQLSVLNETL  SKFAQTGDMD  KILSLFPYMA  IATSEFLGVTL
301 GLFDNIADIF  KWNDSMSGRG  TKTVALNFLP  PLISWLLLP  GFFTAIGASG
351 LAATVWDQGI  IPAMLLYVSP  QKIGAGKTYK  VYGGLWMLV  FLFGIANIAA
401 QVLSQMEVLP  VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA  AAACCCCTTC  ACTGTTCCGGC  GCGCGCATGA  TTATCGCCGG
51  CACGGTCATC  GCGCAGGCA  TGCTCGCCAA  CCCGACCGCC  ACATCCGGCG
101 TATGGTTTAC  CGGCTCGCTG  GCCGTGTTGC  TGTACACCTG  GTTTTCTATG
151 CTTTCAGCG  GCCTGATGAT  TTTGGAAGTC  AACACCCATT  ATCCGCACGG
201 CGCAAGTTTC  GACACGATGG  TCAAAGACCT  GCTCGGACGC  GGCTGGAACA
251 TCATCAACGG  CATCGCCGTC  GCCTTCGTTT  TATACCTGCT  TACTTACGCT
301 TATATCTTCG  TCGGCGGCGA  CCGTACCGCC  AAAGGCTTAG  GCAGCGCGGC
351 AGGCGGCGAC  GTTTCACCTA  CCGTCGGACA  ACTCGTCTTC  TTCGGCATCC
401 TCGCCTTTTG  CGTATGGGCA  TCCGCACGCT  TGGTCGACCG  CTTACCGGCG
451 GTCCCTTATCG  GCGGCATGGT  ATTGACCTTT  ATTTGGGCGG  CCGCGCGGCT
501 GATTGCCGAT  GCCAAGCCGT  CCGTCCTCTT  CGATACCCAA  GCCCCGCGCG
551 GCACAACTA  CTGGATTTAC  GCCGCCACCG  CCCTGCCCGT  CTGCCTCGCT
601 TCCTTCGGGT  TCCACGGCAA  CGTCTCCAGC  CTGCTCAAAT  ACTTTAAAGG
651 CGACGCGCCC  AAAGTGGCTA  AATCCATCTG  GACGGGCACA  CTGATTGCGC
701 TGGTAATTTA  CGTCTCTGG  CAAACGCCA  TCCAAGGCAA  CCTGCCGCGC
751 AACGAGTTCG  CCCCCGTCAT  CGCCGCCGAA  GGGCAAGTCT  CCGTCCTCAT
801 CGAAACCCTG  TCCAAATTCG  CCCAAACCGG  CAATATGGAC  AAAATATTGT
851 CCCTGTTTTT  CTATATGGCG  ATCGCCACCT  CGTTTTTAGG  CGTAACGCTC
901 GGACTCTTCG  ACTACATCGC  CGACATCTTC  AAATGGAACG  ACAGCATCTC
951 CGGCCGACCC  AAAACCGCCG  CGCTGACCTT  CCTGCCGCC  CTGATTTCCT
1001 GCCTGCTCTT  CCCCACCGGC  TTCGTTACCG  CCATCGGCTA  CGTCGGCCTG
1051 GCGGCAACCG  TCTGGACAGG  CATCATCCCC  GCCATGCTGC  TCTACCGTTC
1101 GCGCAAAAAA  TTCGGCGCAG  GCAAAACCTA  TAAAGTTTAC  GCGGGCTTGT
1151 GGCTGATGGT  TTGGGTCTTC  CTTTTCGGCA  TCGTCAACAT  CGCCGCACAG
1201 GTATTGAGCC  AAATGGAAC  CGTCCCGTA  TTTAAGGAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep..
1  MPNKTPSLFG  GAMIAGTVI  GAGMLANPTA  TSGVWFTGSL  AVLLYTWFSM
51  LSSGLMILEV  NTHYPHGASF  DTMVKDLLGR  GWNIINGIAV  AFVLYLLTYA
101 YIFVGGDLTA  KGLGSAAGGD  VSLTVGQLVF  FGILAFVCWA  SARLVDRETF
151 VLIGGMVLTF  IWAAGGLIAD  AKPSVLFDTQ  APAGTNYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWGT  LIALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  QQVSVLIETL  SKFAQTGNMD  KILSLFSYMA  IATSEFLGVTL
301 GLFDYIADIF  KWNDISGRT  KTAALTFLPP  LISCLLFPTG  FVTAIGYVGL
351 AATVWTGIIP  AMLLYRSRKK  FGAGKTYKVY  GGLWLMVWVF  LFGIVNIAAQ
401 VLSQMEVLP  VFKG*

```

m102/g102 86.0% identity in 415 aa overlap

	10	20	30	40	50	60
m102.pep	MPNKTPSLFGGAMIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
g102	MSAKTPSLFGGAMIAGKVIGAGMFPNPTANLGDGLIGSLIVLLYTWFPSSGALMILEV					
	70	80	90	100	110	120
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
g102	NTHNPRGASFDTMVKDLLGRGWNIINGIAVALVYGSTYAYILVGGDLTAKGIGSAVGGK					
	130	140	150	160	170	180
m102.pep	VSLTVGQLVFFGILAFVCWASARLVDRETFVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ					
g102	ISLTVGQLVFFGILAFVCWASARLVDRETFVLIGGMVLTFIWTGGLVADAKPSVLFDTQ					
	190	200	210	220	230	240
m102.pep	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					

a102.seq

1	ATGCCACCA	AAACCCCTTC	ACTGTTTCGGC	GGCGCGATGA	TTATCGCCGG
51	CACGNTCATC	GGCGCAGGTA	TGCTCGCCAA	CCCGACCGCC	ACATCCGGCG
101	TATGGTTATC	CGGCTCGCTG	GCCGTGTTGC	TGTACACCTG	GTTTTCCATG
151	CTCTCGACGC	GCGTGATGAT	TTTGGAAATC	AACACCACT	ACCCCGACGG
201	CGCGANCTTC	GACACCATGG	TAAAGACCT	GCTCGGACGG	AGCTGGAAC
251	TCATCAACGG	CATCGCCGTC	GCCTTCGTTT	TATACCTGCT	TACTTACGCT
301	TATATCTTCG	TCGGCGGCGA	CCTGACCGCG	AAAGCGTTAG	GCAGCGCGCT
351	AGGCGGCAAT	GTTTCATCTA	CCGTCCGGACA	ACTCGTCTTC	TTCCGCAATC
401	TCGCCCTTTG	CGTATGGGCA	TCCGCACGCT	TGGTCGACCG	ATTCACGAGC
451	GTCCTCATCG	GCGGCATGCT	ATTAACCTTT	ATTTGGGCAA	CCGGCGGCCT
501	GATTGCGCAT	GCCAACTCTG	CCGTCTCTTT	CGACACCCAA	GCCCCTACCG
551	GACCAACTA	CTGGATTATT	GTCGCCACCG	CCCTGCCCTG	CTGCCCTTGG
601	TCATTGCGTT	TCACGCGCAA	CGTCTCCAGC	CTGCTCAAA	AACTTTAAAG
651	CGACGCGCCC	AAAGTGGCTA	AATCCATCTG	GACGGGCACA	CTGATTGCGC
701	TGGTAATTTA	CGTCTCTGG	CAAAACGCCA	TCCAANGCAA	CCTGCCGCGC
751	AACAGTTCG	CCCCCGTGAT	TCCCGCCGAA	GGGCAAGTCT	CCGTCNTGAT
801	TGAAACCTCG	TCCAAATTCT	GCCAAACCGG	CAATATGGAC	AAATTAATTG
851	CCCTGTTTT	CTATATGGCG	ATCGCCACCT	CGTTTTTAGG	CGTAACGCTC
901	GGACTCTTCG	ACTACATCGC	CGACATCTTC	AAATGGAACG	ACAGCGTGTC
951	CGGCCCGACC	AAAACCGCCG	CGCTGACCTT	CCTGCCGCCT	NTAATTTTCT
1001	GCCTGCTCTT	CCCCACCGG	TTTGTTACCG	CCATCGGNTA	CGTCCGCGCT
1051	GCGGCAACCG	TCTGGACAGG	CATCATCCCC	GCCATCTGTC	TNTACCGTTC
1101	GCGCAAAAA	TTCCGCGCAG	GCAAAACCTA	TAAAGTTTAC	GGCGGCTTGT
1151	GGCTGATGGT	TTGGGTCTTC	CTTTTCGGCA	TCNTCAACAT	CGCCGCACAN
1201	GTATTGAGCC	AAATGGAAC	CGTCCCCGTA	TTTAAAGGAT	AA
1202					

a102.pap

```

1  MPTKTPSLFG  GAMIIAGTXI  GAGMLANPTA  TSGVWFTGSL  AVLLYTWFMS
51  LSSGLMILEV  NTHYPHGAXF  DTMVKDLLGR  SWNIINGTAV  ATVLYLLTYA
101 YIFVGGLDLA  KGLGSAAGGN  VSLTVQGQVF  FGLAFVCWA  SARLVDRFST
151 VLIGGMVLTF  IWATGGLIAD  AKPLVFLDTQ  APTGTNIWYI  VATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWTFQ  LIALVIYVLW  QTAIQXNLPR
251 NEFAPVIAAE  GQVSXKIETL  SKFAQTGNMD  KILSLFSYMA  IATSFLGVTL
301 GLFDYIADIF  KWNDSVSGRT  KTAALTFLPP  XISCLLFTFG  FVTAIGYVGL
351 AATVWTGIIIP  AMLLYRSRKK  FGAGKTYKVY  GGLWLMVWVF  LFGIXNIAAX
401 VLSQMLELVPV  FKG*

```

m102 / a102. 95.9% identity in 413 aa overlap

	10	20	30	40	50	60
m102.pep	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
a102	MPTKTPSLFGGAMIIAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXFDTMVKDLLGRSWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m102.pep	VSLTVGQLVFFGILAFCVWASARLVDRFTGVLIGGMVLTFFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFCVWASARLVDRFTSVLIGGMVLTFFIWATGGLIADAKLPVLFDTQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m102.pep	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTIALVIYVLW					
a102	APTGTNYWIYVATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTIALVIYVLW					
	190	200	210	220	230	240
	250	260	270	280	290	300
m102.pep	QTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQTGNMDKILSLFSYMAIATSFGLVTL					
a102	QTAIQXNLPRNEFAPVIAAEGQVSVXIETLSKFAQTGNMDKILSLFSYMAIATSFGLVTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m102.pep	GLFDYIADIFKWNDISISGRKTAAALFLPPLISCLLFPTGFVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDISVSGRKTAAALFLPPXISCLLFPTGFVTAIGYVGLAATVWTGIIP					
	310	320	330	340	350	360
	370	380	390	400	410	
m102.pep	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIVNIAAQVLSQMELVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIXNIAAXVLSQMELVPVFKGX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

g105.seq

```

1  Atgtccgcag aacCATACac acAAAtcggc tGGgtaggct taggGcaaat
51  gGgtctgcct atgGTAACGC GGCTCTTGA CCGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCgcg CAAAGGAGCA
151 AAAGTTTACG GCagcACCGC CGAACTCGTC CGCGCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCCG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAACAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAACA CGCTTCCAAA GacctTAACC TCGcegtcaa AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```


This corresponds to the amino acid sequence <SEQ ID 364; ORF 105.ng>:

g105.pep

```

1  MSAETTYQIG WVGLGQMGLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51  KVGYSTAELV RACPVIPLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLILFGG SEAVLNPLQK
151 IFSLVGKKTFF HFGDVGKSG AKLVLSLLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 365>:

m105.seq

```

1  ATGTCCGCAA ACGAATACGC ACAAATCGGC TGGaTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAm ATCATCGTCA ACATGAGCAC CATCTCCCGG
301 ACCGAAAaGC TCGCCGTCAA AGCACTTGTC GAAGCGCAGm GaCAGTTTGC
351 CGAAGCACCC GTTTCGGGAT CGGTCGGGCC CGCCACCAAC GGCACGCTGC
401 TGATTCTGTT CGGCGGCAGC GAAcCGtTTT AAACCGCTG CAAAAAATAT
451 TTTCCCTCGT CGGCAAAAAA ACCTTCCATT TCGGCGATGT CGGCAAAGGT
501 TCGGCGCGCA AACTCGTCTT GAACCTGCTC TTGGGCATTT TCGGCGAaCG
551 TACAGCGAAs GmTgCTGATG GCGCGGCAGT TCGGCATCGA TACCGACACC
601 ATCGTCGAAG CCATCGGSGA CTCGGCAATG GACTCGCCCA TGTTCCAAAC
651 CAAAAAATCC CTGTGGGCAA ACCGCGAATT CCCGmCCGmC TTCGCCCTCA
701 AACACGCCTC CAAAGACCTC AACCTCGCCG TCAAAGAGCT TGAACAGGCA
751 GGCAACACCC TGCCCGCCGT CGAAACCGTT GCTGCCAGCT ACCGCAAAGC
801 AGTCGAAGCC GGCTACGGGA CACAGGACGT TTCCGCGGTT TACCTGAAAC
851 TGGCAGAACA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 366; ORF 105>:

m105.pep

```

1  MSANEYAQIG WIGLGQMGLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51  KVGNTAELV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGX IIVNMSTISP
101 TEKLAVKALV EAQRQFAEAP VSGSVGPATN GTLLILFGGS EPFXTRCKKY
151 FPSSAKKPSI SAMSAKVRAR NSSXTRSWAF SANVQRXXLM ARQFGIDTDT
201 IVEAIGDSAM DSPMFQTKKS LWANREFPXX FALKHASKDL NLAVKELEQA
251 GNTLPAVETV AASYRKAVEA GYGTQDVSGV YLKLAEH

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 105 shows 79.9% identity over a 289 aa overlap with a predicted ORF (ORF 105.ng) from *N. gonorrhoeae*:

m105/g105

	10	20	30	40	50	60
g105.pep	MSAETTYQIGWVGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGSTAEVLV					
m105	MSANEYAQIGWIGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAEVLV					
	10	20	30	40	50	60
g105.pep	RACPVIPLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISP TENLAVKALVEAAGGQFAEA					
m105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGXIIVNMSTISPTEKLAVKALVEAQR-QFAEA					
	70	80	90	100	110	120
g105.pep	RACPVIPLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISP TENLAVKALVEAAGGQFAEA					
m105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGXIIVNMSTISPTEKLAVKALVEAQR-QFAEA					
	70	80	90	100	110	
g105.pep	PVSGSVGPATNGTLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG					
m105	PVSGSVGPATNGTLILFGGSEFPFXTRCKKYFPSSAKKP-SISAMSAKVRARNSSXTRSW					
	120	130	140	150	160	170

	190	200	210	220	230	240
g105.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK					
m105	AFSANVQRXXLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPXXFALKHASK					
	180	190	200	210	220	230
	250	260	270	280	289	
g105.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEH					
m105	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGTQDVSGVYLKLAEH					
	240	250	260	270	280	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 367>:

a105.seq

```

1 ATGTCCGCAA ACGAATACAC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51 GGGTCTGCCT ATGGTAACGC GGCTCTTGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCC CCATCTCCGC CAAAGCGCA
151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GCGCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTG GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCCGCAA
501 AGGTTCGGGC GCGAACTCG TCTTGAATC GCTCTGGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCG GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCCATGTT
651 CCAAACCAA AAATCCCTGT GGGCAAACCG CGAATCCCCA CCCGCCTTCG
701 CCCTCAAACA CGCCTCCAAA GACCTCAACC TCGCCGTCAG AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAATTTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 368; ORF 105.a>:

a105.pep

```

1 MSANEYTIQIG WIGLGQMLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51 KVGNTAELV RDYPIVFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
151 IFSLVGKKTFF HFGDVKGSG AKLVNLSLLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

m105/a105 96.5% identity in 289 aa overlap

	10	20	30	40	50	60
m105.pep	MSANEYAIQIGWIGLGQMLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
a105	MSANEYTIQIGWIGLGQMLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m105.pep	RDYPIVFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAG-QFAEA					
a105	RDYPIVFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
	120	130	140	150	160	179
m105.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLVNLSLLG					
a105	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLVNLSLLG					
	130	140	150	160	170	180
	180	190	200	210	220	230

315

```

m105.pep    IFGDV-QRXMLMARQFGIDTDITVEAIGDSAMDSMPFQTKKSLWANREFPXFALKHASK
||||: :: |||||||||||||||||||||||||||||||||||||||||||||||||||
a105        IFGEAYSEAMLMARQFGIDTDITVEAIGGSAMDSMPFQTKKSLWANREFPPAFALKHASK
                190      200      210      220      230      240

m105.pep    240      250      260      270      280
DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
|||||||||||||||||||||||||||||||||||||||||||||||||
a105        250      260      270      280      290
DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 369>:

g105-1.seq

```

1  ATGTCCGCAG AACATACAC ACAATCGGC TGGGTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCGAC AAAACTGCCC CCATCTCCGC CAAAGGAGCA
151 AAAGTTTACG GCAGCACC GCAGACTCGT CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GCGCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCCG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGTTCCGGC GCGAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAACAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAACA CGCTTCCAAA GACCTTAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTGCGA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 370; ORF 105-1.ng>:

g105-1.pep

```

1  MSAETYTOIG WVGLGQMLP MVTRLDDGI EVGVNRS PD KTA PISARGA
51  KVGYSTAELV RACPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
151 IFSLVGKRTF HFGDVGRKSG ARLVLNSLLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 371>:

m105-1.seq

```

1  ATGTCCGCAA ACGAATACGC ACAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GCGCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCCG GCCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGTTCCGGC GCGAACTCG TCTTGAATC GCTCTTGGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGSGACTCG GCAATGGACT CGCCCATGTT
651 CCAAACAAA AAATCCCTGT GGGCAAACCG CGAATTCCCG CCCGCCTTCG
701 CCCTCAAACA CGCCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTGCGA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAACTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 372; ORF 105-1>:

m105-1.pep

```

1  MSANEYAQIG WIGLQMLP MVTRLDDGI EVGVNRS PD KTA PISAKGA
51  KVGYNTAELV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP

```


316

101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
 151 IFSLVGKKTFF HFGDVGKSG AKLVNLSLLG IFGEAYSEXM LMARQFGIDT
 201 DTIVEAIGDS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

m105-1/g105-1 96.9% identity in 289 aa overlap

	10	20	30	40	50	60
m105-1.pep	MSANEYAQIGWIGLQMG	LPMTLLDGGIEVGVY	NRSPDKTAPISAKGAK	VYGN	TAE	LV
g105-1	MSAETYTIQIGWVGLQMG	LPMTLLDGGIEVGVY	NRSPDKTAPISAKGAK	VYG	STA	ELV
	10	20	30	40	50	60
m105-1.pep	RDYPVIFLMVSDYAAVCDIL	NGVRDGLAGKIIIVNM	STISPTENLAVKALVEA	AGGQFAEA		
g105-1	RACPVIFLMVSDYAAVCDIL	NGVRDGLAGKIIIVNM	STISPTENLAVKALVEA	AGGQFAEA		
	70	80	90	100	110	120
m105-1.pep	PVSGSVGPATNGTLLILFGG	SEAVLNPLQKIFSLVGKKT	FFHFGDVGKSGAKLVN	LSLLG		
g105-1	PVSGSVGPATNGTLLILFGG	SEAVLNPLQKIFSLVGKKT	FFHFGDVGKSGAKLVN	LSLLG		
	130	140	150	160	170	180
m105-1.pep	IFGEAYSEXMLMARQFGIDT	DTIVEAIGDSAMDSPMFQTK	KSLWANREFPPAFALKHASK			
g105-1	IFGEAYSEAMLMARQFGIDT	DTIVEAIGDSAMDSPMFQTK	KSLWANREFPPAFALKHASK			
	190	200	210	220	230	240
m105-1.pep	DLNLAVKELEQAGNTLPAVE	TVAASYRKAVEAGYGEQDVS	GVYLKLAEHX			
g105-1	DLNLAVKELEQAGNTLPAVE	TVAASYRKAVEAGYGEQDVS	GVYLKLAEHX			
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 373>:

a105-1.seq

1 ATGTCGCCAA ACGAATACAC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
 51 GGGCTGTCCT ATGGTAACGC GGCTCTTGGA CGCGCGCATC GAAGTCGGCG
 101 TATACAACCG CTCGCCCGAC AAAACTGCCC CCATCTCCGC CAAAGCGCA
 151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
 201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCTG AACGGAGTCC
 251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
 301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
 351 TGCCGAAGCA CCCGTTCCG GATCGGTCCG GCCCGCCACC AACGGCACGC
 401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
 451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCGGCG ATGTCGGCAA
 501 AGGTTCGGGC GCGAAACTCG TCTTGAATC GCTCTTGGGC ATTTTCGGCG
 551 AAGCTACAG CGAAGCGATG CTGATGGCGC GGCAATTCGG CATCGATACC
 601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCCATGTT
 651 CCAACCCAAA AAATCCCTGT GGGCAAACCG CGAATCCCA CCCGCCTTCG
 701 CCCTCAAACA CGCCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
 751 CAGGCAAGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
 801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTC GCGGTTTACC
 851 TGAAATTGGC AGAACACTGA

This corresponds to the amino acid sequence <SEQ ID 374; ORF 105-1.a>:

a105-1.pep

1 MSANEYTIQIG WIGLQMG LPMVTRLLDGGI EVGVYNRSPD KTAPISAKGA
 51 KVGNTAEILV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
 101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
 151 IFSLVGKKTFF HFGDVGKSG AKLVNLSLLG IFGEAYSEAM LMARQFGIDT
 201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

a105-1/m105-1 99.0% identity in 289 aa overlap

	10	20	30	40	50	60
a105-1.pep	MSANEYTIQIGWIGLQMG	LPMVTRLLDGGIEVGVY	NRSPDKTAPISAKGAK	VYGN	TAE	LV

m105-1	MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTEALV
	10 20 30 40 50 60
	70 80 90 100 110 120
a105-1.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
m105-1	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
	70 80 90 100 110 120
	130 140 150 160 170 180
a105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFHFQDVGKGS GAKLVNLSLLG
m105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFHFQDVGKGS GAKLVNLSLLG
	130 140 150 160 170 180
	190 200 210 220 230 240
a105-1.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
m105-1	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK
	190 200 210 220 230 240
	250 260 270 280 290
a105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
m105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
	250 260 270 280 290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

```

g107.seq
1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGGTTG CCGATGCCAA
51  ACCGTCCGTC CTCTTCGACA CCCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCCttggta atttacgtcc
251 TCTggcaaac cgccatCcaa agcaaccTGC cgcgcaacga gttcgcCCCCc
301 gtgattgccg ccgagaggca actCTCCGTC CTgaatgaaa cccTgtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc cacctccttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cggcaccaaa
501 accgtcgcgc tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

```

g107.pep
1  MVLTFIWATG GLVADAKPSV LFDTQAPVGT GYWIYAATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAAERQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSF LGVTILGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

```

m107.seq
1  ATGGTATTGA CCTTTATTTG GGCGGCCGGC GGGCTGATTG CCGATGCCAA
51  GCGGTCCGTC CTCTTCGATA CCCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGs CACCGCCCTG CCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TCGCTGGTA ATTTACGTCC
251 TCTGGCAAAc CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTCGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

```

m107.pep..
1  MVLTFIWAAG GLIADAKPSV LFDTQAPAGT NYWIYAXTAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP

```


101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTGLGLFDY
151 IAHLMERQH LRAAPKPPR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng) from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
g107	MVLTFIWTGGLVADAKPSVLFDTQAPVGTGYWIYAATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	: : : : :					
g107	KGDAPKVAKSIWAGTLVALVIYVLWQTAIQSNLPRNEFAPVIAAERQLSVLNETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSF LGVTGLGLFDYIA-HLMERQHLRAAPKPPR					
	: : : : :					
g107	TGDMDKILSLFFPYMAIATSF LGVTGLGLFDNIAGHLMERQYVRAAPKPSR					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTTATTG GGCACCGGC GGCCTGATTG CCGATGCCAA
51  ACTGCCCGTC CTCTTCGACA CCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTCGC CACCGCCCTG CCGTCTGCC TTGCGTCATT CGGTTTCCAC
151 GGCAACGTCT CCAGCTGCT CAAATACTT AAAGCGCAGC CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGGGCA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTGCCCCAA ACCGGCAATA TGGACAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTGACTAC
451 ATCGCCGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCCGCGCTG ACCTTCCTGC CGCTCTAAT TTCCTGCCTG CTCTTCCCA
551 CCGGCTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCGTCTGG
601 ACAGGCATCA TCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTCGG
651 CGCAGGCAAA ACCTATAAAG TTACGGCGG CTTGTGGCTG ATGTTTGGG
701 TCTTCCTTTT CGGCATCGTC AACATCGCCG CACAGGTATT GAGCCAAATG
751 GAACTCGTCC CCGTATTAA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWTG GLIADAKLPV LFDQTAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTGLGLFDY
151 IADIFKWNDS VSGRTKTAAL TELPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKEGAGK TYKVYGGWLW MVWVLEFGIV NIAAQVLSQK
251 ELVPVFKG*

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
a107	MVLTFIWTGGLIADAKLPVLFDTQAPTGTNYWIYVATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60

	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPERNEFAPVIAAEGQVSVLIETLSKFAQ					
a107	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPERNEFAPVIAAEGQVSVLIETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIAHLQMERQHLRAAPKPPRX					
a107	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIADIFKWNDVSVSGRTKTAALTFLPPLISCL					
	130	140	150	160	170	180
a107	LFPTGFVTAIGYVGLAATVWTGIIPAMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIV					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

```

g108.seq
1   ATGttgccgg gCTTCAACCG GATATTCAaa cggTTTGCTC CAACACTCGG
51  AAcggCGCAT AAAACGCCGc cTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATCCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGCTAT TTTGCCGGCG GCAATCTTAC TCGGCGGGTG
201 CGCCGCCGGC GGCAACACAT TCGGCAGCTT AGACGGCGGC ACGGGTATGG
251 GTGGCAGCAT CGTCAAAATG ACGGTAGAAA gccAATGCCG TCGGGAATTG
301 GACAGGCGCA GCGAATGGCG TTTGACCGCG CTGGCGATGA GTGCCGAAAA
351 ACAGGCGGAA TGGGAAACA AGATTTCGGG CTGCGCTACC GAAGAAGCAC
401 CTAACCAGCT GACCGGCAAC GATGTGATGC AGATGCTGaa ccagtccacG
451 CGCaatcagg cacTtgccgc CctgaccgTC AAAacggtTT CcgctgcTT
501 CAaacgcctg tACCGCTaa

```

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

```

g108.pep
1   MLPGFNRIFK RFAPTLGTAH KTPPFALSRT GRLIRSYRHK RRGFNRKGIE
51  MNKTLSILPA AILLGGCAAG GNTFGSLDGG TGMGGSIVKM TVESQCRABL
101 DRRSEWRLTA LAMSAEKQAE WENKICGCAT EEAPNQLTGN DVMQMLNQST
151 RNQALAAALT KTVSACFKRL YR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

```

m108.seq
1   ATGTTGCCGG GCTTCAACCG GATATTCAAA CGGTTTGTTT CAACACTCGG
51  AACGGCGCAT AAAACGCCGC CCTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATTCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGCTAT TTTGCCGGTG GCAATCTTAC TCGGCGGCTG
201 CGCCGCCGGA GCGGTAACA CATTCCGCAG CTTAGACGGT GGCACAGGCA
251 TGGGCGGCAG CATCGTCAAA ATGGCGGTTG GGAGCCAATG CCGTGCGGAA
301 TTGGACAAAC GCAGCGAATG GCGTTTGACC GCGCTGGCGA TGAGTGCCGA
351 AAAACAGGCG GAGTGGGAAA ACAAGATTG CGCTTGGCTC GCCCAAGAAG
401 CACCCGAACG GATGACCGGC AACGATGTGA TGCAGATGCT GGCTCCGTCC
451 ACGCGCAATC AGGCATTGCG CGCCCTGACC GCCAAAACGG TTTCCGCCTG
501 CTTCAAACAC CTGTACCGCT AA

```

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

```

m108.pep
1   MLPGFNRIFK RFVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNRKGIE
51  MNKTLSILPV AILLGGCAAG GGNTFGSLDG GTMGGSIVK MAVGSQCRAE
101 LDKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPERMTG NDVMQMLAPS
151 TRNQALAAALT AKTVSACFKH LYR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng) from *N. gonorrhoeae*:

m108/g108

320

	10	20	30	40	50	60
m108.pep	MLPGFNRIFKRFVPTLGTAKHTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKLSILPV					
g108	MLPGFNRIFKRFAPTLGTAKHTPPFALSRTGRLIRSYRHKRRGFNRKGIEMNKLSILPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCAAGGNTFGSLDGGTGMGGSIVKMAVGSQCRAELDKRSEWRLTALAMSAEKQA					
g108	AILLGGCAAGG-NTFGSLDGGTGMGGSIVKMTVESQCRAELDRRSEWRLTALAMSAEKQA					
	70	80	90	100	110	
	130	140	150	160	170	
m108.pep	EWENKICACVAQEAPERMTGNDVMQMLAPSTRNQALAALTAKTVSACFKHLYRX					
g108	EWENKICGCATEEAPNQLTGNDVMQMLNQSTRNQALAALTAKTVSACFKRLYRX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 385>:

a108.seq

```

1  ATGTTGCCGG  GCTTCAACCG  GATATTCAA  CGGTTTGTC  CAACACTCGG
51  AACGGCGCAT  AAAACGCCG  CCTTCGCGT  ATCCCGAAC  GGGCGGCTAA
101 TCAGATTCTA  TCGCCATAA  AGGCGGGGT  TCAACCGAA  AGGAATTGAG
151 ATGAATAAAA  CCTTGTCTA  TTTGCCGGT  GCAATCTTA  TCGGCGGCTG
201 CGCCGCCGGG  GCGGTAACA  CATTCCGCG  CTTAGACGG  GGCACAGGTA
251 TGGGCGGCAG  CATCGTCAA  ATGGCGGTG  AAAGCCAAT  CCGTCCGGA
301 TTGAACAAAC  GCAGCGAAT  GCGTTTGAC  GCGCTGGCG  TGAGTGCCGA
351 AAAACAGGCG  GAATGGGAA  ACAAGATTG  CGCTTGCGT  GCCCAAGAAG
401 CACCAACCA  GCTGACCGG  AACGATGTG  TGCAGATGT  GGATCCGTCC
451 ACGCGCAAT  AGGCACTTG  CGCCCTGAC  GCCAAACGG  TTTCCGCTG
501 CTTCAACAC  CTGTACCGT  AA

```

This corresponds to the amino acid sequence <SEQ ID 386; ORF 108.a>:

a108.pep

```

1  MLPGFNRIFK  RFVPTLGT  AHTPPFALS  RTGRLIRF  YRHKRRGF  NRKGIEMN  KLSILPV
51  MNKLSILPV  AILLGGCA  AGGNTFGS  LDG GTGMG  GSIVKMAV  ESQCRAE
101 LNKREWRLT  ALAMSAEK  QA EWENK  ICACV AQEAPN  QLTG NDVMQ  MLDPS
151 TRNQALAAL  TKTVSAC  FKH Lyr*

```

m108/a108 96.5% identity in 173 aa overlap

	10	20	30	40	50	60
m108.pep	MLPGFNRIFKRFVPTLGTAKHTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKLSILPV					
a108	MLPGFNRIFKRFVPTLGTAKHTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKLSILPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCAAGGNTFGSLDGGTGMGGSIVKMAVGSQCRAELDKRSEWRLTALAMSAEKQA					
a108	AILLGGCAAGGNTFGSLDGGTGMGGSIVKMAVESQCRAELNKRSEWRLTALAMSAEKQA					
	70	80	90	100	110	120
	130	140	150	160	170	
m108.pep	EWENKICACVAQEAPERMTGNDVMQMLAPSTRNQALAALTAKTVSACFKHLYRX					
a108	EWENKICACVAQEAPNQLTGNDVMQMLDPSTRNQALAALTAKTVSACFKHLYRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:

This corresponds to the amino acid sequence <SEQ ID 388; ORF 109.ng>:

1 ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTTGGC
51 AGCCGGTATT GAGCGTAGCC TTGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CACCGTGGTG TTCTCTCCG CTTGGTCAAT CCGGTTTTCG GCTGGGCGTT

322

```

201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAAA GAGCGCAGCG
251 CGCAATTAGG TTTCACCGGA CGCGTATTGA TACCCGTAGT AGGTTTCTTG
301 ATCTTGTGTG TGGCGATGGG TCGGTCGGG ATGCTGCCCG GTATCCCGCC
351 GTTTTGGAG CACTTCAAT CTTTGGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 392; ORF 109>:

a109.pep

```

1 MYRRVVGSL DGLGDLAAGI ERSLGRRRIL TAFSGHGNDA AQRQNHPIRR
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFTG RVLIPVVGFL
101 ILCVAMGAVG MLPGIPPFLE HFKSLG*

```

m109/a109 97.6% identity in 126 aa overlap

	10	20	30	40	50	60
m109.pep	MYRRVVGSLDGLGDLAAGIERSLGRRIITAFSGHGNDAQRQNHPIRRHRGVLFRLVN					
a109	MYRRVVGSLDGLGDLAAGIERSLGRRIITAFSGHGNDAQRQNHPIRRHRGVLFRLVN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m109.pep	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
a109	PVFGWALTMLLDNLGLIGCKERSAQLGFTGRVLIPVVGFLILCVAMGAVGMLPGIPPFLE					
	70	80	90	100	110	120
m109.pep	HFKSLGX					
a109	HFKSLGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 393>:

g111.seq

```

1 ATGCCGCTCTG AACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAAATAC AAAAGCGCAT
201 TGATGATGCG CTAAAGAAG TCAACCGGCA GATGtccACC TACCAGACCG
251 ATTCCGAAAT CAGCCGGTTt atacagacan atgctggaga gctcttcgcg
301 tntcatgcag nttctataac tgattccgcc gaagactgtc tgcctaatac
351 gcctatctca tcggcgctct ga

```

This corresponds to the amino acid sequence <SEQ ID 394; ORF 111.ng>:

g111.pep

```

1 MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLOGET MGTITYVKYL
51 SNNRDKLPSP AKIQKRIDDA LKEVNRQMSY YQTDSEISRQ IQTAGELFAH
101 ASITDSAEDC LPNTPISSAL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 395>:

m111.seq

```

1 ATGCCGCTCTG AACACGCCT GCCGAACCTT ATCCGCGCTCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAAACGCAT
201 CGATGACGCG CTAAAGAAK TCAACCGGyA GATGTCCACC TATCAGCCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCC GC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACACAC GGCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCCG CCCGACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA

```


323

```

601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GGCGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCGATG
901 ACGCGGACG GCTTGTCAC AGGATTATTC GTATTGGCGC AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAATCTCG TGTTTTCCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAACTGcTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 396; ORF 111>:

```

m111.pep
1  MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLOGET MGTITYXVKYL
51  SNNRDKLPSP AEIXKRIDDA LKEXNRXMST YQPDSEISR FNOHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
151 IKQAASYTGI DKIIILKQGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPR IGIEQPNIVQ GGNTQIIVPL
251 NNRLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

ORF 111 shows 88.7% identity over a 97 aa overlap with a predicted ORF (ORF 111.ng) from *N. gonorrhoeae*:

```

m111.pep/g111.pep

      10      20      30      40      50      60
m111.pep  MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLOGETMGTITYXVKYLSNNRDKLPSP
          |||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g111       MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLOGETMGTITYXVKYLSNNRDKLPSP
          10      20      30      40      50      60

      70      80      90      100     110     120
m111.pep  AEIXKRIDDALKEKNRKMSTYQPDSEISR FNOHTAGKPLRISSDFAHVTA EAVRLNRLTH
          |:| |||||:| ||||| ||||| ||||| |:|:|
g111       AKIQKRIDDALKEVNROMSTYQTDSEISRFIQT XAGELFAXHXSITDSAEDCLPNTPI S
          70      80      90      100     110     120

      130     140     150     160     170     180
m111.pep  GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIIILKQGDYASLSKTHPK
g111       SALX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 397>:

a111.seq

```

1  ATGCCGCTCTG AACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTGC
51  CCTGAGTTT ATCTTCCTGA ACGCCTGTTT GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGTTTC AACCAACACA CAGCCGGCAA GCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG
351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTTCG CCCGACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCAAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAACG CGCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GGCGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA

```


801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
 851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTGCAGTG
 901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
 951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTG ATTGTCAGGG
 1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAAGTCTC
 1051 CGCTAA

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

1 MPSETRLPNF IRTLIFALSE IFLNACSEQT AQTVTLQGET MGTTYTVKYL
 51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR
 101 ISSDFAHVTA EAVHLNRLTH GALDVTGVL VNLWGFGPK SVTREPSPEQ
 151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
 201 LEKYGIQNYL VEIGGELHGK GKNARGEPR IGIEQPNIVQ GGNTQIIVPL
 251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPISHNLA SISVADSAM
 301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
 351 R*

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQT AQTVTLQGETMGTTYXVKYLSNNRDKLPSP					
a111	MPSETRLPNFIRTLIFALSFIFLNACSEQT AQTVTLQGETMGTTYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISDFAHVTA EAVHLNRLTH					
a111	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISDFAHVTA EAVHLNRLTH					
	70	80	90	100	110	120
m111.pep	130	140	150	160	170	180
	GALDVTGVLVNLWGFGPKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
a111	GALDVTGVLVNLWGFGPKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
	130	140	150	160	170	180
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGNARGEPRIGIEQPNIVQ					
a111	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGNARGEPRIGIEQPNIVQ					
	190	200	210	220	230	240
m111.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNNKRPISHNLASISVADSAM					
a111	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNNKRPISHNLASISVADSAM					
	250	260	270	280	290	300
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

1 ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
 51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTT GGAACAAACC GCGCAAACCG
 101 TTACCCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
 151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAAATAC AAAAGCGCAT
 201 TGATGATGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TACCAGACCG


```

251 ATTCGGAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ATTTCCGACA CGTTACCGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACTCAC GGCGCACTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGGTTCGG CCCCGACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGCAACA
501 AGGCAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAA GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAATAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCggcGAGTT
651 GCACGGCAA GGCAAAATG CGCACGGCGA ACCGTGGCGC ATCGGTATAG
701 AGCAACCCAA TATcatccaa gycggcaata cgcAGattat cgtcccgcgtg
751 aaCaaccgtt cgtttgccac ttccggcgAT taccgtATT tccacgtcgA
801 TAAAAACGGC Aaacgccttt cccacATCAT CAATCCCAAC AACAAACGAC
851 CCATCAGcCA CAacctcgcc tcCATCagCg TGGTCTCAGA CAGTGCATG
901 ACGCGGAGC GTTTATCCAC AGGATTATT GTTTTAGGCG AAACCGAAGC
951 CTTAAGGCTG GCAGAACAAG AAAAATCTGC TGTTCCTTA ATTGTCGGG
1001 ATAAGGACGG CTACCGCACC GCCATGTCTT CCGAATTGTC CAAGCTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 400; ORF 111-1.ng>:

g111-1.pep

```

1 MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLQGET MGTITYVKYL
51 SNNRDKLPSP AKIQKRIDDA LKEVNROMST YQTDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFGPDK SVTREPSPEQ
151 IKQAASYTGI DKIIKQGGK YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHCK GKNHAGEPWR IGIEQPNIIQ GGNTQIIIVPL
251 NNRLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNL A SISVVSAMS
301 TADGLSTGLF VLGETEALRL AEQEKLAFL IVRDKGYRT AMSSEFAKLL
351 R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 401>:

m111-1.seq

```

1 ATGCGCTCTG AAACACGCCT GCCGAACTTT ATCCGCGTCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAAACCG
101 TTACCTCTGA AGCGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAACGCGAT
201 CGATGACCGG CTTAAAGAG TCAACCGGCA GATGTCACCT TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGATTCGG CCCCGACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAGAT TACGCTTCCT TGAGCAAAAC CCACCCAAAG GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAATAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAA GGCAAAACG CGCGCGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GCGCGCAATA CGCAGATTAT CGTCCCGCTG
751 AACACCCGTT CGCTTGCCAC TTCGCGCAT TACCGTATT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTGCAGA CAGTGCATG
901 ACGCGGAGC GCTTGCCAC AGGATTATC GTATTGGGCG AAACCGAAGC
951 CTTAAGCTG GCAGAGCGG AAAAATCTGC TGTTCCTTA ATTGTCAGG
1001 ATAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGTA AAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 402; ORF 111-1>:

m111-1.pep

```

1 MPSETRLPNF IRVLIIFALGF IFLNACSEQT AQTVTLQGET MGTITYVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNROMST YOPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFGPDK SVTREPSPEQ
151 IKQAASYTGI DKIIKQGGK YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHCK GKNARGEPR IGIEQPNIVQ GGNTQIIIVPL
251 NNRLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNL A SISVVSAMS
301 TADGLSTGLF VLGETEALKL AEREKLAFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111-1/g111-1 96.6% identity in 351 aa overlap

```

          10      20      30      40      50      60
m111-1.pep MPSETRLPNFIRVLIIFALGFIFLNACSEQTAQTVTLQGETMGTITYVKYLSNNRDKLPSP
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
g111-1      MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLQGETMGTITYVKYLSNNRDKLPSP

```


	10	20	30	40	50	60
	70	80	90	100	110	120
m111-1.pep	AEIQKRIDDALKEVNROMSTYQPDSEISRNFQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
g111-1	AKIQKRIDDALKEVNROMSTYQTDSEISRNFQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m111-1.pep	GALDVTVGPLVNLWGFGPDKSVTREPSPEQIKQAASYTGIDKIIKQGGDYASLSKTHPK					
g111-1	GALDVTVGPLVNLWGFGPDKSVTREPSPEQIKQAASYTGIDKIIKQGGDYASLSKTHPK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m111-1.pep	AYLDLSSIAKGFVGVKAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQ					
g111-1	AYLDLSSIAKGFVGVKAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIIQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m111-1.pep	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPI SHNLASISVVADSAM					
g111-1	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPI SHNLASISVVSDSAM					
	250	260	270	280	290	300
	310	320	330	340	350	
m111-1.pep	TADGLSTGLFVLGETEALKLAEREKLAFLIVRDKGGYRTAMSSEFEKLLRX					
g111-1	TADGLSTGLFVLGETEALRLAEQKLAFLIVRDKGYRTAMSSEFAKLLRX					
	310	320	330	340	350	

g111-1/p44550

sp|P44550|YOJL HAEIN HYPOTHETICAL LIPOPROTEIN HI0172 PRECURSOR.>gi|1074292|pir||C64144
 hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)
 lipoprotein, putative [Haemophilus influenzae Rd] Length = 346
 Score = 349 bits (885), Expect = 2e-95
 Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQTVTLOGETMGTTYXVKYLSNNRDKLPSPAEIXKRIDDALKEXNRXMTYQ 82
 L AC ++T + ++L G+TMGTTY VKYL + S + + I+ LK+ N MSTY+
 Sbjct: 17 LAACQKET-KVISLSGKTMGTTYHVKYLDGGSITATS-EKTHEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRNFQHT-AGKPLRISSDFAHVTAEAVRLNRLTHGALDVTVGPLVNLWGFGPDKS 141
 DSE+SRNFQ+T P+ IS+DFA V AEA+RLN++T GALDVTVGP+VNLWGFGP+K
 Sbjct: 75 KDSELSRNFQNTQVNTPIEISADFAKVLAEAIRLNKVTEGALDVTVGPVVNLWGFGPEKR 134

Query: 142 VTREPSPEQIKQAASYTGIDKIIKQGGDYASLSKTHPKAYLDLSSIAKGFVGVKAGELE 201
 ++P+PEQ+ + ++ GIDKI L K+ A+LSK P+ Y+DLSSIAKGFVGV+VA +L
 Sbjct: 135 PEKQPTPEQLAERQAWVGIDKITLDTNKEKATLSKALPQVYVDLSSIAKGFVGVQVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQGGNTQIIIVPLNNRSLATSGDY 261
 E+ QNY+VEIGGE+ KGKN G+PW+I IE+P + ++ LNN +A+SGDY
 Sbjct: 195 EQLNAQNYMVEIGGEIRAKGNIEGKRPWQIAIERPTTGERAVEAVIGLNNMGMASSGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNKRPI SHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321
 RI+ ++NGKR +H I+P PI H+LASI+V+A ++MTADGLSTGLFVLGE +AL++A
 Sbjct: 255 RIY-FEENGKRAHEIDPKTGYPHQHHLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLAFLIVRDKGGYRTAMSSEFEKL 349
 E+ LAV+LI+R G+ T SS F+KL
 Sbjct: 314 EKNNLAVYLIIRTDNGFVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

a111-1.seq

```

1  ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTCG
51  CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101  TTACCTCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151  TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201  CGATGACGCG CTTAAGAAG TCAACCGCA GATGTCCACC TATCAGCCCG
251  ACTCCGAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCCGC
301  ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCGTCC ACCTGAACCG

```



```

351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCCG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GCAAAAACG CGCGCGGCGA ACCTTGCGCG ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAGCGGC AAACGCCCTC CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAATCGC TGTTCCTCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

```

a111-1.pep
1  MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLOGET MGTITYTKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTGVL VNLWFGPDK SVTREPSPEQ
151 IKQAASVTGI DKIIILKQGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHKG GKNARGEPR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPISHNLA SISVVDASAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

a111-1.pep	10	20	30	40	50	60
	MPSETRLPNFIRTLIFALSFI FLNACSEQTAQTVTLQGETMGTITYTKYLSNNRDKLPSP					
m111-1	MPSETRLPNFIRVLIFALGFI FLNACSEQTAQTVTLQGETMGTITYTKYLSNNRDKLPSP					
	10	20	30	40	50	60
a111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVHLNRLTH					
m111-1	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH					
	70	80	90	100	110	120
a111-1.pep	130	140	150	160	170	180
	GALDVTGVLPLVNLWFGPDKSVTREPSPEQIKQAASVTGIDKIIILKQGDYASLSKTHPK					
m111-1	GALDVTGVLPLVNLWFGPDKSVTREPSPEQIKQAASVTGIDKIIILKQGDYASLSKTHPK					
	130	140	150	160	170	180
a111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKGFVGVKAGELEKYGIQNYLVEIGGELHKGKKNARGEPRIGIEQPNIVQ					
m111-1	AYLDLSSIAKGFVGVKAGELEKYGIQNYLVEIGGELHKGKKNARGEPRIGIEQPNIVQ					
	190	200	210	220	230	240
a111-1.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPISHNLA SISVVDASAM					
m111-1	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPISHNLA SISVVDASAM					
	250	260	270	280	290	300
a111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
m111-1	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

```

g114.seq
1  ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51  GACTTTTTTA TGTCCGCCGG GCGGGACGAG TATGGGGCGG TCAATGTCGG

```


g114.ppe

m114.seq

m114.pep

all4.seq

1	ATGCCGGAGG	CAAGCATCGC	CTCCATCACT	TCGCCGCTGC	ACGGGGCGCA
51	ACAGGAATGC	AGCAAGACTT	TTTTATGTCC	GCCGGGCGGG	ACGAGTATGG
101	GGCGGTCATC	GTCGGTAACG	GTAGGTTTGT	TTTGTGTTTC	CATTAACCTA
151	ACGATATCTG	TCGAAATACG	TTGAAGCGGC	TATTTATCA	GAGCCGCCGC
201	ATGTAAACA	GGGTGTCAGG	GCATCAGCCC	GAGCTGCCTG	ACGAACCGGA
251	CGGTTTGCGC	CGTTACGATA	AAATGGTCGA	GCAGCGACAC	ATCGACCAGC
301	GACATTGCCT	GTCGCCAGCG	CCTTGTGAAC	ATGATGCTT	CCTGCGAAGG
351	TTCCGGCCGAG	CCGCCGGAT	GCTTGTGCGC	GATAATCAGG	CTGTCCGCAT
401	ATTCTGCCAA	TGCCAGTTTG	AGGATTTCAC	GGATGTAA	

This corresponds to the amino acid sequence <SEQ ID 410; ORF 114.a>:

a114.pep

```

1  MPEASIASIT SPLHGAQOEC SKTFLCPPGG TSMGRSMSVT VGLFCVSINL
51  TISVEYG*SG YFIRAAACKT GCQGISPSCL NERTVCAVTI KWSSSDTSTS
101 DIACASRLVN MMSSCEGSGE PPGWLCAIIR LSAYSSNASL TISM*
```

m114/a114 92.9% identity in 140 aa overlap

```

              10      20      30      40      50
m114.pep      MASITSPLHGAHRECSKTFLCPPGGTSIGRSMSTVGLFCVSINLTISVEYGXSG
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           MPEASIASITSPLHGAQOECSTFLCPPGGTSMGRSMSTVGLFCVSINLTISVEYGXSG
              10      20      30      40      50      60

              60      70      80      90      100     110
m114.pep      YFIRAAACKTECQGINPSCLEQTLXVTIKWSSSDTSTSDIACASRLVNMSSCEXSSE
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           YFIRAAACKTGCGISPSCLNERTVCAVTIKWSSSDTSTSDIACASRLVNMSSCEGSSE
              70      80      90      100     110     120

              120     130     140
m114.pep      PPGWLCAIIRLSAYSSNASLTISM*
              :|||||:|||||:|||||:|||||:|||||:|||||
a114           PPGWLCAIIRLSAYSSNASLTISM*
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 411>:

g117.seq

```

1  atggtcgacg aactcgacCT GCTGCCCGAT GCCGTGCGCG CCACCCTGCT
51  TGCGGACATC GGACGCTACG TCCCGGATTG GAACCTATTG GTTTCGAGC
101 GCTGCAACAG CACCGTCGCC GAGCTGGTCA AAGGTgtgga CGAAGTGCAG
151 AAACCTACCC ACTTCGCCCG GGTGGACAGC CTCGCCACGC CGGAAGAACG
201 CGCACAGCAA GCGGAAACCA TCGGAAAAT GCTGCTGGCG atggttaccg
251 Acatccgcgt cgtATTATC AAACCTGGCGA TCGGTacgcg caccCTGcta
301 ttTTtaagCA ACGCCCCGA CAGCCCTGAA AAACgcgccG TCgcaaAga
351 aacctCGAC ATCTTCGCC CGCTCGCCAA CCGCTTGGGC GTGTGGCAGC
401 TCAATGGCA GCTCGAAGAT TTGGGCTTCC GCCATCAAGA ACCCGAAAAA
451 TACCGCGAAA TCGCCCTGCT TTTGGACGAA AAACGCACCG AACGCTCGA
501 ATACATCGAA AACTTCTCTG ATATCTCTCG TACGGAATC AAAAAATACA
551 ATATCCACTT TGAAGTCGCC GGCCGTCCGA AACACATCTA CTCCATTAC
601 AAAAAAATGG TGAAGAAAAA ACTCAGCTTC GACGgctGT TCGACATCCG
651 CGCCGTGCGG ATTCTGGTGG ATACCGTCCC CGaGTGTTAC ACCACGCTGG
701 gcaTCGTCCA CAGCTCTGG CAGCCCATTC CCGCGagtt CGAcgactAC
751 ATCGCCAACC CCAAAGgcaA CGgttATAAA AgtTTGCACA CCGTCATCGT
801 cggcccGGAA gacaaaggtg tggaaGtgCA AATCCGCACC TTCGAtatGC
851 accAATTCAa CgaatTcgT gtcgcccGCC ACTGGCGtta caaagaaggc
901 ggcaaaggcg attccGCtA cgaacaaAAA ATcgccTggt TGCgccaACT
951 CTTGGACTGG CGCGAAAATA TGGCGGAAAG CGGCAAGGAA GACCTCGCCG
1001 CCGCCTTCAA AACCGAGCTT TTCAACGACA CGATTATGT TTTGACCCCG
1051 CACGGCAAAG TCCTCTCTCT GCCAACGGGC GCNACCCCA TCGACTTCGC
1101 CTACGCCCTG CACAGCAGCA TcgCGACCG CTGCCGGGGC GCGAAAGTCG
1151 AaggGCAGAT TGTGCCGCTG TCCACCCCGC TCGAAAACGG ACAGCGCGTC
1201 GAAATcatta cCGCcaaAGA AGGGCATCCT TCCGTCAACT GGCTTTACGA
1251 AGGctgGGtc aaATCCGGCA AGGCCATCGG caaAATCCGC GCCTAcatCC
1301 GCCAGcaaAa cgCgaCACC GTGCGCGAAG AAGGCCGTGT CCAACTCGAC
1351 AAGCAGCTTG CCAAACCTAC GCCCAAACCC AACCTGCAAG AGCTTgcca
1401 aaATCTCGGC taaaaAAGC cagaagacct ctacacCGCc gtcggacaag
1451 gcgaaatttc caaccgcgcc atCaaaaaag cctgcgccac GCTgaacgaa
1501 ccgccccCGG TGCCCGTCAG CGCAACCACC ATCGTCAAC AGTCCAAAT
```



```

1551 CAAAAAAGGT GGCAAAACCG GCGTGCTCAT CGACGGCGAA GACGGCTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAACCCG CGCCGCCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTC GTCCACCGCA AAACCTGCCC
1701 CTCTTTCCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAGGAA GGGCAAGTGT TCGCCGTCGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCGG GCTTTTGCGC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTTA CCGCCGTGCA AACCCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTTACAG CTCGAAGTCA AACAAGtCAA CGacCTCCCG
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAA GCGGTATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

g117.pep

```

1 MVDEL DLLPD AVAATLLADI GRYVPDWNLL VSERCNSTVA ELVKGVDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVLI KLAMRTRTLL
101 FLSNAPSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHQEPEK
151 YREIALLLDE KRTERLEYIE NPLDILRTEL KKYNHFEVA GRPKHIYSIY
201 KKMVKKLSF DGLFDIRAVR ILVDTVPECY TLGIVHSLW QIPGEFDDY
251 IANPKGNGYK SLHTVIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 KGKDSAYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLTP
351 HGKVLSLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQRV
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIRQONADT VREEGRVQLD
451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
501 PPPVPVSATT IVKQSKIKGK GKTGVLIDGE DGLMTTLAKC CKPAPPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTAQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLGDVK GVLSTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

m117.seq (partial)

```

1 ..GTGAACTCA AGAAATACAA TGTCCATTTC GAAGTCGCCG GCCGCCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCCTCTT TGACATCCGC GCCGTGCGAA TTCTGGTTGA TACCGTCCCC
151 GAGTGTACCA CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCCATTC
201 CGGCGAGTTC GACGACTACA TCGCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTGCACAC CGTCATCGTC GGCCCGGAAG ACAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATTCAAC GAATTCGGTG TCGCCGCCCA
351 CTGgCGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAACTC TTGGACTGGC GCGAAAACAT GGCGGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAA ACCGAGCTTT TCAACGACAC
501 GATTTATGTT TTGACCCCGC ACGGCAAAGT CCTCTCCCTG CCCACGGGCG
551 CGACCCCAT CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCGCGGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCGCT
651 CGAAAACGGA CAGCGCGTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CCTACATCCG CCAGCAAAAC GCGGACACCG TGCGCGAAGA
801 AGGCCGCGTC CAACTCGACA AACAGCTTGC CAAACTCACG CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGCT ACAAAGGCC AGAAGACCTC
901 TACACCGCCG TCGGACAAGG CGAAATTTCC AACCAGCGCA TCCAAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCCGT ACCCGTCAGC GAAACCACCA
1001 TCGTCAAACA GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCACGCTT GCCAAATGCT GCAAACCCGC
1101 GCGGCCGAC GATATTATCG GCTTCGTTAC CCGCGAGCGC GgCATTTCAC
1151 TGCACCGCAA AwyyTkCyCG TCTTTCCAAC ACCTCGCCGA ACACGCGCC
1201 GAwAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCCGTCGAT ATCGAAATCC GCGCCCAAGA CCGCTCCGGG CTTTTGCGCG
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAAC TCAACGTTAC CGCCGTGCAA
1351 ACCCAGTCCC GCGACTTGA AGCCAGCATG AGGTTCACGC TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCCGC GCGTCTCGC CAGCCTCGGC GACGTCAAAG
1451 GCGTATTGAG CGTTACCCCG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

m117.pep (partial)


```

1...VKLKKYNVHF EVAGRPKHIY SIYKKMVKKK LSFGLFDIR AVRILVDTVP
51 ECYITLGIHV SLWQIPGEF DDYIANPKGN GYKSLHTVIV GPEDKGVEVQ
101 IRTFDMHQFN EFGVAHWRY KEGGKGSAY EQKIAWLRQL LDWRENMAES
151 GKEDLAAAFK TELFNDTIYV LTPHGKVLSL PTGATPIDFA YALHSSIGDR
201 CRGAKVEGQI VPLSTPLENG QRVEIITAKE GHPSVNWLYE GWVKSNAIG
251 KIRAYIRQON ADTVREEGRV QLDKQLAKLT PKPNLQELAE NLGYKKPEDL
301 YTAVGQGEIS NRAIQKACGT LNEPPPPVPS ETTIVKQSKI KKGKNGVLI
351 DGEDGLMTTL AKCKPAPPD DIIGFVTRER GISVHRKXXX SFQHLAEHAP
401 XKVLDASWAA LQEGQVFAVD IEIRAQDRSG LLRDVSDALA RHKLNVTAVQ
451 TQSRDLEASM RFTLEVQVN DLPRVLASLG DVKGVLVTR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 117 shows 97.6% identity over a 490 aa overlap with a predicted ORF (ORF 117.ng) from *N. gonorrhoeae*:

m117/g117

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
g117				:	:	:
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVP	ECYITLGIHSLWQIPGEF	DDYIANPKGNGYKSLHTVIV		
g117		:	:	:	:	:
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQIRTFDMHQFN	EFGVAHWRYKEGGKGSAY	EQKIAWLRQLLDWRENMAES		
g117		:	:	:	:	:
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYV	LTPHGKVLSP	TGATPIDFAYALHSSIGDR	CRGAKVEGQIV	
g117		:	:	:	:	:
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQRVEIITAKE	GHPSVNWLYEGWVKSNAIG	KIRAYIRQONADTVREEGRVQ		
g117		:	:	:	:	:
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAEN	LGYPKPEDLYTAVGQGEIS	NRAIQKACGT	LNEPPPPVPS	
g117		:	:	:	:	:
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKI	KKGKNGVLIDGEDGLMTTL	AKCKPAPPDDIIGFVTRER	GISVHRKXXXS	
g117		:	:	:	:	:
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPXKVLDA	SWAALQEGQVFAVDIEIRAQDRSG	LLRDVSDALARHKL	NVTAVQT	

a117.seq

1	ATGTTTCATG	AACTCGACCT	GCTCCCGCAT	GCCGTCGCCG	CCACCTTGCT
51	TGCCGACATC	GGACGCTACG	TCCCGGACTG	GAACCTATTG	GTTTCCGAAC
101	GCTGCAACAG	TACCGTCGCC	GAGCTGGTCA	AAGGTTGGGA	CGAAGTGCAG
151	AAACTCACC	ACTTCGCCCC	GGTGGACAGC	CTCGCCACGC	CGGAAGAAGC
201	CGCCGACGAG	CGAGAAACTA	CTCGGAAATC	GCTGCTGGCG	ATGGTTACCG
251	ACATCCGCGT	CGTGTTAATC	AAACTGGCGA	TGCGTACGCG	CACCCTGCAA
301	TTTTTAAGCA	ACGCCCCGGA	CAGCCCCGAA	AAACGCGCCG	TGCGCAAAG
351	AACCCTCGAC	ATCTTGCGCC	CGCTCGCCAA	CGGTTTGGGC	GTGTGGGACG
401	TCAAATGGCA	GCTCGAAGT	TTGGGCTTCC	GCCATCAAGA	ACCCGAAAA
451	TACCGCGAAA	TGCCCTTGCT	TTGGACGAA	AACGCGACCG	AACGCGTCGA
501	ATACATCGAA	AACTTCTTTA	ATATCCTGCG	TACGGAACCT	AAAAAATACA
551	ATATCCACTT	TGAAGTCGCG	GGCCGTCGCA	AACACATCTA	CTCCATTTAC
601	AAAAAATG	TGAAGAAAAA	ACTCAGCTTC	GACGGGTTGT	TGCAACTCCG
651	CGCCGTGCGG	ATTCTGGTTG	ATACCGTCCC	CGAGTGTTAC	ACACACTGG
701	GCATTGTCCA	CAGCCTCTGG	CAGCCCATTC	CCGGCGAGTT	CGACGACTAC
751	ATCGCCAACC	CGAAAGGCAA	CGGCTATAAA	AGTTTGACA	CCGTCATCGT
801	CGGCCCGGAA	GACAAAGGCG	TGGAAGTGCA	AATCCGCACC	TTCGATATGC
851	ACCAATTCAA	CGAATTGGGT	GTCGCGCGCG	ACTGGCGTTA	CAAGAGGGCG
901	GGCAAAGGCG	ATTCCGCTTA	CGAACAAAAA	ATCGCCTGGT	TACGCCAACT
951	TTTGGACTGG	CGCGAAAAA	TGGCGGAAAG	CGGCAAGGAA	GACCTCGCCG
1001	CGCCCTPCAA	AACCGAGCTT	TTCAACGACA	CGATTTATGT	TTTGACCCCG
1051	CACGGCAAAG	TCCTTCTCCCT	GCCCACAGGC	GCGACCCCCA	TCGACTTCGC
1101	CTACGCGCTG	CACAGACGCA	TCCGGCAGCG	TTGCCGCGGT	GCGAAGTTCG
1151	AAGGGCAGAT	TGTGCCGCTG	TCCACCCCGC	TCGAAAACGG	ACAGCGTGTC
1201	GAAATCATTA	CCGCCAAAGA	AGGGCATCCT	TCCGTCAACT	GGCTTTACGA
1251	AGGCTGGGTC	AAATCCAACA	AGGCAATCGG	CAAAATCCCG	CCCTACATCC
1301	GCCAGCAAAA	CGCCGACACC	GTCGCGGAAG	AAGGCCGCGT	CCAACCTCGAC
1351	AAACAGCTTG	CCAAACTCAC	CGCCAAACCC	AACCTGCAAG	AGCTTGCCGA
1401	AAATCTCGGC	TACAAAAAGC	CAGAAGACCT	CTACACCGCC	GTGCGACAAG
1451	GCGAAATTTT	CAACCGCGCC	ATCCAAAAAC	CCTGCGGCAC	GCTGAACGAA
1501	CCGCGCGCCG	TACCCGTTCG	CGGAACCAAC	ATCGTCAAA	AGTCCAAAA
1551	CAAAAAGAGC	GGCAAAAAACG	CGGTGCTCAT	CGACGCGGAA	GACGGTCTGA
1601	TGACCACGCT	TGCCAAATGC	TGCAAACCCG	CGCGGCCCGA	CGACATTGTC
1651	GGCTTGCTTA	CCGCGCATCG	CGGCATTTG	GTACACCGCA	AAACCTGCCC
1701	CTCTTTCCGA	CACCTCGCCG	AACACGCGCT	CGAAAAAGTA	CTGGACGCAA
1751	GTTGGGCGCG	GTTGCAGGAA	GGACAAGTGT	TGCGCGTCA	TATCGAAATC
1801	CGCGCCCAAG	ACCGCTTCGG	GCTTTTGGCG	GACGATATCC	ACGCGCTCGC
1851	CCGCCACAAA	CTCAACGTTA	CCGCGGTGCA	AACCCAGTCC	CGCGACTTGG
1901	AAGCCAGCAT	GAGGTTACAG	CTCGAAGTCA	AACAAGTTAC	CGACCTCCCA
1951	CGCGTCTCTG	CCAGCCTCGG	CGACGTCAAA	GGCGTATTGA	GCGTTACCCG
2001	GCTTTTAA				

a117.pap

1	MVHELDLLPD	AVAATLLADI	GRYPVDWNL	VUSERCNSTVA	ELVKGVDVQ
51	KLTHFARVDS	LATPEERAQD	AETMRKMLLA	MVTDIRVULI	KLAMRTHTEQ
101	FLSNAPDSPE	KRAVAKETLD	IFAPLANRLE	VWLQKQWLED	LGFRHQEPEK
151	YREIALLLDE	KRTERLEYIE	NFLNILRLE	KKYNHFEVA	GRPKHIYSYI
201	KKMVKKKLSF	DGLFDIRAVR	ILVDTVPECY	TTLGIVHSLW	QPPIGEFDDY
251	IANPKSNGYK	SLHTVIWGPE	DKGEVQISRT	FDMHQFNEFG	VAAHWRVYKEG
301	KGKDSAYEQK	IAWLRQLLDW	RENMAESQKE	DLAAAFKTLE	FNDTYIVLTP
351	HGKVLSLPTG	ATPIDFAYAL	HSSJGDRCRG	AKVEGOIVPL	STPLENGORV

401 EIITAKEGHP SVNWLYEGWV KSNKAIGKIR AYIRQQNADT VREEGRVQLD
 451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLINE
 501 PPPVPVSETT IVKQSKIKGK GKNGLIDGE DGLMTTLAKC CKPAPPDDIV
 551 GFVTRDRGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
 601 RAQDRSGLLR DVSDALARHK LNVTAQTQS RDLEASMRFT LEVKQVTDLP
 651 RVLASLGDVK GVLSTRL*

m117/a117 98.0% identity in 490 aa overlap

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
a117				: :		
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIPGFDDYIANPKGNGYKSLHTVIVG				
a117						
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESG				
a117						
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYVLTTPHGKVLSTPGATPIDFAYALHSSIGDRCRGAKVEGQIV				
a117						
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQORVEIITAKEGHP SVNWLYEGWV KSNKAIGKIRAYIRQQNADTVREEGRVQ				
a117						
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAENLG YKKPEDLYTAVGQGEISNRAIQKACGTLINEPPVPVSE				
a117						
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKIKGKNGVLIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKXXXS				
a117						
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPXKVLDA SWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQT				
a117						
	570	580	590	600	610	620
m117.pep		460	470	480	490	
		QSRDLEASMRFTLEVQVNDLPRVLASLGDVKGVLSVTRLX				
a117						
	630	640	650	660		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTCGCTGG CGCAGGAACA TTATCCTGCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GCGCGAAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCGCGGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC ACAGCAAGCG GAAACCATGC GGAATAAGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT ATTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCGTCAATTT TTAAGCAACG CCCCAGACAG CCCTGAAAAA CGCGCCGTCG
551 CCAAGAAAC CCTCGACATC TTCGCCCGC TCGCAACCG CTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAGAACC
651 CGAAAAATAC CGCGAATCG CCCTGCTTTT GGACGAAAAA CGACCCGAAC
701 GCCTCGAATA CATCGAAAC TTCTCGATA TCCTGCGTAC GGAACCAAA
751 AAATAACAATA TCCACTTTGA AGTCGCCGCG CGTCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGCCTGTTCT
851 ACATCCGCGC CGTGGCGATT CTGGTCGATA CCGTCCCGGA GTGTTACACC
901 ACGCTGGGCA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGagtttCGA
951 cgactACATC GCCAACCCCA AAGgcaACGg ttATAAAAGt TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtgg aagtgcAAAT CCGCACCTTC
1051 GATATGcacc AATTcCaaCga ATTcGGTgTC GCCGCCCACT GGCgTTACAA
1101 AGAAGCGCGC AAAGGCGATT CCGCCTACGA ACAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGCGCG GAAAAATATG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CTTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCCATCG
1301 ACTTCCGCTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAAA TCCGGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGTGTCCA
1551 ACTCGACAAG CAGCTTGCCA AACTCAGGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACGCGCGTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTGC CCGTCAGCGC AACCACCATC GTCAAAACAGT
1751 CCAAAATCAA AAAAGGTGGC AAAACCGCGC TGCTCATCGA CGCGGAAGAC
1801 GGCTTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTGCCGCG TTCGTTACCC GCGAGCGCGG CATTTCCGTC CACCGCAAAA
1901 CCTGCCCTC TTTCCGACAC CTGCGCGAAC ACGCGCCGA AAAAGTACTG
1951 GACGCAAGT GGGCGCGGTT GCAGGAAGGG CAAGTGTTCG CCGTCGATAT
2001 CGAAATCCCG GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAA CAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAA AAGTCAACGA
2151 CCTCCGCGC GTCTCGCGC GCCTCGGCGA TGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFDSYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNIHFEVAG RPKHIYSIYK KMVKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKGNKYKS LHTVIVGPPE KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTEH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQORVE IITAKEGHPS VNWLYEGWVK SGKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGETSNRAI QKACGTLNEP PPVPVSATTI VKQSKIKKGG KTGVLIDGED
601 GLMTTLAKCC KPAPPDDIAG FVTRERGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLAGLGDVKG VLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

g117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

```



```

51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCGG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTTGCTGG CGCAGGAACA TTACCCCGCC
151 GATGCCGCGCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GCGCGAAATG GTTCATGAAC TCGACCTGCT CCCCGATGCC GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301 TCCGAACGCT GCAACAGTAC CGTCGCGGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC CCAGCAGGCA GAAACTATGC GGAATATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCCAGAAA CGCGCCGTCG
551 CCAAAGAAAC CCTCGACATC TTCGCCCGCG TCGCCAAACG TTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCGCGC ATCAAAAGCC
651 CGAAAAATAC CGCGAAATCG CGCTGCTTTT GGACGAAAA CGCACCAGAC
701 GCCTCGAATA CATCGAAAAC TTCTCAACA TCCTGCGCGG TGAACCTAAG
751 AAATACAATG TCCATTTCGA AGTCGCCGCG CGCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAAT CAGCTTCGAC GGCCTCTTTG
851 ACATCCGCGC CGTGCGAATT CTGGTTGATA CCGTCCCGGA GTGTACACC
901 ACGCTGGGTA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAATCCCA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCGG CCCGGAAGAC AAAGGCGTGG AAGTACAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCCGTTGC GCCGCCCACT GCGGTTACAA
1101 AGAGGCGCGC AAGGGCGATT CCGCCTACGA ACAGAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CTTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCGCGCA GGCAAAAGTCC TCTCCCTGCC CACGGGCGCG ACCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAAACGGACA
1401 GCGCGTCGAAT ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CCGGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCAGCCC CAAACCAAC CTGCAAGAGC
1601 TFGCGGAAA TCTCGGCTAC AAAAAAGCCAG AAGACCTCTA CACCGCGCTC
1651 GGACAGGGCG AAATTTCCAA CCGCGCCATC CAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAACAGT
1751 CCAAAATCAA AAAAGCGCGC AAAAAAGCGG TGCTCATCGA CGCGGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCGACGA
1851 TATTATCGGC TTCGTTACCC GCGAGCGCGG CATTTCAAGT CACCGCAAAA
1901 CCTTCCCGTC TTTCCAACAC CTCGCCGAAC ACGCGCCCGA AAAAGTGCTG
1951 GACGCAAGCT GGGCGGCATT GCAGGAAGGA CAAGTATTCG CCGTCGATAT
2001 CGAAATCCCG GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAACTC AACGTTACCG CCGTGCAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGCG GTCCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

m117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFDSYCAALP DNDKNLIGTA WLLAQEHYPA
51  DAATPYGEPL PDHFLGAAOM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMILLAM
151 VTDIRVVLIK LAMRTRLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WOLKWQLEDL GFRHQKPEKY REIALLLDEK RTERLEYIEN FLNILRGELK
251 KYNVHFEVAG RPKHIYSIYK KMVKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKGNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESCKED
401 LAAAFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQORVE IITAKEGHPS VNWLVEGWVK SNKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKNKG KNGVLIDGED
601 GLMTTFLAKC KPAAPPDDIIG FVTRERGISV HRKTCPSFQH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLASLGDVKG VLSVTRL*

```

m117-1/g117-1 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFDSDYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFDSDYCAALPDNDKNLIGTAWSLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120

m117-1.pep	PDHFLGAAQMVHEDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
g117-1	PDHFLGAAQMVDELDPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
	70 80 90 100 110 120
m117-1.pep	130 140 150 160 170 180
	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
g117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
	130 140 150 160 170 180
m117-1.pep	190 200 210 220 230 240
	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQKPEKYREIALLLDEKRTERLEYIEN
g117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQEPEKYREIALLLDEKRTERLEYIEN
	190 200 210 220 230 240
m117-1.pep	250 260 270 280 290 300
	FLNILRGELKKYNVHFEVAGRPKHIYSIYKMMVKKLSFDGLFDIRAVRILVDTVPECYT
g117-1	FLDILRTELKKYNIHFEVAGRPKHIYSIYKMMVKKLSFDGLFDIRAVRILVDTVPECYT
	250 260 270 280 290 300
m117-1.pep	310 320 330 340 350 360
	TLGIVHSLWQPIPGFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV
g117-1	TLGIVHSLWQPIPGFDDYIANPKGNGYKSLHTVIVGPEEKGVEVQIRTFDMHQFNEFGV
	310 320 330 340 350 360
m117-1.pep	370 380 390 400 410 420
	AAHWRYKEGGKDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH
g117-1	AAHWRYKEGGKDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH
	370 380 390 400 410 420
m117-1.pep	430 440 450 460 470 480
	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
g117-1	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
	430 440 450 460 470 480
m117-1.pep	490 500 510 520 530 540
	VNWLYEGWVKSNAKIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
g117-1	VNWLYEGWVKSNAKIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
	490 500 510 520 530 540
m117-1.pep	550 560 570 580 590 600
	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKI KGGKNGVLIDGED
g117-1	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSATTIVKQSKI KGGKTGV LIDGED
	550 560 570 580 590 600
m117-1.pep	610 620 630 640 650 660
	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLASWAALQEG
g117-1	GLMTTLAKCKPAPPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLASWAALQEG
	610 620 630 640 650 660
m117-1.pep	670 680 690 700 710 720
	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVAVQTQSRDLEASMRFTLEV KQVNDLPR
g117-1	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVAVQTQSRDLEASMRFTLEV KQVNDLPR
	670 680 690 700 710 720
m117-1.pep	730
	VLASLGDVKGVLVSVTRLX
g117-1	VLASLGDVKGVLVSVTRLX
	730

m117-1/RelA

sp|P55133|RELA_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744
 Score = 536 bits (1366), Expect = e-151
 Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATLLADI---GRVVPDWNLLVSERCNSTVAELVKGVDEVQKLTHFARVDSL 130
 L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S
 Sbjct: 68 LSMADATLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQGVQMCAIS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEKRAVAKETLDI 190
 A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I
 Sbjct: 122 AEETAQAAQVDNIRRMLLSMVDDFRCVVIKLAERICNLREVQDQFDEV-RRAAAQECANI 180

Query: 191 FAPLANRLGVWQLKWQLEDLGRHQKPEKYREIALLLDEKRTERLEYIENFLNIRGELK 250
 +APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K
 Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDTYKQIAKQLSERRIDREDYITHFVDDLS DAMK 240

Query: 251 KYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTPVECYTTLGIVHSLWQ 310
 N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++
 Sbjct: 241 ASNIRAEVQGRPKHIYSIWRKMQKSLFEDLFDVRAVRIVAEELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTDMHQFNEFGVAAHWRYKEG- 369
 +P EFDDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAHW+YKEG
 Sbjct: 301 HLPKEFDDYVANPKNGYQSIHTVVLGPEGKTIEIQIRTKMHSESELGVAHWRYKEGT 360

Query: 370 --GKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPHGKVLSP 427
 G SAY++KI WLR+LL W+E M++SG ++ +++++F+D +Y TP G V+ LP
 Sbjct: 361 ASGGAQSAYDEKINWLRKLLAWQEEMSDSG--EMLDELRSQVFDREVYAFTPKGDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQRVEIITAKEGHPVSNWLYE- 486
 + ATP+DFAY +HS +G RC GARVEG+IVP + L+ G +VEIIT KE +PS +WL
 Sbjct: 419 SNATPLDFAYHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAKIGKIRAYIRQONADTVREGRVOLDKQLAKL--TPKPNLQELAENLGYPK 543
 G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P
 Sbjct: 479 LGFVTSRRARAKVHAWFRKQDRDKNIAGKEILEAELVKIHA TLKDAQYAAKRFNVKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQKACGTLNEPPVPVSETTIVKQSKI-----KKGKNGV 594
 E+LY +G G++ N+ I +N+P + + K S+ KK ++ V
 Sbjct: 539 EELYAGIGSGDLRINQVINHINALVNKPTAEEDQQLLEKLSEASNKQATSHKKPQDAV 598

Query: 595 LIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFOHLAEHAPEKVLDAW 654
 +++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W
 Sbjct: 599 VVEGVDNLMTLHARCCQIPGDDIQGFVTQGRGISVHRMDCEQLEELRHHAPERIIDTVW 658

Query: 655 AALQEGQVFAVDIEIRAQDRSGLLRDVSALARHKLNVAVQTQ--SRDLEASMRFTLEV 712
 G + + + + A +R+GLL++++ L K+ V +++++ + + M F LE+
 Sbjct: 659 GGGFVGN-YTITVRVTASERNGLLKELTNTLMNEKVKVAGMKSRVDYKKQMSIMDFEEL 717

Query: 713 KQVNDLPRVLASLGDVKGVLVSVTRL 737
 + L RVL + VK V RL
 Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

al17-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACAACGATA
101  AAAAACTTGT CTTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151  GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201  GCGCGAAATG GTTCATGAAC TCGACCTGCT CCCCGATGCC GTCGCCGCCA
251  CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301  TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351  AGTGACAGAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401  AAGAAGCGCG CCAGCAGGCA GAAACTATGC GGAAATGCT GCTGGCGATG
451  GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501  CTGCAATTT TTAAGCAACG CCCCCGACAG CCCCAGAAAA CGCGCCGTCG
551  CCAAGAAAC CCTCGACATC TTCGCCCGC TCGCCAACCG TTTGGGCGTG
601  TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCCTCCGCC ATCAAGAACC
651  CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCAGAC
701  GCCTCGAATA CATCGAAAC TTCCTTAATA TCCTGCGTAC GGAAC TCAA
751  AAATACAATA TCCACTTGA AGTCGCCGCG CGTCCGAAAC ACATCTACTC
801  CATTTACAAA AAAATGGTGA AGAAAAAAGT CAGCTTCGAC GGGTTGTTCC

```



```

851 ACATCCGCGC CGTGGCGGATT CTGGTTGATA CCGTCCCGGA GTGTTACACC
901 ACACTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAACCCEGA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCCG CCCGGAAGAC AAAGGCGTGG AAGTGCAAAAT CCGCACCTTC
1051 GATATGCACC AATTCACAGA ATTCCGGTGC GCCGCGCACT GCGGTTACAA
1101 AGAGGGCGCG AAAGGCGGATT CCGCTACGA AAAAAAATC GCCTGGTTAC
1151 GCCAACTTTT GGACTGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGGCGCGC CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCGCGCG GCCAAAGTCC TCTCCCTGCC CACAGGCGCG ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAACCGGACA
1401 GCGTGTGCAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCAGGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAAGCCAG AAGACCTCTA CACGCGCGTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CGTCAAGCGA AACCACCATC GTCAAAACAGT
1751 CCAAAATCAA AAAAGGCGGC AAAAAGCGCG TGCTCATCGA CGCGCAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 CATTGTGCGC TTCGTTACCC GCGATCGCGG CATTTCGGTA CACCGCAAAA
1901 CCTGCCCTCT TTTCCGACAC CTCGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGA CAAAGTGTTC CCGTCGATAT
2001 CGAAATCCCG GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAAC CAGTCCCGC
2101 GACTTGGGAA GCGAGCATGAG GTTACGCTC GAAGTCAAAAC AAGTTACCGA
2151 CCTCCACGCG GTCCTCGCCA GCCTCGCGCA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

all17-1.pep

```

1  MTAISPIQDT QSATLQELRE WFDSYCTALP NNDKRLVLAA RSLAEAHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLNLRTELK
251 KYNIHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKGNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWRQLLDWR ENMAESGKED
401 LAAAEKTELF NDTIYVLTPL GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQVE IITAKEGHP S VNWLYEGWVK SNKAIGKIRA
501 YIRQONADTV REEGRVQLDK QIAKLTTPKN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDVKG VLSVTRL*

```

all17-1/ml17-1 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
ml17-1.pep	MTAISPIQDTQSATLQELREWFDSYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
all17-1	MTAISPIQDTQSATLQELREWFDSYCTALPNNDKRLVLAA RSLAEAHYPAATPYGEPL					
	10	20	30	40	50	60
ml17-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
all17-1	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
	70	80	90	100	110	120
ml17-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLK LAMRTRTLQFLSNAPDSPEK					
all17-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLK LAMRTRTLQFLSNAPDSPEK					
	130	140	150	160	170	180
ml17-1.pep	RAVAKETLDI FAPLANRLGVWQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN					
all17-1	RAVAKETLDI FAPLANRLGVWQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN					
	190	200	210	220	230	240

	250	260	270	280	290	300
m117-1.pep	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
a117-1	FLNILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m117-1.pep	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
a117-1	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m117-1.pep	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH					
a117-1	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH					
	370	380	390	400	410	420
	430	440	450	460	470	480
m117-1.pep	GKVLSTPGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
a117-1	GKVLSTPGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
	430	440	450	460	470	480
	490	500	510	520	530	540
m117-1.pep	VNWLIEGWVKSNAIGKIRAYIRQONADTVREEGRVOLDKQLAKLTPKPNLQELAENLGY					
a117-1	VNWLIEGWVKSNAIGKIRAYIRQONADTVREEGRVOLDKQLAKLTPKPNLQELAENLGY					
	490	500	510	520	530	540
	550	560	570	580	590	600
m117-1.pep	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKI KGGKNGVLIDGED					
a117-1	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKI KGGKNGVLIDGED					
	550	560	570	580	590	600
	610	620	630	640	650	660
m117-1.pep	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWAALQEG					
a117-1	GLMTTLAKCKPAPPDDIVGFVTRDRGISVHRKTCPSFRHLAEHAPEKVLDAASWAALQEG					
	610	620	630	640	650	660
	670	680	690	700	710	720
m117-1.pep	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEV KQVNDLPR					
a117-1	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEV KQVNDLPR					
	670	680	690	700	710	720
	730					
m117-1.pep	VLASLGDVKGVLVSVTRLX					
a117-1	VLASLGDVKGVLVSVTRLX					
	730					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 423>:

```

g118.seq
1   ATGTGCGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGCTG GAGAAATGATT TAATcgaGGT TAGGAGAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAATTG GGAGCTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCTGAT AGCGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTTGAT TATTACAaCA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 424; ORF 118.ng>:

```

g118.pep
1   MCEFKDFRRN IPCFEEYDEN SFIGKWYDDG VWDDEEYWL ENDLIEVRRK
51  YPYPMIDIPRD IVIGIGTIID FLMVFNWELF EIKASPWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YYNKK*

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```
m118.seq
1  ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTCATTG GAATCGGTAC
201 CATTATTGAT TTCTTAATGG TTCCAAATTG GAAACTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```
m118.pep
1  MCEFKEIIRN VPFEGYDEN SFIGKYYDDG VWDDEEYWKL ENDLIEVRKK
51  YPYPM DIPRY VVIGIGTIID FLMVPNWKLF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YNNKK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```
m118/g118

          10      20      30      40      50      60
m118.pep  MCEFKEIIRNVPFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:
g118       MCEFKEIIRNVPCFEEYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10      20      30      40      50      60

          70      80      90     100     110     120
m118.pep  VVIGIGTIIDFLMVPNWKLF EIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g118       IVIGIGTIIDFLMVPNWKLF EIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          70      80      90     100     110     120

m118.pep  YNNKKX
          |||||
g118       YNNKKX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```
a118.seq
1  ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAATTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```
a118.pep
1  MCEFKEIIRN IPCFEEYDEN SFIGKYYDDG VWDDEEYWKL ENDLIEVRKK
51  YPYPM DIPRD IVIGIGTIID FLMVPNWKLF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YNNKK*
```

m118/a118 93.6% identity in 125 aa overlap

```
m118.pep          10      20      30      40      50      60
MCEFKEIIRNVPFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
|||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a118       MCEFKEIIRNVPCFEEYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10      20      30      40      50      60
```


	70	80	90	100	110	120
m118.pep	VVIGIGTIIDFLMVPNWKLFEIKASPWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD					
	:	:	:	:	:	:
a118	IVIGIGTIIDFLMVPNWELFEIKASPWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD					
	70	80	90	100	110	120

m118.pep	YYNKKX
a118	YYNKKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

g120.seq

```

1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAAGGCTACC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGTA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAATCC GCGCGTACGG TTGTCCGCAA TACCCTGCAC CCTGCCTACT
251 ATAAAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTTGCCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGTCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGCGGCC TGAATAAGGC GGTACGGGA AAATACAGCA Taggcggcgt
501 gGAAACCGAA GTCGTCAAAT ATCGGTGCG GCGCGGCGAC GATACGGTAA
551 CGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGAcgaCG GCAAAACCTA TACGCTGAAG CTCAAATCGG TGCAGATCAA
651 CGGACAGGCC GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

g120.pep

```

1  MMKTFKNIFS AAILSAAALPC AYAARLPQSA VLHYSGSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PAYYKDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DVTYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

m120.seq

```

1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGTA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGTACGG TTGTCCGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCCGCCGAC
301 GGCAGCGTAA CTTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTTGCCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGCGGTT TGAATAAGGC GGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG

```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

m120.pep

```

1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLXYSYSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP

```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
g120	MMKTFKNIFSAAILSAALPCAYAARLPQSAVLHYSGSYGI PATMTFERSGNAYKIVSTIK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTY GKAGESKTEQSPKAM					
g120	VPLYNIRFESGGTVVGNTLHPAYYKDIRRGKLYAEAKFADGSVTY GKAGESKTEQSPKAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VVKYRVRRGD					
g120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VVKYRVRRGD					
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA AKP					
	:					
g120	DTVTYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA AKPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120.seq

```

1  ATGATGAAGA CTTTAAATAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGTACGG TTGTCCGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAACGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTTC ACGCTTGCCTG CGAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGCGCT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGGC GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120.pep

```

1  MMKTFKNIFS AAILSAALPC AYAAGLPQSA VLHYSGSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNTLH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
a120	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLHYSGSYGI PATMTFERSGNAYKIVSTIK					

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	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
a120	VPLYNIRFESGGTVVGNLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVKYRVRRGD					
a120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVKYRVRRGD					
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDGKTYTLKLKSVQINGQAAKPX					
a120	DAVMYFFAPSLNNIPAQIGYTDGKTYTLKLKSVQINGQAAKPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51  GCGGATGCC GTGCTGGTAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCTGACC GGTTCGCGCG CAAATTGCTG
151 GATTTGCAGG ACACAGGCAC AGACGAAGTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACACGCAAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAAGTga cgcggatttt TACCGTCggc gacttcCGCA
401 GCGCGACCTT TGCTGCCGGC GGacaAGGTG CGCGCTCGT CCGGCCTTT
451 CCGAAGCCCT TGTTCCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CCGCGGGATT GCCAACATCA GCGTACTCCC CCGCGCGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cactGGcagc TGCCTTACGA CAAAacggt gcAAAGgcgg cacAAGGCAA
651 catatTGcgc cAACTGCTCG gcaggctGCT CGCCcaccCG TATTCTCAC
701 AACCcacc aaAAGCAGC GGgcGCGaAc Tgtttgccct AAattggctc
751 gaaacctAcc ttgacgcgcy cgaaaaccga tacgacgtat tgcggacgct
801 ttcccgattc accgcgcaaA ccgTttggga gcgcgtctca CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCTGACACAG
951 CACGCGCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gcgcATTtg
1001 cgtggttggC GCGTGTGTGG ATTAACGCA TTCCCGGTAG TCCGCACAAA
1051 GCGACGCGCG CATCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM SGTSMGADA VIVRMDGGKW LGAEGHAFTP YPDLRRKLL
51  DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPC DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVWDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAFWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTCGCGCG CCAATTGCTG

```



```

151 GATTTCGAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTG
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATT
351 GCCGCTGCTG GCGXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
401 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
451 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
501 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
551 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
601 XXXXXCAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCCG TATTTGCGAC
701 AACGCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGCGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCAG CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGCGAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQLL
51  DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSEPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKW LGAEGHAFTPYPGRLLRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKW LGAEGHAFTPYPDRLLRKLDDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
g121	HRSRMLSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	AXXX					
g121	AELTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDAVSHAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAE LNLDPOQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYY					
g121	GAGYYYY					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGCGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCG TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCGCGACCT TCGCGCCGGC GGACAAGGCG CGCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCGACGCA CCCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TCGGGACGCT
801 TTCCCGATTG ACCGCGCAAA CCGTTTTTCA CGCCGTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGCGC GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCGGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTTC
1001 CATGGATGGC GGCCTGTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCAAACC GTGTATTCTG GGC CGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAP
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGPG NMLMDAWMOA
201 HWQLPYDKNG AKAAQGNILP QLIDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPOQWVEA AAFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTYPGRLLRRQLLDLQDTGADEL					
a121	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTYPGRLLRRKLLDLQDTGADEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAELLCSONLAPSDITALGCHGQTVRHAPEHGYISIQDLADLPLL					
a121	HRSRILSQELSRLYAQTAELLCSONLAPSDITALGCHGQTVRHAPEHSYSVQLADLPLL					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m121.pep	AXXX					
	:	:	:	:	:	:
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLEPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
	:	:	:	:	:	:
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICDGGIRNPV					
	:	:	:	:	:	:
a121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFVDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	:	:	:	:	:	:
a121	LMADLAECFGTRVSLHSTAEINLDPOWVEAAAFAWMAACWVNRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
	:	:	:	:	:	:
a121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAACAC  AGCTTTACAT  CGGCATCATG  TCGGGAACCA  GCATGGACGG
51  GCGGGATGCC  GTACTGATAC  GGATGGACGG  CGGCAATGG  CTGGGCGCGG
101 AAGGGCAGCG  CTTTACCCCG  TACCCCGGCA  GGTACGCCG  CCAATTGCTG
151 GATTTGCAGG  ACACAGCGCG  AGACGAACTG  CACCGCAGCA  GGATTTTGTC
201 CAAAGAACTC  AGCCGCCTAT  ATGCGCAAAC  CGCCGCCGAA  CTGCTGTGCA
251 GTCAAAACCT  CGCACCGTCC  GACATTACCG  CCCTCGGCTG  CCACGGGCAA
301 ACCGTCCGAC  ACGCGCCGGA  ACACGGTTAC  AGCATACAGC  TTGCCGATTT
351 GCCGCTGCTG  GCGGAACGGA  CGCGGATTTT  TACCGTCGGC  GACTTCCGCA
401 GCCGCGACCT  TCGGGCCGGC  GGACAAGGCG  CGCCACTCGT  CCCCGCCTTT
451 CACGAAGCCC  TGTTCGCGCA  CAACAGGGAA  ACACGCGCGG  TACTGAACAT
501 CGGCGGGATT  GCCAACATCA  GCGTACTCCC  CCCGACGCA  CCCGCTTCG
551 GCTTCGACAC  AGGGCCGGGC  AATATGCTGA  TGGACGCGTG  GACGCAAGCA
601 CACTGCGAGC  TTCCTTACGA  CAAAACGGT  GCAAAGCGCG  CACAAGGCAA
651 CATATTGCCG  CAACTGCTCG  ACAGGCTGCT  CGCCACCCG  TATTTCGCAC
701 AACCCACCCC  TAAAAGCACG  GGGCGCGAAC  TGTTCGCCCT  AAATTGGCTC
751 GAAACCTACC  TTGACGGCGG  CGAAAACCGA  TACGACGTAT  TCGGACGCT
801 TTCCCGTTTT  ACCGCGCAAA  CCGTTTGCGA  CGCCGTCTCA  CACGCAAGCG
851 CAGATGCCCG  TCAAATGTAC  ATTTGCGGCG  GCGGCATCCG  CAATCCTGTT
901 TTAATGGCGG  ATTTGGCAGA  ATGTTTCGGC  ACACGCGTTT  CCCTGCACAG
951 CACCGCCGAC  CTGAACCTCG  ATCCGCAATG  GGTGGAAGCC  GCCGNATTTG
1001 CGTGGTTGGC  GCGGTGTTGG  ATTAATCGCA  TTCCCGGTAG  TCCGCACAAA
1051 GCAACCGGCG  CATCCAAACC  GTGTATTCTG  ANCGCGGGAT  ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  METQLYIGIM  SGTSMGDADA  VLIRMDGGKW  LGAEGHAFTP  YPGRLRRQLL
51  DLQDTGADEL  HRSRILSQEL  SRLYAQTAAE  LLCSQLNAPS  DITALGCHGQ
101 TVRHAFEHGY  SIQLADLPLL  AERTRIFTVG  DFRSRDLAAG  GQGAPLVPAF
151 HEALFRDNRE  TRAVLNIGGI  ANISVLPPDA  PAFGFDTGPG  NMLMDAWTQA
201 HWQLPYDKNG  AKAAQGNILP  QLLDRLLAHP  YFAQPHPKST  GRELFALNWL
251 ETYLDGGENR  YDVLRTLSRF  TAQTVCDAVS  HAAADAROMY  ICGGGIRNPV
301 LMADLAECFG  TRVSLHSTAD  LNLDPOWVEA  AXFAWLAACW  INRIPGSPHK
351 ATGASKPCIL  XAGYYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

a121-1.seq

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

a121-1.pgp

1	METQLYIGIM	SGTSMGDADA	VLIRMDGGKW	LGAEGHAFTP	YPGRLRRKLL
51	DLQDTGADEL	HRSRMLSQEL	SRLYAQTTAE	LLCSONLAPS	DITALGHGQG
101	TVRHAPAEHS	SVQLADLPQL	AERTQITFAE	PFPSRDLAAG	QGQAPLVPAP
151	HEALFRDDRE	TRAVLNTGGI	ANISVLPPDA	DADRSDTGPQ	NMLMDAWNOA

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201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
 351 ATGASKPCIL GAGYYY*

m121-1/a121-1 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAF	TPYPGR	LRQLLDLQDTGADEL	
a121-1	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAF	TPYPGR	LRQLLDLQDTGADEL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQ	TVRHAPEHGY	SIQLADLPLL	
a121-1	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQ	TVRHAPEHGY	SIQLADLPLL	
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDF	RSRDLAAGGQGA	PLVPAFHEALFR	DNRETRAVLN	IGGIANISVL	PPDA
a121-1	AERTQIFTVGDF	RSRDLAAGGQGA	PLVPAFHEALFR	DNRETRAVLN	IGGIANISVL	PPDA
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTGPGN	MLMDAWTQAHWQ	LPYDKNGAKAAQ	GNILPQLLDRL	LAHPYFAQPH	PKST
a121-1	PAFGFDTGPGN	MLMDAWTQAHWQ	LPYDKNGAKAAQ	GNILPQLLDRL	LAHPYFAQPH	PKST
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWL	ETYLDGGENRYD	VLRTLSRFTAQ	TVCDVASHAA	ADARQMYICG	GGGIRNPV
a121-1	GRELFALNWL	ETYLDGGENRYD	VLRTLSRFTAQ	TVCDVASHAA	ADARQMYICG	GGGIRNPV
	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	LMADLAECFG	TRVSLHSTADL	NLDPOWVEAAX	FAWLAACWIN	RIPGSPHKAT	GASKPCIL
a121	LMADLAECFG	TRVSLHSTADL	NLDPOWVEAAX	FAWLAACWIN	RIPGSPHKAT	GASKPCIL
	310	320	330	340	350	360
m121-1.pep	XAGYYYY					
a121	GAGYYYY					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

```

1  ATGGCTTTAC TGAGCATCCG CAAGCTGCAC AAACAATACG GCAGCGTAAC
51  CGCCATCCAA TCCTTAGACT TGGACTTGGA AAAAGCGGAA GtcatCGTAC
101 TGCTGGGCCC gTccggetgc ggCAAATCCA CCCTcctgcg ctgcgctcaaC
151 GGTTTGGAGC CGCACCAagg cgGCAGCATC GTGATGGACG GTgtcgCGCA
201 ATTcggcAAA GACGTTTCCT GGCAAACCGC CCGCAAAAa gtcggtatgg
251 tctttcaaag taacgAactg Tttgcccaca tgaccgtcat cgAaaacatc
301 ttcttAggcC CGGTAAagga aCAAAAcCgc gaccgtgccg aagcaGAGGC
351 gCAAGCCGCG AAactGttgg aacgcgTCGG actgctAGAC CGCAAAAACG
401 CCTATCCGCG CGAACTTTCC GGCGGTCAGA AACAGCGCAT CGCCATTGTC
451 CGCGCCCTGT GCCTGAATCC GGAAGTCATC CTGCTGGACG AAATCACC GC
501 CGCACTTGAC CCCGAAATGG TGCGCGAAGT CTTGGAAGTG GTTTTGAAC
551 TCGCCCGCGA AGGGATGAGT ATGCTCATCG TAACCCACGA AATGGGGTTC
601 GCACGCAAAG TTGCCGACCG CATCGTCTTT ATGGACAAAG GCGGCATCGT
651 CGAATCGTCC GACCCCGAAA CCTTTTTTTC CGCACCAAAA AGCGAACGCG
701 CCCGCCAATT TCTGGCAGGT ATGGACTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 446; ORF 122.ng>:

1	MALLSIRKLH	KQYGSVTAIQ	SLDLBLEKGE	VIVLLGPSGC	GKSTLLRCVN
51	GLEPHQGGSI	VMDGVGEFGK	DVSQWTARQK	VGMVFQSNEL	FAHMTVIENI
101	FLGPVKEQNR	DRABAEAAQAG	KLLERVGLED	RKNAYPRELS	GGQKORIAIV
151	RALCLNPEVI	LLDEITAAAL	PEMVRVGLLV	VLELAREFMS	MLIVTHEMGF
201	ARKVADRIVF	MDKGGIVESS	DPETFFSAFK	SERARQFLAG	MDY*

m122.seq

1	GTTGTTCATGA	TTAAAAATCCG	CAATATCCAT	AAGACCTTTG	GCGAAAAACAC
51	TATTTTTCGCG	GGCATCGATT	TGGATGTGTG	CAAAGGGCAG	GTGGTCGTCA
101	TCCTCGGGcC	TTCCGGCTCA	CGCAAAACGA	CGTTTCTGCG	ATGCGCTAAAC
151	CGGTGTGGAA	TGCCCGAAGA	GGCACAACCT	GAGTTCGACA	ACGAGCGACC
201	GCTGAAATC	GATTTTCTA	AAAAACCAAG	CAAAACACAT	ATTTTGGCAC
251	TGCGCCGCAA	ATCAkGCATG	GTGTTTCAAC	AATACAyCT	CTTTCGCAC
301	AAAACCGCCT	TGAAAAACGT	AATGGAAGGA	CCGGTTGCCG	TACagGGCAA
351	GCCTGCGGCC	CAAGCGCGCG	AAGAGGCTCT	GAAACTGC TG	GAAAAAGTCG
401	GCTTGGGCGA	CAAAGTGGAT	TTGTATCCCT	ACCAGCTTTC	CGGCGGTCAG
451	CAGCAGCGCG	TCGGCATTGC	CCGCGCATTG	GCGATTACAG	CTGAACGTAT
501	GCTGTTTGAC	GAACCGACTT	CCGCGCTCGA	TCTGTAATTG	GTGCAAGATG
551	TTTTGGATmC	CATGAAGGAA	TTGGCGCAAG	AAGGCTGGAC	CATGGTTGTC
601	GTTACGCATG	AAATCAAGTT	CGCCTTAGAA	GTGGCAACCA	CCGwCGTCGT
651	GATGGACrCG	GGCGTTATTG	TCGAACAAGG	CAGCCC GCAA	GATTTGTT CG
701	ACACCCCCAA	ACACGAACGG	ACGCGGAGAT	TTTTAAGCCA	AATCCAATCT
751	ACCAAGATTT	GA			

m122.pcp

1	VVMIKIRNII	KTFGENLTILR	GIDLDVCKGQ	VVVLGPSPGS	GKTTFLRLCLN
51	ALEMPEDGQI	EFVDNERPLKI	DFSCKPSKHD	ILALRRKSXM	LYPQYNLFGH
101	KTALENVMGE	PVAVQGKPAK	QAREALKLLE	EKVLGDKDVM	VFFQYQLSPQ
151	QQRVGIARAL	AIQPELMLFD	EPTSALDPEL	VQDVLDMKE	LAQEGWTMNV
201	VTIEKFALE	VATTXVMDX	GVIVEQGSQP	DLFDHPKHER	TRRFLSLIQS
251	TKI *				

Homology with a predicted ORF from *N. gonorrhoeae*

m122/q122

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFTGENTILRGIDLDVCKGVVVVLGPSGGKTTFLRCLNALEMPEDGQI					
	: : : : : : :	: : : :	: :	: : : :	:	:
g122	MALLSIRKLHKQYGSVTAIQSLDLDLEKEGEIVLLGPSGCCGSTLLRCVNGLPEPHQGCSI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSXMVFQQYNLFPHKTALENVMEGFPVAVQKGPA					
	: :	: :	:	: :	: : :	:
g122	VMDGVGFPGKDVSQWTA-----RQKVGMVFQSNELFAMHTVIENIFLGPVKQEQRDR					
	70	80	90	100	110	
	130	140	150	160	170	180
m122.pep	QAREEALKLLEKVGLGDVKVDLYPYQLSGGQQRVGIARALAIQPELMFLFEPTSALDP					
	: : :	: :	: :	: :	: : : :	: :
g122	EAEAQAAGKLLERVGLLDRKNAYPRELSGGQKORIAVRALCLNPEVILLDEITAALDP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m122.pep	VQDVLDXMKELAQEGWTM VVVTHEIKFALEVATTXVMDXGVIVEEQSQDLDFDHPKHER					
	: : :	: :	: :	: :	: :	:
g122	VREVLEVVLLELAREGMSMLIVTHMGFARKVADRIVFMDDKGGIVESSDPETFFSAPKSE					

350

	180	190	200	210	220	230
	250					
m122.pep	TRRFLSQISTKIX					
	: : :					
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```

a122.seq
1   GTTGTTCATGA TTAAATCCG CAATATCCAT AAGACCTTCG GCAAAAATAC
51  CATTTTGCGC GGCATCAATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGCC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAA TGCCCGAAGA CGGACAAATC GAGTTCGACA ACAGCGGACC
201 GCTGAAAATC GATTTTCTA AAAAACCAAG CAAACACGAT ATTTTGGCAC
251 TCGCGCGCAA ATCAGGCATG GTGTTTCAAC AATACAACCT CTTCCGCAC
301 AAAACCGCCT TGGAAAACGT GATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTGAT
451 CAGCAGCGCG TCGGCATTGC CCGAGCATTG GCGATTGAGC CCGAGCTGAT
501 GTTGTGTTGAC GAACCCACTT CCGCGCTTGA CCCCAGTTG GTGCAAGACG
551 TGTTGAACGC CATGAAGGAA TTGGCGCGGG AAGGTTGGAC GATGGTCGTC
601 GTTACCCACG AAATCAAGTT CGCGCTGGAA GTTGCCACGA CCGTTGTCGT
651 GATGGACGGC GCGGTTATCG TAGAGCAGGG CAGCCCGAAA GAGTTGTTCT
701 ACCACCCCAA ACACGAACGG ACGCGGAGAT TTTTAAGCCA AATCCAATCT
751 ACCAAGATTG GA

```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```

a122.pep
1   VVMIKIRNIH KTFGKNTILR GINLDVCKGQ VVILGPSGS GKTFLRCLN
51  ALEMPEDGQI EFDNERPLKI DFSKKPSKHD ILALRRKSGM VFQYQYNLFPH
101 KTALENVMEG PVAVQGKPAQ QAREEALKLL EKVGLGDKVD LYPYQLSGGQ
151 QQRVGIARAL AIQPELMLFD EPTSALDPEL VQDVLNAMKE LAREGWTMNV
201 VTHEIKFALE VATTVVVMDG GVIVEQGSPP ELFDHPKHER TRRFLSQIQS
251 TKI*

```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFGENTILRGIDLVDCKGQVVILGPSGSGKTTFLRCLNALEMPEDGQI					
a122	VVMIKIRNIHKTFGKNTILRGINLDVCKGQVVILGPSGSGKTTFLRCLNALEMPEDGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSGMVQYQYNLFPHKTALENVMEGPVAVQGKPAQ					
a122	EFDNERPLKIDFSKKPSKHDILALRRKSGMVQYQYNLFPHKTALENVMEGPVAVQGKPAQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m122.pep	QAREEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
a122	QAREEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m122.pep	VQDVLDMKELAQEGWTMNVVTHEIKFALEVATTXVMDXGVIVEQGSPPDLFDHPKHER					
a122	VQDVLNAMKELAREGWTMNVVTHEIKFALEVATTVVMDGGVIVEQGSPPDLFDHPKHER					
	190	200	210	220	230	240
	250					
m122.pep	TRRFLSQISTKIX					

a122 |||||
 TRRFLSQIQTIX
 250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATT
51 GCGCGGCATC GATTGGATG TGGGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TGCCTGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG
201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC
301 GTGTTGGAAC ACGTGATGGA AGGCGCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTTTGAAGT GCTGGAAAAA GTCGGCTTGG
401 GCGATAAAGT GGATTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGTGTCGGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT
501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTTGG
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCACGCT GGAAGTTGCC ACGAAGCTCG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGCGAGCCC GAAAGAGTTG TTCGACCACC
701 TCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTGCAAG
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep
1 MIKIRNIHKT FGENTILRGI DLDVKGQV VILGPSGSGK TFLRCLNAL
51 EMPEDGQIEF DNARPLRIDF SKKTSKHDIL ALRRKSGMVF QYNLFPKHT
101 VLENVMEGPV AVQGKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT
201 HEIKFTLEVA TNVVMDGGV IVEQGSFKEL FDHLKHERTR RFLSQIQSAK
251 I*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA AACTATTTT
51 GCGCGGCATC GATTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAATCAGG CATGGTGTTC CAACAATACA ACCTCTTTC GCACAAAACC
301 GCCTTGGAAC ACGTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGCAAAAGT GGATTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGCGTCGCGA TTGCGCGCGC ATTGGCGATT CAGCCTGAAC TGATGCTGTT
501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG
551 ATACCATGAA GGAATTGGCG CAAGAAGGCT GGACCATGGT TGTCGTTACG
601 CATGAAATCA AGTTCCGCTT AGAAGTGGCA ACCACCGTCG TCGTGATGGA
651 CGGCGGCGTT ATTGTGCAAC AAGGCGAGCC GCAAGATTG TTCGACCACC
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep
1 MIKIRNIHKT FGENTILRGI DLDVKGQV VILGPSGSGK TFLRCLNAL
51 EMPEDGQIEF DNARPLRIDF SKKPSKHDIL ALRRKSGMVF QYNLFPKHT
101 ALENVMEGPV AVQGKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA QEGWTMVVVT
201 HEIKFALEVA TTVVMDGGV IVEQGSQDL FDHPKHERTR RFLSQIQTIX
251 I*

m122-1/g122-1 94.8% identity in 251 aa overlap

	10	20	30	40	50	60
m122-1.pep	MIKIRNIHKTFGENTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
g122-1	MIKIRNIHKTFGENTILRGIDLDVKGQV VILGPSGSGKTTFLRCLNALEMPEDGQIEF					

352

	10	20	30	40	50	60
m122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGFPVAVQGKPAAQA					
g122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTVLENVMEGFPVAVQGKPAAQA					
	70	80	90	100	110	120
m122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					
g122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					
	130	140	150	160	170	180
m122-1.pep	190	200	210	220	230	240
	DVLDTMKELAQEGWMTMVVTHEIKFALEVATTVVMDGGVIVEQGSQDLFDHPKHHERTR					
g122-1	DVLDTMKELAQEGWMTMVVTHEIKFTLEVATNVVMDGGVIVEQGSQDLFDHPKHHERTR					
	190	200	210	220	230	240
m122-1.pep	250					
	RFLSQIQSTKIX					
g122-1	RFLSQIQSAKIX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

a122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTCGGCAAAA ATACCATTTT
51  GCGCGGCATC AATTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAA ACGACGTTT TCGGATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTT GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTT GCACTGCGCC
251 GCAAATCAGG CATGGTGTTC CAACAATACA ACCTCTTTCC GCACAAAACC
301 GCCTTGGAAG ACGTGATGGA AGGACCGGT GCGGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCAAGAGG CTCTGAACT GCTGGAAGAA GTCGGCTTGG
401 GCGACAAAGT GGATTTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGCGTCGGCA TTGCCCGAGC ATTGGCGATT CAGCCCGAGC TGATGTTGTT
501 TGACGAACCC ACTTCCGCGC TTGACCCCGA GTTGGTGCAA GACGTGTGTA
551 ACGCCATGAA GGAATTGGCG CGGGAAGGT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCGCGCT GGAAGTTGCC ACGACCGTTG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 CCAAAACAGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

a122-1.pep

```

1  MIKIRNIHKT FGKNTILRGI NLDVCKGQVV VILGPSGSGK TFLRCLNAL
51  EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENVMEGPV AVQGKPAAQA REEALKLEK VLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLNAMKELA REGWMTMVVT
201 HEIKFALEVA TTVVMDGGV IVEQGSQREL FDHPKHHERTR RFLSQIQSTK
251 I*

```

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1.pep	MIKIRNIHKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRNIHKTFGKNTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
a122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGFPVAVQGKPAAQA					
m122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGFPVAVQGKPAAQA					
	70	80	90	100	110	120
a122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					
m122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					

353

	130	140	150	160	170	180
	190	200	210	220	230	240
a122-1.pep	DVLNAMKELAREGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGSPEKELFDHPKHERTR					
	: : : : : : : : : : :					
m122-1	DVLDTMKELAQEGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGSPODLFDHPKHERTR					
	190	200	210	220	230	240
	250					
a122-1.pep	RFLSQIQSTKIX					
m122-1	RFLSQIQSTKIX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 457>:

g125.seq

```

1  ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGGT
51  TTGGTTCCGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACGCTGC
101 TCGCCCCCTT GGGCTGGCAG CGCGGTCTGG CGGCCCTGCT TTTGGGTCAT
151 GCCGTCCGCG GCGCGCTGTT TTTTGC GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GTGTGCGCCT GTCGTTCCGC AAATGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGTCGGCGC AacggTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACggc gaATCCTTTG TCTGGTGGGC ATTGGCAAAC GGC GCACTGA
401 TCGTGCTGTG GCTGGTTTTT GCGCACGCA GAACGGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GCTTGCCGTG TTGTGTTGA GCGTCGAAGT
501 GTTCGCTTCG TCCGGCACA ACGCCGCGCC CGCCGTTCA GACGGCATGA
551 CCTTCGGAAC GGCAGTCGAA CTGTCCGCCG TCATGCCGCT TTCCTGGCTG
601 CCGCTGGCCG CCGACTACAC GCGCCAAGCA CGCCGCCCGT TCGCGGCAAC
651 CCTGACGGCA ACGCTCGCCT ATACGCTGAC GGGCTGCTGG ATGTATGCCT
701 TGGGTTTGGC GCGGCTCTG TTTACGGAG AAACGACGT GCGGAAAATC
751 CTGTTGGGCG CGGGCTTGGG CATAACGGGC ATTCTGGCAG TCGTCCTCTC
801 CACCGTTACC ACAACGTTTC TCGATACCTA TTCCGCCGGC GCGAGTGCGA
851 ACAACATTTT CGCGGTTTTT GCGGAAATAC CCGTCGCTGT CGGCGTTACC
901 CTGatccgca ccgtgcttgc cgtcatgctg cccgttaccg aatataaaaa
951 cttctctgctg cttatccgct cggatatttg gccgatggcg ggtgggtttg
1001 attgccgaCT TTTtgtctt AAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 458; ORF 125.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 459>:

m125.seq

```

1  ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCTCCGCCA TCGGGCTGAT
51  TTGGTTCCGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACGCTGC
101 TTGCGCCTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTACT TTTGGGTCAT
151 GCCGTCCGCG GCGCGCTGTT TTTTGC GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGC CCGCTTCGCG AAACGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGCGCG AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GGC GCGCTGA
401 TTGTGCTGTG GCTGGTTTTT GCGCACGCA AAACGGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGCGGTT CTGTGGCTGA GTGCCGAAGT
501 CTTTTCCACG GCAGGCAGCA CCGCCGCACA GGTTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTTA TGCCGCTTTC CTGGCTGCCG
601 CTTGCCGCCG ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCTT
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGTGGATG TATGCCTTGG
701 GTTTGGCAGC GCGGTTGTTC ACCGAGAGAA CCGACGTGGC AAAAATCCTG
751 CTGGGCGCAt GTTTGgGTGC GGCAGGCATT TTGGCGGTCG TCCTCTCCAC
801 CGTTACCACA ACGTTTCTCG ATGCCTATT CCGCCGCGCG AGTGCGAACA

```


851 ACATTTCGGC GCGTTTTCGG GAAACACCCG TCGCTGTCrG CGTTACCCTG
 901 ATCGGCACGG TACTTGCCGT CATGCTGCCC GTTACCGAAT ATGAAAACCT
 951 CCGCTGCTT ATCGGCTCGG TATTGCGCC GATGGCGGc GGTTTTGATT
 1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

This corresponds to the amino acid sequence <SEQ ID 460; ORF 125>:

m125.pep
 1 MSGNASSPSS SSAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
 51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSVA NMLQLAGWTA
 101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
 151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
 201 LAADYTRHAR RPFATLTAT LAYTLTGCWM YALGLAALF TGETDVAKIL
 251 LGAXLGAAGI LAVVLSTVTT TFLDAYSAGA SANNISARFA ETPVAVXVTL
 301 IGTVLAVMLP VTEYENFLLL IGSVFAPMAG GFDCRLFRLE TA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 125 shows 92.1% identity over a 343 aa overlap with a predicted ORF (ORF 125.ng) from *N. gonorrhoeae*:

m125/g125

	10	20	30	40	50	60
m125.pep	MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQRLAALLLGHAVGGALFFAA					
g125	MSGNASSPSSSSAIGLVWFGAAVSIAEISTGTLLAPLGWQRLAALLLGHAVGGALFFAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m125.pep	AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
g125	AYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMIYVAGATVSSALGKVLWDG					
	70	80	90	100	110	120
	130	140	150	160	170	179
m125.pep	ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQ-VS					
g125	ESFVWWALANGALIVLWLVFGARRTGGLKTVSMLLMLLAVLWLSVEVFASSGTNAAPAVS					
	130	140	150	160	170	180
	180	190	200	210	220	230
m125.pep	DGMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCWMYALGLAAL					
g125	DGMTFGTAVELSAVMPLSWLPLAADYTRQARRPFAATLTATLAYTLTGCWMYALGLAAL					
	190	200	210	220	230	240
	240	250	260	270	280	290
m125.pep	FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT					
g125	FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTYSAGASANNISARFAEIPVAVGVT					
	250	260	270	280	290	300
	300	310	320	330	340	
m125.pep	LIGTVLAVMLPVTEYENFLLLIGSVFAPMAGGFDCRLFRLETAX					
g125	LIRTVLAVMLPVTEYKNFLLIRSVFGPMAGGFDCRLFCLKTAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 461>:

a125.seq
 1 ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGAT
 51 TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCAGC GGTACACTGC
 101 TTGCGCCTTT GGCCTGCAG CGCGGTCTGG CGGCTCTGCT TTTGGGTCAT


```

151 GCCGTCGGCG GCGCGCTGTT TTTTGC GGCG GCGTATATCG GCGCACTGAC
201 CCGACGCAGC TCGATGGAAA GCGTGCCCT GTCGTTCCGGC AACGCGGTT
251 CAGTGCTGTT TTCCTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGG ATTGGCAAAC GCGCGCTGA
401 TTGTGCTGTG GCTGGTTTTC GGCGCACGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGGCTGA GTGCCGAAGT
501 CTTTTCCACG GCAGGCAGCA CCGCCGACAC GGTTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTGA TGCCGCTTTC TTGGCTGCCG
601 CTGGCGCCCG ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCTT
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTTGGCAGC GCGTGTGTT ACCGGAGAAA CCGACGTGGC AAAAATCCTG
751 CTGGGCGCAG GTTTGGGTGC GGCAGGCATT TTGGCGGTGC TCCTGTCGAC
801 CGTTACCACC ACTTTTCTCG ATGCCTACTC CGCCGGCGTA AGTGCCAACA
851 ATATTCCCGC CAAACTTTTCG GAAATACCCA TCGCCGTGCG CGTCGCCGTT
901 GTCGGCACAC TGCTTGCCGT CCTCCTGCCC GTTACCGAAT ATGAAAACCT
951 CCTGCTGCTT ATCGGCTCGG TATTTGCGCC GATGGCG.GC GGTTTTGATT
1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 462; ORF 125.a>:

```

a125.pep
1  MSGNASSPSS SAAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLGH
51  AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLSVA NMLQLAGWTA
101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
201 LAADYTRHAR RPFATLTAT LAYTLTGCM YALGLAAALF TGETDVAKIL
251 LGAGLGAAGI LAVLSTVTT TFLDAYSAGV SANNISAKLS EPIAVAVAV
301 VGTLLAVLLP VTEYENFLLL IGSVFAPMAX GFDCRLFRLE TA*

```

m125/a125 95.6% identity in 342 aa overlap

```

          10      20      30      40      50      60
m125.pep  MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQRLAALLLGHAVGGALFFAA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a125       MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQRLAALLLGHAVGGALFFAA
          10      20      30      40      50      60

          70      80      90      100     110     120
m125.pep  AYIGALTGRSSMESVRLSFGKRGSVLSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a125       AYIGALTGRSSMESVRLSFGKRGSVLSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
          70      80      90      100     110     120

          130     140     150     160     170     180
m125.pep  ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a125       ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD
          130     140     150     160     170     180

          190     200     210     220     230     240
m125.pep  GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMYALGLAAALF
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a125       GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMYALGLAAALF
          190     200     210     220     230     240

          250     260     270     280     290     300
m125.pep  TGETDVAKILLGAXLGAAGILAVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVTL
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a125       TGETDVAKILLGAGLGAAGILAVLSTVTTTFLDAYSAGVSANNISAKLSEPIAVAVAV
          250     260     270     280     290     300

          310     320     330     340
m125.pep  IGTVLAVMLPVTEYENFLLIGSVFAPMAGGFDCRLFRLETAX
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a125       VGTLLAVLLPVTEYENFLLIGSVFAPMAXGFDCRLFRLETAX

```


310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

```
g126.seq
1   AtgccgtcTG AAaccCcaaa ggcACGCCGC CGGCTTTCAG ACGGCATCGC
51  GTCCGACAAC CATACCAAAG AATCCATCAT GTCACCctg tacggcGAAA
101 CTTTCCCTTC GCGGCTGCTg cteggcacgG cggcctacCC GACCCCTGAA
151 ATCCTCAAAC AATCCGTCCG AACCGCCCCG CCCGCGATGA ttaccGTCTC
201 GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTGGT
251 CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301 CAAAGCGTGC AGGAAGCGGT. AACGACGGCG CAAATGGCGC GCGAAGTGTT
351 TGAACCGAT TGGATAAAAT TGGAACTCAT CGGCGACGAC GACACCTTGC
401 AGCCGGACGT GTTCCAATC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451 GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CCTGCCGCCG
501 CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551 GCACGGGTTT GGGGGCGGTT CACGCCTATG CGCTCAAAT CCTGCGCGAA
601 CGCCTGCCCG ACACGCCGCT GATTATCGAC GCGGGCTTGG GTTTGCCTTC
651 CCAAGCGGCA CAAGTGATGG AATGGGGTTT TGACGGCGTA TTGTTAAACA
701 CCGCCGTTTC CCGCAGCGGC GACCCGTCA ACATGGCGCG CGCCTTCGCA
751 CTCGCCGTCG AATCCGGACG GCTGGCATTT GAAGCCGGGC CGGTCGAAGC
801 GCGAACCAAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTTGGC
851 ATTCGGCGGA ATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

```
g126.pep
1   MPSETPKARR RLSGDIASDN HTKESIMLTLY YGETFPSRL LGTAAYPTPE
51  ILKQSVRTAR PAMITVSLRR TCGGGEAHGQ GFWSLQLQETG VFPVLPNTAGC
101 QSVQEAHTTA QMAREVFETD WIKLELIGDD DTLQPDVFQL VEAAILIKD
151 GFKVLPYCTE DLIACRRLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201 RLPDTPLIID AGLGLPSQAA QVMEWGFQDV LLNTAVSRSG DPNVMARAF
251 LAVESGRLEF EAGFVEARTK AQASTPTVGQ PFWHSAEY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

```
m126.seq (partial)
1   ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACCTTTCCC
51  CTCGCGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCCC GAAATCCTCA
101 AACAATCCAT CCAAACCGCC CAGCCTGCGA TGATTACCGT CTCGCTGCGC
151 CGCGCGGGAA GCGGCGGCGA GCGGCACGGT CAGGGGTTTT GGTGCTGCT
201 TCAAGAAACC GCGTTCCTCG TCCTGCCGAA CACGGCAGGC TGCCAAAGCG
251 TGCAGGAAGC GGTAAACGAC GCGCAAATGG CGCGCGAAGT GTTTGAAACC
301 GATTGGATAA AATTGGAAT CATCGGAGAT GACGACACCT TGCAGCCGGA
351 TGTGTTCCAG CTTGTGGAAG CGGCGGAAAT CCTGATTAAA GACGGCTTCA
401 AAGTGCTGCC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCCTGCTC
451 GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCGGA TCGGCACGGG
501 TTTGGGCGCG GTTCACGCCT ACGCGTTGAA CGTCCTGCGC GAACGCCTGC
551 CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601 GCACAAGTGA TGGAATGGGG CTTTGACGGC GTGCTTTTGA ATACTGCCGT
651 TTCCCGCAGC GCGATCCGG TCAATATGGC ACGCGCCTTC GCACTCGCCG
701 TCGAATCCGG ACGGCTGGCA TTTGAAGCCG GACCGGTCGA AGCACGCGAC
751 AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTTT GGCATTGCGC
801 GGAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

```
m126.pep (partial)
1   ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP BILKQSIQTA QPAMITVSLR
51  RAGSGGEAHG QGFWSLQET GVPVLPNTAG QSVQEAHTT AQMAREVFET
```



```

101 DWIKLELIGD DDTLQPDVFQ LVEAAEILIK DGFKVLPYCT EDLIACRRLI
151 DAGCQALMPW AAPIGTGLGA VHAYALNVLR ERLPDTPLII DAGLGLPSQA
201 AQVMEWGFDG VLLNTAVSRS GDPVNMARAF ALAVESGRLA FEAGPVEARD
251 KAQASTPTVG QPFWHSAEY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 126 shows 95.9% identity over a 269 aa overlap with a predicted ORF (ORF 126.ng) from *N. gonorrhoeae*:

m126/g126

```

                                10      20      30      40
m126.pep                      HYTKPEIMLTLYGETFPSRLLLGTAAYPTPEILKQSIQTAQ
                                ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      MPSETPKARRRLSDGIASDNHTKESIMLTLYGETFPSRLLLGTAAYPTPEILKQSVRTAR
                                10      20      30      40      50      60

                                50      60      70      80      90      100
m126.pep      PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                ||||| ||||| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      PAMITVSLRRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                70      80      90      100      110      120

                                110     120     130     140     150     160
m126.pep      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                130     140     150     160     170     180

                                170     180     190     200     210     220
m126.pep      APIGTGLGAVHAYALNVLRERLPDTPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                ||||| ||||| ||||| :| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      APIGTGLGAVHAYALKILRERLPDTPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                190     200     210     220     230     240

                                230     240     250     260     270
m126.pep      DPVNMARAFALAVESGRLAFEAGPVEARDKAQASTPTVGQPFWHSAEYX
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      DPVNMARAFALAVESGRLAFEAGPVEARTKAQASTPTVGQPFWHSAEYX
                250     260     270     280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 467>:

a126.seq

```

1   TTGTTAATCC ACTATACAAA GGAACCCATT ATGCTCACCC TGTACAGCGA
51  AACTTTCCCT TCGCGGCTGC TGCTCGGCAC AGCCGCCTAC CCGACCCCTG
101 AAATCCTCAA ACAATCCGTC CGAACCGCCC GGCCCGCGAT GATTACCGTC
151 TCGCTGCGCC GCGCGGGATG CGGCGGCGAG GCGCACGGTC AGGGGTTTGT
201 GTCGCTGCTT CAAGAAACCG GCGTTCCTCGT CCTGCCGAAC ACGGCAGGCT
251 GCCAAAGCGT GCAGGAAGCG GTAACGACGG CGCAAATGGC GCGCGAAGTG
301 TTTGAAACCG ATTGGATTAA ACTCGAATC ATCGGCGACG ACGACACCTT
351 GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC GGCGGAAATC CTGATTAAAG
401 ACGGCTTCAA AGTGCTGCCT TATGCAACG AAGACCTGAT TGCTTGCCGC
451 CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG ATGCCGTGGG CGGCCCCGAT
501 CGGCACGGGT TTGGGCGCGG TTCACGCCTA CGCGTTGAAC GTCTTGCGCG
551 AACGCCTGCC CGACACGCCG CTGATTATCG ACGCGGGCTT GGGTTTGCCC
601 TCACAGGCGG CACAAGTGAT GGAATGGGGC TTTGACGGCG TGCTTTTGAA
651 TACTGCCGTT TCCCGCAGCG GCGATCCGGT CAATATGGCA CGCGCCTTCG
701 CACTCGCGGT CGAATCCGGA CGGCTGGCAT TTGAAGCCGG ACCGGTCGAA
751 GCACGCGACA AAGCGCAAGC CAGCACGCCG ACAGTCGGAC AACCGTTTTG
801 GCATTGCGCG GAATATTGA

```


This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
1  LLIHYTKEPI MLTYSETFP S RLLLGTAAY PTPEILKQSV RTARPAMITV
51  SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101 FETDWIKLEL IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR
151 RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201 SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251 ARDKAQASTP TVGQPFWWSA EY*
```

m126/a126 98.1% identity in 269 aa overlap

```

              10      20      30      40      50
m126.pep      HYTKEPIMLTLYGETFPSRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           LLIHYTKEPIMLTLYSETFPSRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGE
              10      20      30      40      50      60

              60      70      80      90      100     110
m126.pep      AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPD
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPD
              70      80      90      100     110     120

              120     130     140     150     160     170
m126.pep      VFQVLEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           VFQVLEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              130     140     150     160     170     180

              180     190     200     210     220     230
m126.pep      VLRERLPDTP LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           VLRERLPDTP LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESG
              190     200     210     220     230     240

              240     250     260     270
m126.pep      RLAFEAGPVEARDKAQASTPTVGQPFWWSAEYX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           RLAFEAGPVEARDKAQASTPTVGQPFWWSAEYX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
1  ATGCTCACCC TGTACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51  GGCCGCCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACC GCCC
101 GGCCGCCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACC GCCC
151 GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAACTC
301 ATCGCGCAGC ACGACACCTT GCAGCCGGAC GTGTTCCAAC TCGTCGAAGC
351 GGCGGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ATGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCCTA
501 TGCGCTCAAA ATCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCTT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601 TTTGACGGCG TATTGTTAAA CACCGCCGTT TCCCGCAGCG GCGACCCCGT
651 CAACATGGCG CGCGCCTTCG CACTCGCGGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG GCCGTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCCTTTTG GCATTCGGCG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
1  MLTYSETFP S RLLLGTAAY PTPEILKQSV RTARPAMITV SLRRTGCGGE
```



```

51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWWSA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

m126-1.seq

```

1 ATGCTCACCC TATACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51 GGCTGCCTAC CCGACCCCTG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAATC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTGTTCACAG TTGTCGAAGC
351 GCGGGAATAT CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCGCAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCTGCCG CGACACGCGG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTGCGCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTGT GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

m126-1.pep

```

1 MLTYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTYGETFP S R L L L G T A A Y P T P E I L K Q S I Q T A Q P A M I T V S L R R A G S G G E A H G Q G F W S L L					
g126-1	MLTYGETFP S R L L L G T A A Y P T P E I L K Q S V R T A R P A M I T V S L R R T G C G G E A H G Q G F W S L L					
	70	80	90	100	110	120
m126-1.pep	Q E T G V P V L P N T A G C Q S V Q E A V T T A Q M A R E V F E T D W I K L E I G D D D T L Q P D V F Q L V E A A E I					
g126-1	Q E T G V P V L P N T A G C Q S V Q E A V T T A Q M A R E V F E T D W I K L E I G D D D T L Q P D V F Q L V E A A E I					
	130	140	150	160	170	180
m126-1.pep	L I K D G F K V L P Y C T E D L I A C R R L L D A G C Q A L M P W A A P I G T G L G A V H A Y A L N V L R E R L P D T P					
g126-1	L I K D G F K V L P Y C T E D L I A C R R L L D A G C Q A L M P W A A P I G T G L G A V H A Y A L K I L R E R L P D T P					
	190	200	210	220	230	240
m126-1.pep	L I I D A G L G L P S Q A A Q V M E W G F D G V L L N T A V S R S G D P V N M A R A F A L A V E S G R L A F E A G P V E					
g126-1	L I I D A G L G L P S Q A A Q V M E W G F D G V L L N T A V S R S G D P V N M A R A F A L A V E S G R L A F E A G P V E					
	250	260				
m126-1.pep	A R D K A Q A S T P T V G Q P F W W S A E Y X					
g126-1	A R T K A Q A S T P T V G Q P F W W S A E Y X					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

a126-1.seq

```

1 ATGCTCACCC TGTACAGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51 AGCCGCTTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCGCGGATG CGGCGGCGAG

```


360

```

151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCTCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATTAA ACTCGAACTC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAT GTGTTCACAC TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCCTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCCGC AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTTG GCATTCCGGC GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

a126-1.pep

```

1  MLTYLSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
51  AHGQGFWSLL QETGVVPLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVAAEI LIKDGFKVLP YCTEDLIACR RLDDAGCQAL
151 MFWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

a126-1/m126-1 98.1% identity in 262 aa overlap

	10	20	30	40	50	60
a126-1.pep	MLTYLSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE AHGQGFWSLL					
m126-1	MLTYLGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE AHGQGFWSLL					
	10	20	30	40	50	60
a126-1.pep	QETGVVPLP NTAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
m126-1	QETGVVPLP NTAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
	70	80	90	100	110	120
a126-1.pep	QETGVVPLP NTAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
m126-1	QETGVVPLP NTAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
	70	80	90	100	110	120
a126-1.pep	LIKDGFKVLP YCTEDLIACR RLDDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
m126-1	LIKDGFKVLP YCTEDLIACR RLDDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
	130	140	150	160	170	180
a126-1.pep	LIKDGFKVLP YCTEDLIACR RLDDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
m126-1	LIKDGFKVLP YCTEDLIACR RLDDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
	130	140	150	160	170	180
a126-1.pep	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
m126-1	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
a126-1.pep	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
m126-1	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
a126-1.pep	ARDKAQASTP TVGQPFWWSA EYX					
m126-1	ARDKAQASTP TVGQPFWWSA EYX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

g127.seq

```

1  ATGGAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCGATACG
51  CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTTCCGCATC
151 GAAAGCAAGC GCGGTTTTTT GGTGCCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCCTGGCAT TTATCTGGTC GCGCAAAAT CAAACGCTGG
251 CTTTGTGAT GTTTGCGGTG GCGGCGGCGG TCGTCGTGGC GACAAAAGAA
301 CTGATTATGT GTCTGTCGGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA

```



```

551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 TCAGCGGTAT TTGGAAAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGGCC GCGCGTTACC CGCGTACCGT ACGACGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGCAGGTACA ATACCGCCTG TTAAATCATC
851 CCGCCGgtc cgAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

g127.pep

```

1 MEIWNMLNTW PDAVPIRAEA AESVAVAAL LLARALLLNI HFRRHDPFGI
51 ESKRRFLVAS RNITLLLVL F SLAFIWSAQI QTLALSMFAV AAAVVVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNSLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

m127.seq

```

1 ATGGAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCGATACG
51 TCGGAGGCG GTCGAATCCG TGGCGGCGGT TCGGGCTTGG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCCGCATC
151 GAAAGCAAGC GGCGGTTTTT GGTGTCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GGCGCAAATC CAAACGCTGG
251 CTTTGTGCGAT GTTTGCGGTG GCGGCGGCGG TCGTCTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTCGGG CAGTATTTTA AGGCTGCGCA CCCAGCAATA
351 CTCGGTCCGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGACAGC TTGCGGGAAC CACCGTTTCT TTCCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA
551 CCGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 CCAACGGsAT TTGGAAAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGACC GCGCGTTACC CGCGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCTTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGCAGGTACA ATACCGCCTG TTAAATCACC
851 CCGCGGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

m127.pep

```

1 MEIWNMLDTW LGAVPIRAEA VESVAVAAL LLARALLLNI HFKRHDPFGI
51 ESKRRFLVAS RNITLLLVL F SLAFIWSAQI QTLALSMFAV AAAVVVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNSLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng)

from *N. gonorrhoeae*:

m127/g127

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAESVAVAALLLARALLLNIHFKRHDPFGIESKRRFLVAS					
	: : : : : : : :					
g127	MEIWNMLNTWPDVPIRAEAESVAVAALLLARALLLNIHFRRHDPFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVA AVVVATKELIMCLSGSILRSATQQYSVG					
	: : : : : : : :					
g127	RNITLLLVLFSLAFIWSAQIQTALSMFAVA AVVVATKELIMCLSGSILRSATQQYSVG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

```

a127.seq
1   ATGGAAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCAGATACG
51  TGC GGAGGCG GTCGAATCCG TGGCGGTGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GGCGGTTTTT GGTGCGCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCAAATC CAAACGCTGG
251 CTTTGTCGAT GTTTGCGGTG GCGGCGCGG TCGTCGTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTCGGG CAGCATTTTA AGGTCTGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTGCGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAC GTCATCCATA
551 CGGTGCGAAT CCCGTTTCCC ATCCATTGG ATTCTGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCTACA TCCCCGCCAT
651 CCAACGGCAT TTGGAACACG TGCAGCGCGA AAACTGTTT ATCAGCCCCG
701 CCGCCAAACC GCGCGTTACC CGCGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GCGCGTTATG GACGAATTTT TCGCGTACA ATACGCCTG TTAAATTACC
851 CCGCCGGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

```

a127.pep
1   MEIWNMLDTW LGAVPIRAEA VESVAVVAAL LLARALLNI HFKRHPDFGI
51  ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAHVVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNLSLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRH LENVQAEKLF ITPAAKPRVT RVPYDDKAYR
251 IIVRFASPVSKRLEIQQAVM DEFLRVQYRL LNPAGSETL *

```

m127/a127 98.6% identity in 290 aa overlap

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLLNHFKRHPDFGIESKRRFLVAS					
a127	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLLNHFKRHPDFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAHVVATKELIMCLSGSILRSATQQYSVG					
a127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAHVVATKELIMCLSGSILRSATQQYSVG					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNLGDY					
a127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNLGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRHLENVQAEKLFITPAAKPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNYPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

```

1  atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTTaatca
51  aatccaaacc gaagACatca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCAGCACC
401 TGCGCGATT TCGTATTGAGC GCGCGGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGCGCGC CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCG
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCGCG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGccaaa cTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACAGCGCC GAACAGGTTT TAAACTTCCT GACGACCTC
901 GCCGCGCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAACACCTCG GTCTCGCCGA CCCGCGCCG TGGGACTTGA
1001 GCTACGCGCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AACTCTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTCGC
1101 CCAAATCAAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCTG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGactaca AAGGCCGCG CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AacCGGCCAC GSACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCGGGCAT CAACggcgTA GAATGGGACG CGGTGGAAT GCCCAGCCAG
1501 TTTATGGAAA ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgGCGAGC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TcgCGCCAA AACTTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCCGAGG CTATTACAGC TACGCATGGG CCGAAGTCCt
1851 cAGCACCGAT GCCTACGCGC CTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAACG CTTCTGGCAA GAAAtccttg ccgtcggcgg ctCCCGCAGC
1951 gcgGCGGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC

```


2001 ACTGCTGCGC CAAagcggtT TCGACAACGC gGcctgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

g128.pep

```

1 MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTTGWA
51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNPLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKQVR YFELQQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AESFKAFRG REPSIDALLR QSGFDNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

m128.seq (partial)

```

1 ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51 AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCG GAACCTGCGC
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAAACTC AACCAAC
1 TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51 wGTCAAAAAA TAYTTCCcyG TCGGCAAwGT ATTAAACGGA CTGTTGCGCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGGTC
151 TGGCACAAG ACGTGCCTA TtkTGAATTG CAACAAAACG GCGAAMCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTaka ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAAT TTCGTTTGGG AATACAATGT CTGGGCACAA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAA ACTTCCAAsG CGGCATGTT yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTta GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTGCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAAATCC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

m128.pep (partial)

```

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTTGWA
51 NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

```

//

```

1 YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTVPV
51 WHKDVRYXEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSGDGL
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEPALF DMMIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT

```


301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHSGF DNAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g128

g128.pep	10	20	30	40	50	60
	MIDNALLHLGEEPRFNIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT					
g128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFTIKNSPEFA					
m128	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFTIKNSPEFD					
g128.pep	130	140	150	160	170	180
	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAPGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
g128.pep			340	350	360	
			YAGEKLREAKYAFSETEVKKYFPVGKVLG			
m128			YASEKLREAKYAFSETXVKKYFPVGKVLNG			
			10	20	30	
g128.pep	370	380	390	400	410	420
	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
g128.pep	430	440	450	460	470	480
	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSGDTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
g128.pep	490	500	510	520	530	540
	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
g128.pep	550	560	570	580	590	600
	LVRQMEFALFDMMIYSEDEGRLLKNWQQVLDVSRKEVAVIQPEYNRNFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDEGRLLKNWQQVLDVSRKKVAVIQPEYNRNFALSFGHIFAGGY					
	220	230	240	250	260	270
g128.pep	610	620	630	640	650	660
	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330


```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTGCGG GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTGAC CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAACTC AACCACGATC
401 TGCGCGATT CGTCCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCCGCGAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCGCA CAACCGCAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTGCG
1101 CCAAAATCAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTTCA GACGCGACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCAACCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCTGCAAC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAT ATTTCGTTT GGAATACAAT GTCTTGGCGC AAATGTCGCG
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AACTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATCCGCGAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCGC CTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQF WDLGYAGEKL REAKYAFSET
351 EVKKYFPVKG VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKRRRRFS DGTQLQPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDDELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAANKFQ RGMFLVRQME

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551 FALFDMMIYS EDDEGRILKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPFRDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPFRDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIGVGVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIGVGVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130	TLSPAQKTKLNH-----				
a128	130	140	150	160	170	180
	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128.pep	-----					
a128	190	200	210	220	230	240
	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHILAVIQYADNRKLREQIYRAYV					
m128.pep	-----					
a128	250	260	270	280	290	300
	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVINFLHDL					
m128.pep	-----YASEKLREAKYAFSETXVKKYFPVGX					
a128	310	320	330	340	350	360
	ARRAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETXVKKYFPVGK					
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	370	380	390	400	410	420
	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQONGEXIGGVYMDLYAREGKRGGAWM					
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVD					
a128	430	440	450	460	470	480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD					
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDXLAAKNFQ					
a128	490	500	510	520	530	540
	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDEGRILKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	550	560	570	580	590	600
	RGMFLVRQMEFALFDMMIYSEDEGRILKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					


```

          400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRG
          |||||: |||||||||||||||||||||||||||||||||||||||||: |||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
          610      620      630      640      650      660

          460      470
m128.pep  REPSIDALLRHSGFDNAVX
          |||||: |||||
a128      REPSIDALLRHSGFDNAAX
          670

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 487>:

g128-1.seq (partial)

```

1  ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51  AATCAAAACC GAAGACATCA AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCGGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGGTG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CGGCACAAA AACCAGCTC GATCAGGACC
401 TGCGCGATTT CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAA CGAAGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACCGCA CGACGCGTT CGGCATTTC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTATACC AATACGCCG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG GCGCTACGTT ACCCGTGCCA GCGAAGCTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACGCG ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TAAAAATTA CGCCGAATG TCGCTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCGG CCAAACCCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCCG GAACACCTCG GTCTCGCCGA CCCGCGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAAATG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTCCG
1101 CCAAAATCAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGCGACAA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACCGGCGCG
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCCGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 488; ORF 128-1.ng>:

g128-1.pep (partial)

```

1  MIDNALLHLG BEPRFNQIKT EDIKPAVQTA IABARGQIAA VKAQHTTGWA
51  NTVRLTGIT ERVGRWGVV SHLNSVVDTP ELRAVYNELM PEITVFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LIGFKNYKEL SLATKMDTP EQVENFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSYAGEKL REAKYAFSET
351 EVKIFYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKRRRFA DGTLLQPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 489>:

m128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT

```



```

201 GGGCGTGGTG TCGCACCTCA ACTCGTTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAAATC AACCACGATC
401 TGCGCGATTT CGTCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCCTC
501 CCAAAATGCTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 ACACCTACCTC GCCGTATCC AATACGCGGA CAACGCGGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAACTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCG CCAAACCTTA GCGCGAAAA GACCTCGCG AAGTCAAAGC
951 CTTCGCGCG GAAAGCCTGA ACCTCGCGGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAACTG CGCGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTGCG
1101 CCAATCAAAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGCG TTTATATGA TTTGTACGA CGCGAAGCA AACCGCGCG
1251 CGCGTGGATG AACGACTACA AAGGCGCGC CCGTTTTCA GACGCGACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTCGCCCC ACCGTGCGC
1351 GGCAGGAAG CCCGCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACCGGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAAGTGGCG
1451 TATCCGCGAT CAACGGCGTA GAATGGGACG CGGTGGAAT GCCAGCCAG
1501 TTTATGGAAT ATTTCGTTG GGAATACAAT GTCTTGGCAC AAATGTACGC
1551 CCACGAAGAA ACCGCGGCTC CCTGCGCGA AGAACTCTT GACAAAATGC
1601 TCGCCGCGCA AAATCTTCAA CGCGGCATGT TCCTCGTCCG GCAAAATGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGCG CAACAGGTTT TAGACAGCGT GCGCAAAAA GTCCCGCTCA
1751 TCCAGCGCGC GAATACAAC CGCTTCGCT TGAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCGG CTATTACAGC TACGCGTGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCG CCTTTGAAGA AAGCGAGAT GTCGCGCCA
1901 CAGGCAAAAC CTTTGGCAG GAAATCTCG CCGTCGGCG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGC CGCGAACCGA GCATAGACGC
2001 ACTCTTGGC CACAGCGGT TCGACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pcp.

```

1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVPLTGIT ERVGRINGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRP KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKPSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTAK LLGFKNYABL SLATKMADTP EQVLNPLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVKG VLNGLFAQIK KLYGIGFTEK TVPVWHKQVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLPLTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 PMENFVWEYN VLAQMSAHBE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLLKNW QQVLDSVRKK VAVIQPPEYN RFALSPGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

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m128-1/g128-1 94.5% identity in 491 aa overlap

	10	20	30	40	50	60
g128-1.pcp	MIDNALHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128-1.pcp	ERVGRINGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128-1	ERVGRINGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120

370

	130	140	150	160	170	180
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKPSQNVLDATDAFGIY					
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKPSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g128-1.pep	FDDAAPLAGIPEDALAMFAAAQSEKKTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAQSEKKTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
g128-1.pep	TRASELSNDGKPDNTANIDRTLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
m128-1	TRASELSDDGKPDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
g128-1.pep	ARRAKPYAEKDLAEVKAPAREHLGLADPQPWDLSYAGEKLRKAKYAFSETEVKKYFPVVGK					
m128-1	ARRAKPYAEKDLAEVKAPARESLNADLPQPWDLGYASEKLRKAKYAFSETEVKKYFPVVGK					
	310	320	330	340	350	360
	370	380	390	400	410	420
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWM					
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFPAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFPAPPVGGREARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	490					
g128-1.pep	ELGVSGINGVK					
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCGGCCCT GCAAACCGCC ATTGCGGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAGCCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CGGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCACGATC
401 TGCGCGATTT CGTCCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTGGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCGGTCATCC AATACGCGCA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCGCGGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCTT GCAGGACCTC
901 GCCGCGCGGC CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCCG GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCGCG CGAAAAATCG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTTCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCTCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGCGG TTTATATGGA TTGTACGCA CGCGAAGGCA AACCGGCGCG

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1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGCACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTCGTTTG GGAATACAAT GTCTTGGGCG AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAACCTCCAA CGCGGAATGT TCCTCGTCCG CCAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCGAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCCAAGC CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

a128-1.pep

```

1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVFPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFPTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQTKL NHDRLDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLPQ WDLGYAGEKL REAKYAFSET
351 EVKKYFPVKG VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQQNGET
401 IGVVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLPHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAANKFP RGMFLVRQME
551 PALPDMMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAAAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESEKAFRG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 97.8% identity in 677 aa overlap

	10	20	30	40	50	60
a128-1.pep	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHGTWANTVEPLTGIT					
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a128-1.pep	ERVGRWGVVSHLNSVTDTPELRAAYNELMPEITVFPTEIGQDIELYNRFKTIKNSPEFD					
m128-1	ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFPTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
a128-1.pep	TLSHAQTKLNLNHDRLDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128-1	TLSPAQTKLNLNHDRLDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
a128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAAQSESKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
a128-1.pep	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPPEQVLNFLHDL					
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPPEQVLNFLHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
a128-1.pep	ARRAKPYAEKDLAEVKAFARESLGLADLPQWDLGYAGEKLREAKYAFSETEVKKYFPVKG					


```

m128-1      ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGAYASEKLREAKYAFSETEVKKYFPVGK
              310      320      330      340      350      360

              370      380      390      400      410      420
a128-1.pep  VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
              |||||
m128-1      VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
              370      380      390      400      410      420

              430      440      450      460      470      480
a128-1.pep  NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
              |||||
m128-1      NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHGLHLLTQVD
              430      440      450      460      470      480

              490      500      510      520      530      540
a128-1.pep  ELGVSGINGVEWDAVELPSQPMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKNFQ
              |||||
m128-1      ELGVSGINGVEWDAVELPSQPMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKNFQ
              490      500      510      520      530      540

              550      560      570      580      590      600
a128-1.pep  RGMFLVRQMEFALFDMMIYSEDDDEGRLLKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
              |||||
m128-1      RGMFLVRQMEFALFDMMIYSEDDDEGRLLKNWQQVLDVSRKKVAVIQPPEYNRFANSFGHIF
              550      560      570      580      590      600

              610      620      630      640      650      660
a128-1.pep  AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFPWQEILAVGGSRSAAESFKAFRG
              |||||
m128-1      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFPWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660

              670      679
a128-1.pep  REPSIDALLRHSGFDNAAX
              |||||
m128-1      REPSIDALLRHSGFDNAVX
              670

```

a128-1/ P44573

sp|P44573|OPDA_HABIN OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlc) homolog
- Haemophilus influenzae (strain Rd KW20)

>gi|1573174 (U32706) oligopeptidase A (prlc) [Haemophilus influenzae Rd] Length = 681

Score = 591 bits (1507), Expect = e-168

Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)

```

Query: 4  NALLHLGEEPRFDQIKTEDIKPALQTXXXXXXXXXXXXXXXXXTHGWANTIVEPLTGITERV 63
          N LL++ P F QIK E I+PA++ H W N + PLT +R+
Sbjct: 5  NPLINIQGLPPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHFTWENFILPLTETNDRL 64

```

```

Query: 64  GRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFDTLS 123
          R W VSHLSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S
Sbjct: 65  NRAWSPVSHLNSVKNSTELREAYQTCPLLSSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

```

```

Query: 124 HAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183
          AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++
Sbjct: 125 IAQKKAIEENSLRDFELSGIGLSEKQORYGEIVARLSELNSQFSNNVLDATMGWEKLIEN 184

```

```

Query: 184 AAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYVTRA 243
          A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE++YRAY TRA
Sbjct: 185 EAELAGLPESALQAAQQAESKGLKGYRFTLEIPSYLPVMTYCENRALREEMYRAYATRA 244

```

```

Query: 244 SELSDD-GKFDNTANIDRTLENALQTAKLLGFKNYAEBSLATKMADTPEQVLNFLHDLAR 302
          SE + GK+DN+ ++ L ++ AKLLGF Y ELSLATKMA+ P+QVL+FL LA
Sbjct: 245 SEQQPNAGKWDNSKVMKEILTLRVELAKLLGPNYTYELSLATKMAENPQQVLDPLDHLAE 304

```

```

Query: 303 RAKPYAEKDLAEVKAFARESLGLADLPWDLGAYAGEKLREAKYAFSETEVKKYFPVGKVL 362
          RAKP EK+L E+K + + G+ +L PND+G+ EK ++ YA ++ E++ YFP +V+
Sbjct: 305 RAKPQGEKELQLKGYCEKEFGVTELPWDIGFYSEKQKQHLAYAINDEBLRPYPENRVI 364

```


Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QQNGETIGGVYMDLYAREBGKRGGAWM 420
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGGAWM
 Sbjct: 365 SGLFELIKRIFNIRAVRKGVDTHWKDVRFFDLIDENDQLRGSFYLDLYAREHKRGGAWM 424

Query: 421 NDYKGRRRFS DGTLLQPTAYLVCNFTPPVGGKEARLSHDEIXXXXXXXXXXXXXXXXXXQVD 480
 +D GR+R DG+++ P AYL CNF P+G K A +H+E+ Q+D
 Sbjct: 425 DDCIGRKRKLDGSIETFPVAYLTCNFNAPIGNKPALFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ 540
 V+GINGV WDAVELPSQFMEN+ WE LA +S H ETG PLPKE ++L AKNFQ
 Sbjct: 485 VSDVAGINGVPWDAVELPSQFMENWCWEEELAFISGHYETGEPLPKEKLTQLLKAKNFQ 544

Query: 541 RGMFLVRQMEFALFDMMIYSEDDEGRLEKNWQVLDVSRKEVAVVRPPEYNRPFANSFGHIF 600
 MF++RQ+EF +FD ++. D + L SV+ +VAV++ ++ R +SF HIF
 Sbjct: 545 AAMFILRQLEFGIFDFRLHHTFDAEKTNQILDTLKSVKSQVAVIKGVDWARAPHFSFSHIP 604

Query: 601 XXXXXXXXXXXXXWAEVLSADAYAAFEESDDV-AATGKRFWQEILAVGGSRSAAESFKAFR 659
 WAEVLSADAY+ FEE TKG F EIL GGS E FK FR
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYSRFEEGIFNPITGKSFLDEILTRGGSEEPMEFLFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676
 GREP +DALLRH G N
 Sbjct: 665 GREPQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq
 1 ATGCTTTTAC CTCCTCGGCG TAAAACGGCG GCACATCAAT CAAGCCGTCT
 51 TTCATTTGCG TGCGGAAAAA ATGCGGCGTG TTGCCGTGAT CAAAATCAAT
 101 ATCGTGACAG ATCCAGCCCA AATCGCGGTT TGCTTCGCTT TCCGATAACG
 151 CCGACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTGCGC ATTTGCCCTT
 201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GGCGGTCGAA TCCTGTTTCA
 251 TCCGACAAAA CGCGTTGGCA GTCGGAATAA CCGCCCGGCC GTGTCAAATA
 301 ATGCGTTACT TTGGCCGGGT CTGTCTCTTT GTAAGCGGCG GTCITTTTTT
 351 GC CGCCATC CGCATCTGTT TGGCGCATG GCAAACGGCG GCTGCCGTAC
 401 AATCAAAATG TTTGGCGATT TCATGCAGAC AGGCATCCGG ATGCCGCCCG
 451 ACATATCGAG CCGGTTTTTG CCTATCCGAT TTGGCGGCAT TTAGGCCGGT
 501 AACTTGA

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep
 1 MLSPRRKTA AHQSSRLSFA CGKNAACCRD QNQYRAASSP NRGLPRFPIT
 51 PTAAAVHPYP RFRHLPPQAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI
 101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP
 151 TYRAGFCLSD LAAFRPVT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)
 1 ..TATCTGCGCT TTCACTATTT GCCCTTTTCTAG GCTGCGGGCA TAGGGACGGA
 51 ACAGGTAGCG GTCAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
 101 GAAATTCGG CCGGCTGTGT CAAATAATGC GTTACTTTGG CCGGGTCTTG
 151 TTCTTTGTAA GTGGTGGTCT TTTTGTGCGC GTTATCCCCA TCTGTTTGAG
 201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTCAT
 251 GCAGATAGGC ATCCGGGTGT TGCCCAACAT ATTGAGCCGG TTTTGCCTA
 301 TCCGATTGTA CGGCATTGAG ACCGGTAACT TGA

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)
 1 ..YLRPHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL
 51 FVSGGLFLR VIPICLSAQ MVAHVQSKCL AISCRXASGC CPTYXAGFCL
 101 SDLTAFRPVT *

Computer analysis of this amino acid sequence gave the following results:

m129/g129

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

m129/a129 98.2% identity in 110 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

g130.seq

```
1 ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCCT
51 TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAAGC
101 TGGCGGGCAG TGGATCGTTT GGCAGATGTCG ATGCCACTAC GGAAGCGGCA
151 ACGCAGACCC GCATCCAGCC TGTCGGACAA TTGACGATGG GTGACGGGCA
201 CCCCGTCGGC GAACGCCAAG GCGAACAGAT TTTCGGCAAA ATCTGTATCC
```


375

```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACCGCGACT GGGCGCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAATC AAACGGGCGA TTACCTACAT GCGCAATAAA
451 AGCGCGGTT CTTTCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCCG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAGGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGCAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
  1 MKQLRDNKAQ GSALFTLVSG IVIVIAVLYF LIKLAGSGSF GDVDATTEAA
 51 TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFOHAL NGFNAMPAKG GAADLTQDEL KRAITYMANK
151 SGGSPNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKKGKETH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
  1 ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CCGCGGACAG
 51 CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACCGC
101 GTATCGCAA GGCTTCGATA CCTTGTTCCA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAACCTT
201 AAACGGGCGA TTACTTACAT GGCGAACAAA AGCGGCGGTT CTTTCCGAA
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACCCC TCGGTCGGC GTTGACGGTA AAAAAGTCTT CGAAGCAACC
401 TGTCAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCG GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGACAA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAAG CGCAATGCA
551 GGTGTTGAGC ATGACGAAGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
  1 ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQGFDT LFOHALNGFN
 51 AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAAPAEA KAKDKGAAPA VGVDGKKVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPAXKG NAGLSDDEVK AAVDYMANQS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng) from *N. gonorrhoeae*:

```

m130/g130

          10      20      30
m130.pep          GEQIFGKICIQCHAADSNVPNAPKLEHNGD
                  |||
g130      DATTEAATQTRIQPVGQLTMDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
          50      60      70      80      90     100

          40      50      60      70      80      89
m130.pep      XAPRI-QGFDTLFOHALNGFNAMPAKGGAADLTQDELKRAITYMANKSGGSFPNPDEAAP
              |||
g130      WAPRIAQGFDTLFOHALNGFNAMPAKGGAADLTQDELKRAITYMANKSGGSFPNPDEAAP
          110     120     130     140     150     160

```


376

	90	100	110	120	130	140
m130.pep	ADNAASGTASAPADSAAAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
g130	ADNAASGTASAPADSAAAPAEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
	170	180	190	200	210	220
	150	160	170	180	190	200
m130.pep	KKDDWAPRIKKGKETLHKHALEGFNAMPAXGNAGLSDDDEVKAAVDYMANQSGAKFX					
g130	KKDDWAPRIKKGKETLHKHALEGFNAMPAXGGNAGLSDDDEVKAAVDYMANQSGAKFX					
	230	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130.seq
  1  ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCTT
 51  TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAAGC
101  TGGCGGGCAG CGGCTCGTTC GCGATGTCG ATGCCACTAC GGAAGCAGCA
151  ACGCAGACCC GTATCCAGCC TGTCGGACAA TTGACGATGG GCGACGGCAT
201  CCCCCTCGGC GAACGCCAAG GCGAACAGAT TTTCGGCAA ATCTGTATCC
251  AATGCCACGC GCGCGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301  AACGGCGATT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCT
351  ACACGCGCTG AACGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGTAG
401  ACCTGACCGA TCAGGAATC AAACGGGCGA TTAATTACAT GCGGAACAAA
451  AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCTG CCGACAATGC
501  CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551  CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601  AAAAAAGTCT TCGAAGCAAC CTGTCAGGTG TGCCACGGCG GTTCGATTCC
651  CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701  AAGGCAAGA AACCTGCAC AAACACGCCC TTGAAGGCTT TAACGCGATG
751  CCTGCCAAG GCGCAATGC AGGTTGAGC GATGACGAAG TCAAAGCGGC
801  TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130.pep
  1  MKQLRDNKAQ GSAFLTIVSG IVIVIAVLYF LIKLAGSGSF GDVDATTEAA
 51  TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101  NGDWAPRIAQ GFDTLFQHAL NGFNAMPAGK GAVDLTDQEL KRAITYMANK
151  SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVDG
201  KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251  PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

m130/a130 97.6% identity in 206 aa overlap

				10	20	30
m130.pep				GEQIFGKICIQCHAADSNVPNAPKLEHNGD		
a130	DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD					
	50	60	70	80	90	100
	40	50	60	70	80	89
m130.pep	XAPRI-QGFDTLFQHALNGFNAMPAGGGAADLTDQELKRAITYMANKSGGSFNPDEAAP					
a130	WAPRIAQGFDTLFQHALNGFNAMPAGGGAADLTDQELKRAITYMANKSGGSFNPDEAAP					
	110	120	130	140	150	160
	90	100	110	120	130	140
m130.pep	ADNAASGTASAPADSAAAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
a130	ADNAASGTASAPADSAAAPAEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
	170	180	190	200	210	220
	150	160	170	180	190	200
m130.pep	KKDDWAPRIKKGKETLHKHALEGFNAMPAXGNAGLSDDDEVKAAVDYMANQSGAKFX					


```

|||||
a130      KKDDWAPRIKKGKETLHKHALEGFNAMPAGGNAGLSDDEVKAAVDYMANQSGAKFX
           230       240       250       260       270       280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 505>:

```

g132.seq
1  ATGGAAGCCT TCAAAACCCT AATTGGATT ATTAATATTA TTTCGCTTT
51  GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACCTT CGGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTTCGGCTCT
151 GCCGGCAACG CCAACTTcct CagccGCTCG AccGccGTTG CAGCAACAtt
201 tttcttTGca acctgcAtgg gctatggTgt atattcacac CCACACGACA
251 AAACACGGTT TGGACTtcag caacataCGA CAGACTCAGC AagcACCCAA
301 ACCcgtAAGC AATACCGAAC CTTCGCCCC TGTTCCTCAG CAGCAGAAAT
351 AACagtTTTT CAAATgccga caTGgtga

```

This corresponds to the amino acid sequence <SEQ ID 506; ORF 132.ng>:

```

g132.pep
1  MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51  AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QHTTDSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 507>:

```

m132.seq (partial)
1  ATGGAACCCT TCAAAACCTT AATTGGATT GTTAATTTAA TTTCGCTTT
51  GGCCGTCTTC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CGGA...

```

This corresponds to the amino acid sequence <SEQ ID 508; ORF 132>:

```

m132.pep (partial)
1  MEFPKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 132 shows 89.5% identity over a 38 aa overlap with a predicted ORF (ORF 132.ng) from *N. gonorrhoeae*:

m132/g132

```

           10       20       30
m132.pep  MEFPKTLIWIIVNLISALAVFVLVLLQHGKGADAGATFG
           || |||||:|:|||||:|||||:|||||:|||||
g132      MEAFKTLIWIINIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS
           10       20       30       40       50       60

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 509>:

```

a132.seq
1  ATGGAAGCCT TCAAAACCCT AATTGGATT GTTAATATAA TTTCGCTTT
51  GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CGGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTTCGGCTCT
151 GCCGGCAACG CTAACCTTCCT CAGCCGCTCG ACCGCCGTTG CAGCAACATT
201 TTTCTTTGCA ACCTGCATGg GCTATGGTGT ATATTACACAC CCACACGACA
251 AAACACGGTT TGGACTTCAG CAACGTACAA CAAACTCAGC AAGCACCCAA
301 ACCCGTAAGC AATACCGAAC CTTCGCCCC TGTTCCTCAG CAGCAGAAAT
351 AACAGTTTTT CAAATGCCGA CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 510; ORF 132.a>:

```

a132.pep
1  MEAFKTLIWI VNIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51  AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QRTTNSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

```

m132/a132 92.1% identity in 38 aa overlap

378

	10	20	30	
m132.pep	MEPFKTLIWIIVNLISALAVFVLVLLQHGKGADAGATFG			
a132	MEAFKTLIWIIVNIIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

g134.seq

```

1  ATGTCCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCCGATGCGG GTAAAACAC  GCTGACCGAA AAACCTGCTGC
101  TGTTTTCGGG CGCGATTCAA AGCGCAGGCA CGGTGAAAGG TAAGAAAACC
151  GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201  TTCCGTGGCA TCAAGCGTGA TGCAGTTCGA CTACAAAGAC CACACCGTCA
251  ACCTCTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301  GTTTTAACCG CAGTGGACAG CGCCTTGATG GTCATCGACG CGGCAAAAGG
351  CGTGGAAAGC CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCGATA
401  CGCCGATTGT TACCTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCT
451  TTGGAACCTT TGGACGAAGT GGAAGACATC CTGCAAAATCC GCTGCGCGCC
501  CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAGGGGC GTGTACCACA
551  TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCCTGCCG
601  CACGAGTTTC ACATCATCAA AGGCATAAAC AATCCCGAAT TGAACAACG
651  CTTTCGGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701  CGGCTTCCAA CGAATTTAAT CTCGacgaAT TTCTCGcgg CGAACTCAGC
751  CCAGTGTCTC TCGGCTCTGC GATTAAACAAC TTCGGCATTC AGGAAATCCT
801  CAATTCATTG ATTGACTGGG CACCCGCACC GAAACCGCGC GACGCGACCA
851  TGCGCATGGT CGGGCCGGAC GAGCCGAAAT TTTCCGGATT TATCTTTAAA
901  ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATCG CCTTCTTGCG
951  CGTCTGCTCC GGTAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001  TCAACCGCGA AATCGCCGCC TCCAGCGTAG TAACCTTCAT GTCGCACGAC
1051  CGCGAACTGG CGGAAGAAGC CTACGCCGGC GACATCATCG GCATCCCGAA
1101  CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCGGAAGGC GAACAACTGG
1151  CGTTTACCGG CATCCATTG TCGCGCCCG AACTGTTCCG CAGCGTCCGC
1201  ATCAAAAACC CGCTGAAAAT CAAACAACTG CAAAAAGGTT TCAACAACCT
1251  CGGCGAAGAA GGTGCGGTTT AAGTATTCAA ACCGATGAGC GGCGCGGATT
1301  TGATTTTGGG TGCGGTTCGGC GTGTTGCAGT TTGAAGTCGT AACCTCAGC
1351  CTCGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAGCG CATCCATCTG
1401  GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAATG GCGGAATTTG
1451  AAAAAAGCAA CGCAGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501  TACCTCGCCC CCAACCGCGT GAATTTGGGG TTGACGCAAG AACGCTGGCC
1551  GGACATCGTG TTCCACGAAA CGCGCGAACA TTCGGTCAAA CTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

g134.pep

```

1  MSQEILDQVR RRRTPAIISH PDAGKTLTLE KLLLFSGAIQ SAGTVKGKKT
51  GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101  VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151  LELLDEVEDI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201  HEFDIIKGIN NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251  PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATMRMVGPD EPKFSGFIFK
301  IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351  RELAEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401  IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVITSR
451  LANEYGVEAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501  YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

m134.seq

```

1  ATGTCCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCTGACGCGA GTAAAACAC  GTTGACTGAA AAACCTTTCG
101  TGTTTTCGGG CGCGATTTCG AGCGCGGGTA CGGTAAAAGG CAAGAAAACC
151  GGCAAATTCG CCACTTCCGA CTGGATGGAA ATCGAGAAGC AGCGCGGCAT

```



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201 TTCCGTGGCA TCAAGTGTGA TGCAGTTCGA TTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CCGTGGACAG CGCATTAATG GTCATCGACG CGGCAAAAGG
351 CGTGAAGCG CAAACCATCA AGCTCTTAAA CGTCTGCCGC CTGCGCGATA
401 CACCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAACTTT TGGACGAAGT GGAAAACATT TAAAAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA TGAAATTTAT CTCTTTGAAG CTGGCGGCGA ACGCCTGCCG
601 CACGAGTTTG ACATCATCAA AGGCATCGAT AATCCTGAAT TGGAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTTAAT CTCGACGAAT TCCTCGCCGG CGAACTCAGC
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTTCATT ATTGACTGGG CGCCCGCGCC GAAACCGCGC GACGCGACCG
851 TACGTATGGT CGAGCCGGAC GAGCCGAAGT TTTCCGGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG
951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TTACCTTCAT GTCGCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACCTG
1151 CGTTCACCGG CATCCCATT TCGCACCCG AACTGTTCCG CAGCGTACGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAACG CAAAAGGCT TGCAACAGCT
1251 CGCGCAAGAA GGCGCGGTGC AGGTGTTCAA ACCGATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTGCGC GTGTTGCACT TTGAAGTCGT TACCTCGCGC
1351 CTCGCCAAGC AATACGGCGT AGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAACTG GCTGAATTTG
1451 AAAAAAGCAA CGCGGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTGCGA CTCACGCAAG AACGTTGGCC
1551 GGACATCGTG TTCCACGAAA CACGCGAACA TTCGGTCAAA CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

m134.pep

```

1 MSQEILDQVR RRRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWME IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151 LELLDEVENI LKIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKID NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATVRMVEPD EPKPSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPP FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng) from *N. gonorrhoeae*:

m134/g134

	10	20	30	40	50	60
m134.pep	MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME					
g134	MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m134.pep	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA					
g134	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA					
	70	80	90	100	110	120
	130	140	150	160	170	180

380

m134.pep	QTIKLLNVCRRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPIGMGKNFKG
g134	QTIKLLNVCRRLRDTPIVTFMKNKYDREVRDSLELLDEVEDILQIRCAPVTWPIGMGKNFKG
	130 140 150 160 170 180
m134.pep	190 200 210 220 230 240
	VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLF EAGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134.pep	250 260 270 280 290 300
	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATMRMVGPEPKFSGFIFK
	250 260 270 280 290 300
m134.pep	310 320 330 340 350 360
	IQANMDPKHRDRI AFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHRELVEEAYAG
g134	IQANMDPKHRDRI AFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHRELAEAYAG
	310 320 330 340 350 360
m134.pep	370 380 390 400 410 420
	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
	370 380 390 400 410 420
m134.pep	430 440 450 460 470 480
	GAVQVFKPMSGADLILGAVGVQLQFEVVTSRLANEYGV EAVFDSASIWSARWVSCDDKKKL
g134	GAVQVFKPMSGADLILGAVGVQLQFEVVTSRLANEYGV EAVFDSASIWSARWVSCDDKKKL
	430 440 450 460 470 480
m134.pep	490 500 510 520 530
	AEFEKANAGNL AIDAGGNLAYLAPNVRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNL AIDAGGNLAYLAPNVRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

a134.seq

1	ATGTCCCAAG	AAATCCTCGA	CCAAGTGCGC	CGCCGCCGCA	CGTTTGCCAT
51	CATCTCCAC	CCTGACGCAG	GTAAAACCAC	GTTGACTGAA	AAACTCTTGC
101	TGTTTTCAGG	TGCGATTCAA	AGCGCGGGTA	CGGTAAAAGG	CAAGAAAACC
151	GGCAAATTCG	CCACCTCCGA	CTGGATGGAC	ATCGAGAAGC	AGCGCGGCAT
201	TTCCGTGGCA	TCAAGCGTGA	TGCAGTTCGA	CTATAAAGAC	CACACCGTCA
251	ACCTTTTGA	CACGCCGGA	CACCAAGACT	TCTCCGAAGA	CACCTACCGC
301	GTTTGTACCG	CCGTGATAG	TGCCTTGATG	GTCATCGACG	CGGCAAAAGG
351	CGTGGGAAGC	CAAACCATCA	AACCTCTGAA	CGTCTGCCGC	CTGCGCAATA
401	CGCCGATTGT	TACGTTTCATG	AACAAATACG	ACCGCGAAGT	GCGCGATTCC
451	CTGGAATTGC	TGGACGAAGT	GGAAAACATC	CTGCAAATCC	GCTGCGCGCC
501	CGTAACCTGG	CCGATCGGCA	TGGGCAAAAA	CTTCAAAGGC	GTGTACCACA
551	TCCTGAACGA	CGAAATCTAT	CTCTTTGAAG	CGGGCGGCGA	ACGCTTGCCG
601	CACGAGTTCG	ACATCATCAA	AGGCATCGAT	AATCCCGAAT	TGGAACAACG
651	CTTTCGGTTA	GAAATACAGC	AGTTGCGCGA	CGAAATCGAA	TTGGTGCAGG
701	CGGCTTCCAA	CGAGTTCAAT	CTCGACGAAT	TCCTCGCCGG	CGAACTCAGC
751	CCCGTATTCT	TCGGCTCTGC	GATTAACAAC	TTCCGTATTG	AGGAAATCCT
801	CAATTCATTG	ATTGAATGGG	CGCCCGCGCC	GAAACCACGC	GATGCGACCG
851	TGCGTATGGT	CGAGCCGGAC	GAGCCGAAGT	TTTCCGGATT	TATCTTCAA
901	ATCCAAGCCA	ATATGGACCC	GAAACACCGC	GACCGTATTG	CCTTCTTGCG

381

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951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCGGCG GACATTATCG GTATCCCAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACCTGA
1151 CGTTTACCGG CATCCCATTC TTCGCGCCCG AACTGTTCG CAGCGTTCGC
1201 ATCAAAAACC CGCTGAAAAT CAAGCAACTG CAAAAGGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTTCAA ACCAATGAGC GCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAACTG GCGGAATTTG
1451 AAAAAACCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACCGCGT GAATCTGGA CTCACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAAA CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```

a134.pep
1 MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAKGVEA QTIKLLNVCRLRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGID NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLTFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQOLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVAV FDNASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

m134/a134 98.9% identity in 531 aa overlap

	10	20	30	40	50	60
m134.pep	MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME					
a134	MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m134.pep	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAKGVEA					
a134	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAKGVEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m134.pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPIGMGKNFKG					
a134	QTIKLLNVCRLRNTPIVTFMKNKYDREVRDSLELLDEVENILQIRCAPVTWPIGMGKNFKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m134.pep	VYHILNDEIYLFEAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
a134	VYHILNDEIYLFEAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m134.pep	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK					
a134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIEWAPAPKPRDATVRMVEPDEPKFSGFIFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m134.pep	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHRELVEEAYAG					
a134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHRELVEEAYAG					
	310	320	330	340	350	360

382

	370	380	390	400	410	420
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134.pep	GAVQVFKPMSGADLILGAVGVLFQFEVVTSRLANEYGVFAVFDNASIWSARWVSCDDKKKL					
a134	GAVQVFKPMSGADLILGAVGVLFQFEVVTSRLANEYGVFAVFDNASIWSARWVSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134.pep	AEFEKANAGNLAI DAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
a134	AEFEKANAGNLAI DAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

g135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51  TTCGGACgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTCCG GCGCTGGGT TTCAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GTGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CCGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTCGGTT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGCGGGCT CCGGTTCCGC AAACGCGACG GCGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTcggaaa gcgGgGgcag cgttTatgtg gacgaaagtg
851 cggaaacacgc tTgtccgaa caagggaag cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

g135.pep

```

1  MKYKRIVFKV GTSSITRSDG SLRSGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVQGG LLMBEYTNAL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHINHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAESGVPV YICSSLKPDS LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESGGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

m135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGCG AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCCG TGCCTGGGT TTCAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CCGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

```


m135.pep

1	MKYKRIVFKV	GTSSITHSDG	SLSRGKIQTI	TCQLAALHHA	GHELVLVSSG
51	AVAAGFALG	FKRYQPKIAD	KQASAAVQGG	LLMEEYTANL	SSDGIVSAQI
101	LLSRADFADK	RRYQNAGGAL	SVLQRRRQVP	IINENDTVSV	EELKIGDNMT
151	LSAQVAMFIQ	ADLLVLLTDI	DGLYTGPNPS	NPDADVRLDKI	EHNHIEIEM
201	AGGSGSANGT	GGMLTKIKAA	TIAAESGVVP	YICSSLKPDA	LARAAEHQAD
251	GSFFVPRAKG	LRTQKQWLAF	YSESRGSVYV	DEGAEHALSE	QKGSLLMSGI
301	AGIEGHFSRM	DTVTVYSKAT	KQPLGKGRVL	FGSAAAEDLL	KSRKAKGVFI
351	HRDDWISITP	EIRLLLTFF*			

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 135 shows 97.6% identity over a 294 aa overlap with a predicted ORF (ORF 135.ng) from *N. gonorrhoeae*:

m135/q135

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
g135	MKYKRIVFKVGTSSITRSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVQGILLMEEYTANLSSDGIVSAQILLSRADFADKKRYQNAGGAL					
g135	FKKRPVKIADKQASAAVQGILLMEEYTANLSSDGIVSAQILLSRADFADKKRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRRAVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNNS					
g135	SVLLQRRRAIPPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNNS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHINHEIIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDA					
g135	NPDAVRLDKIEHINHEIIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDS					
	190	200	210	220	230	240
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEHALSEQKSLMSGI					
g135	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESGSVYVDESAEHALSEQKACX					
	250	260	270	280	290	300
m135.pep						
g135						
	250	260	270	280	290	300
m135.pep						
g135						
	310	320	330	340	350	360

m135.pep AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

```
a135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACTTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGCGGCG GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACA GGCGGTATGC TGAATAAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCGAAA GCAGGGGCGG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGAATCG AAGGGCATT TTCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCTT TGGGCAAAGG GCGAGTCTTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATTGCGTA AGGCGAAAGG CGTGTTCATC
1051 CATCGGACG ACTGGATTTC CATCACGCCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

```
a135.pep
1  MKYKRIVFKV GTSSITHSDG SLRSGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHNHEIEM
201 AGGSGSANGT GGMLTKIKAA TIATESGVPV YICSSLKPPA LAEADNQAD
251 GSFFVPRAKG LRTQQWLAF YSESRRGVYV DEGAEHALSE QGKSLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLTEF*
```

m135/a135 98.4% identity in 369 aa overlap

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
a135	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRAPVIINENDTVSVEELKIGDNDTSLAQVAAMIQADLLVLLTDIDGLYTGPNPS					
a135	SVLLQRRAPVIINENDTVSVEELKIGDNDTSLAQVAAMIQADLLVLLTDIDGLYTGPNPS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAAESGVVPVYICSSLKPPA					
a135	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAATESGVVPVYICSSLKPPA					
	190	200	210	220	230	240

385

	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRSVYVDEGAEHALSEQGKSLMSGI					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSESRRGGVYVDEGAEHALSEQGKSLMSGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTDTVYISKATKQPLGKGRVLFSGAAEDLLKSRKAKGVFIHRDDWISITP					
a135	AGIEGHFSRMDTDTVYISKATKQPLGKGRVLFSGAAEDLLKLRKAKGVFIHRDDWISITP					
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLTEFX					
a135	EIRLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

```

g136.seq
1  ATGGAATCC  GGTTCAGAC  AGCATTTTTA  CGTTTGGTTC  AGatgaAAAC
51  AAACGCTtca  aTTCTtaccg  caACACGCCT  TGTATTTCCT  GccgCTGCCG
101 CACGGACAGG  GATCGTTCCT  GCCGgtTTTT  TCCCCTTCCC  TCGGACGGT
151 TTGCGGTTTG  TTGATGACCG  CCTGCCAGTA  GCGGTAGATG  Tctgccagcg
201 cgTAAGGCag  tTCGGACgca  agttccgcca  gctcgccctc  ggTGAATTGC
251 AGgcgataa  cgccgtttTC  CTCTTCGTcG  taaatgccgc  ccaactgcat
301 cacgGGGTAA  AACAGCTCTT  CAAACGCTTC  ATCATCGGCG  GCTTCAAACC
351 AATCGGTCGG  CACAATGTCC  AAACCGTAAA  GATAGGCGTT  GCACCAAGTG
401 TAAAAATCGC  TGCCGCCCTC  GCCGTCGTcG  TAGAGCCACA  AATCGGGCAG
451 CTTTTTATCC  GACATCGCGG  CGGTTGTTTT  CATCGCCATT  GCCAAACCA
501 GCCGTTTCGAT  TTCGGAACGT  TCGGCGGCGG  TAAATTGCGA  TTCGTCGCCC
551 AACACTTCGG  GCAGCCAGTC  GAGCGGTGCC  AATTGTCCG  GCCCGCTCAA
601 CAGCGCCGTC  ATAAACCTT  GAACCTCGTC  GCAACGCATC  GTGTTGCCTT
651 GTTCGCTTTT  GGCATCCAAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

```

g136.pep
1  MEIRFQTAFL  RLVQMKTNAS  ILTATRLVFP  AAAARTGIVP  AGFFFPFADG
51  LRFVDDRLPV  AVDVCQVRVQ  FGRKFRQLAF  GELQADNAVF  LFVVNAAHCH
101 HGVKQLFKRF  IIGGFKPIGR  HNVQTVKIGV  APSVKIAAAL  AVVVEPQIGQ
151 LFIHRGGCF  HRHCQNQPF  FGTFGGKLR  FVAQHFGQPV  ERCQFVRPAQ
201 QRRHKTLLV  ATHRVALFAF  GIQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

```

m136.seq
1  ATGGAACAA  ACGCTTCAAT  TCTTACCGCA  ACACGCCTTG  TATTTTCTGC
51  CGTGCCGCA  CGGACAGGGA  TCGTTCCTGC  CTGTTTTTTC  GCCTTCCCTG
101 CGGACGGTTT  GCGGTTTGT  GATGACTGCC  TGCCAGTAGC  GGTAGATATC
151 CGCCAATGCA  TAAGGCAACT  CGGATTCCAG  TTCCGCCAGC  TCGCCTTCTG
201 TGAATTGCAG  ACGGATAGCG  CCGTTTTCCT  CTTCGTCGTA  AATACCGCCC
251 AATGCCATGA  TGGGATAAAA  CAACTCTTCA  AACGCTTCAT  CATCGACGGC
301 TTCAAACCA  TCGGTCGGCA  CAATATCCAA  ACCGTAAAGA  TAAGCATTGC
351 ACCATGTGTA  AAAATCGCTG  CCGCGTCTT  CGTTTTCATA  CAGCCACAAA
401 TCGGGCAGTT  TTTTATCCGA  CATCGCGGCG  GTTGTTCCTA  TCGCCATTGC
451 CAAAACCAGC  CGTTCGATT  CGGAACGTT  GGCGGCGGTA  AATTGCGATT
501 CGTCGCCCAA  CACTTCGGGC  AGCCAGTCGA  GCGGTGTCAA  TTTGTCCGGC
551 CCGCTCAACA  GCGCCGTCAT  AAAACCTTGA  ACCTCGTCGC  AACGCATCGT
601 GTTGCCTTGT  TCGCTTTTGG  CATCCAACAA  TTCGCTCAAC  CGCCGTTTGG
651 ATGCTTCGGT  AAATTTTCGG  GAATCCATCA  TTTTCTTTT  CAAATGGGTT
701 TTGCGCCCTA  TTATCGCCGC  AATGCCGTCT  GA

```

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:

m136.pep

```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRFV  DDCLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVFLFVV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQQRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFPF  QMGFAPYYRR  NAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 136 shows 85.6% identity over a 209 aa overlap with a predicted ORF (ORF 136.ng) from *N. gonorrhoeae*:

m136/g136

```

                                10      20      30      40
m136.pep      METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPV
                |||
g136      MEIRFQTAFLRLVQMKTNASILTATRLVFPAAAAARTGIVPAGFFFPADGLRFVDDRLPV
                10      20      30      40      50      60

                                50      60      70      80      90      100
m136.pep      AVDIRQCIRQLGFQFRQLAFCELOTD SAVFLFVVNTAQCHDGIKQLFKRFIIDGFKPIGR
                |||
g136      AVDVCQRVRQFGRKFRQLAFGELQADNAVFLFVVNAAHCHGVKQLFKRFIIGGFKPIGR
                70      80      90      100      110      120

                                110      120      130      140      150      160
m136.pep      HNIQTVKISIAPCVKIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLR
                |||
g136      HNVQTVKIGVAPSVKIAAALAVVVEPQIGQLFIRHRGGCFHRHCQNQPFDFGTFGGGKLR
                130      140      150      160      170      180

                                170      180      190      200      210      220
m136.pep      FVAQHFGQPVERCQFVRPAQQRHKTTLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIH
                |||
g136      FVAQHFGQPVERCQFVRPAQQRHKTTLNLVATHRVALFAFGIQX
                190      200      210      220

                                230      240
m136.pep      HFPPQMGPAPYYRRNAVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 527>:

a136.seq

```

1  ATGGAAACAA  ACGCTTCAAT  TCTTACCGCA  ACACGCCTTG  TATTTCTGCG
51  CGCTGCCGCA  CGGACAGGGA  TCGTTCCTGC  CTGTTTTTTC  GCCTTCCCTG
101 CGGACGGTTT  GCGGCTTGTT  GATGACCGCC  TGCCAGTAGC  GGTAGATATC
151 CGCCAATGCA  TAAGGCAACT  CGGATTCCAG  TTCCGCCAGC  TCGCCTTCTG
201 TGAATTGCAG  ACGGATAGTG  CCGTTGTCCT  CTTGTCGTA  AATACCGCCC
251 AATGCCATGA  TGGGATAAAA  CAACTCTTCA  AACGCTTCAT  CATCGACGGC
301 TTCAAACCAA  TCGGTCGGCA  CAATATCCAA  ACCGTAAAGA  TAAGCATTGC
351 ACCATGTGTA  AAAATCGCTG  CCGCCGTCTT  CGTTTTATA  CAGCCACAAA
401 TCGGGCAGTT  TTTTATCCGA  CATCGCGGCS  GTTGTTCCTA  TCGCCATTGC
451 CAAAACCAAG  CGTTCGATTT  CGGAACGTC  GCGGCGGTA  AATTGCGATT
501 CGTCGCCCAA  CACTTCGGGC  AGCCAGTCGA  GCGGTGTCAA  TTTGTCCGGC
551 CGCCTCAACA  GCGCCGTCAT  AAAACCTTGA  ACCTCGTCGC  AACGCATCGT
601 GTTGCCTTGT  TCGCTTTTGG  CATCCAACAA  TTCGCTCAAC  CGCCGTTTGG
651 ATGCTTCGGT  AAATTTTCGG  GAATCCATCA  TTTTCCTTTT  CCAATGGGTT
701 TTGCGCCCTA  TTATAGTGGA  TTAAATTTAA  ATCAGGACAA  GGCGACGAAG
751 CCGCAGACAG  TACAAATAGT  ACGGCAAGGC  GAGGCAACGC  CGTACTGGTT
801 TAAATTTAAT  CCACTATATC  GCCGAATGC  CGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 528; ORF 136.a>:

a136.pep

387

```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVEFVI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQQRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFPF  PMGFAPYYSG  LNLNQDKATK
251 PQTQIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

```

10      20      30      40      50      60
m136.pep  METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ
          |||||
a136      METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRLVDDRLLPVAVDIRQCIRQLGFQ
          10      20      30      40      50      60

70      80      90      100     110     120
m136.pep  FRQLAFCELOTD SAVVLFV VNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
          |||||
a136      FRQLAFCELOTD SAVVLFV VNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
          70      80      90      100     110     120

130     140     150     160     170     180
m136.pep  KIAAAVFVFIQ P QIGQFFIRHRGGCFHRHCQNQPFDGTFGGGKLRFVAQHFGQPVERCQ
          |||||
a136      KIAAAVFVFIQ P QIGQFFIRHRGGCFHRHCQNQPFDGTFGGGKLRFVAQHFGQPVERCQ
          130     140     150     160     170     180

190     200     210     220     230     240
m136.pep  FVRPAQQRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPFQMGFAPYYRR
          |||||
a136      FVRPAQQRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPFQMGFAPYYSG
          190     200     210     220     230     240

m136.pep  NAVX
a136      LNLNQDKATKPQTQIVRQGEATPYWFKFNPLYRRNAVX
          250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

```

g137.seq
1  ATGATTATCC  ATCACcaatt  CGATCCCGTC  CTCATCAGTA  TCGGCCCGCT
51  TGCCGTCGCG  TGGTATGCCT  TAAGCTACAT  CCTCGGATTT  ATTCTTTTTA
101 CCTTTCTCGG  CAGAAGGCGC  ATCGCGCAAG  GCTTGTCCGT  TTTTACCAAA
151 GAATCGCTCG  ACGACTTCCT  GACATGGGGC  ATTTTGGGCG  TGATTTTGGG
201 CGGACGCTTG  GGCTATGTCC  TGTTTTACAA  ATTCTCCGAC  TACCTCGCCC
251 ATCCGCTTGA  TATTTTCAAG  GTATGGGAAG  GCGGAATGTC  GTTCCACGGC
301 GGCTTTTGG  GTGTAGTTAT  TGCCATATGG  TTGTTACGCC  GCAAGCACGG
351 CATCGGCTTC  CTCAAAGTGA  TGGACACGGT  CGCGCCGCTC  GTTCCGCTGG
401 GTCTCGCTTC  GGGACGTATC  GGCAACTTTA  TCAACGGCGA  ACTTTGGGGA
451 CGCATPACCG  ACATTAACGC  ATTTTGGGCA  ATGGGCTTCC  CGCAAGCGCA
501 TTACGAAGAT  GCCGAAGCCG  CCGCGCACAA  TCCGCTTTGG  GCAGAATGGC
551 TGCAACAATA  CGGTATGCTG  CCGCGTCATC  CCTCGCAGCT  TTATCAGTTT
601 GCCCTTGAAG  GCATCTGCCT  GTTCGCCGTC  GTTTGGCTGT  TTTCCAAAAA
651 ACCGCGCCCG  ACCGGGCAGA  CTGCCGCGCT  TTTTCTCGGC  GGCTACGGCG
701 TGTTCCGCTT  TATTGCCGAA  TTGCGCGCC  AACCCGACGA  CTATCTCGGG
751 CTGCTGACCT  TGGGGCTGTC  GATGGGGCAA  TGTTGAGCG  TCCCAGATGAT
801 TGTTTTGGGT  ATCGTCGGCT  TTGTCCGCTT  CGGCATGAAA  AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 530; ORF 137.ng>:

g137.pep


```

1  MIIHQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLLDDFLTWG ILGVILGGRL GYVLFYKFS YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RITDINAFWA MGFPQAHYED AEAHAHNPLW AEWLQYQYGM PRHPSQLYQF
201 ALEGICLFAV VWLFSKKPRP TGQTAALFLG GYGVFRFIAE FARQPDYLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 531>:

```

m137.seq
1  ATGATTACCC ATCCCAATT CGATCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATTT ATTCTTTTAA
101 CCTTCTCGG CAGAAGCGC ATCGCGCAAG GCTTGTCCGT TTTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGG GTGTAGTTAT TGCCATACGG TTGTTCCGGC GCAAACACGG
351 CATCGGCTTC CTCAAACTGA TGGATACGGT CGCACCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGCGCG
501 TTACGAAGAT GCCGAAGCCG CCGCGCACA TCCGCTTTGG GCAGAATGGC
551 TGAACAATA CGGTATGCTG CCGGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTCAACGTC ATTTGGCTGT TCTCTAAAAA
651 ACAGCGGTCG ACCGGACAAG TCGCCTCGCT CTTCTCGGC GGCTACGGCA
701 TATTCGCTT CATGCGGAA TTCGACGCC AACCCGACGA CTATCTCGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTAGCG TCCCAGTAT
801 TGTTTGGGT ATCGTCGGCT TTGTCCGGT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 532; ORF 137>:

```

m137.pep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLLDDFLTWG ILGVILGGRL GYVLFYKFS YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIR LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RITDINAFWA MGFPQARYED AEAHAHNPLW AEWLQYQYGM PRHPSQLYQF
201 ALEGICLFTV IWLFSKKQRS TGQVASLFLG GYGVFRFIAE FARQPDYLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 137 shows 95.4% identity over a 283 aa overlap with a predicted ORF (ORF 137.ng) from *N. gonorrhoeae*:

m137/g137

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLLDDFLTWG					
g137	MIIHQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLLDDFLTWG					
	10	20	30	40	50	60
m137.pep	ILGVILGGRLGYVLFYKFSYLAHPLDIFKVVWEGGMSFHGGFLGVVIAIRLFSRKHGIGF					
g137	ILGVILGGRLGYVLFYKFSYLAHPLDIFKVVWEGGMSFHGGFLGVVIAIWLFGRKHGIGF					
	70	80	90	100	110	120
m137.pep	LKLMDTVAPLVPLGLASGRIGNFINDELWGRVTDINAFWAMGFPQARYEDAEAAHNPLW					
g137	LKLMDTVAPLVPLGLASGRIGNFINDELWGRITDINAFWAMGFPQAHYEDAEAAHNPLW					
	130	140	150	160	170	180
m137.pep	AEWLQYQYGM PRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGFIRFIAE					
g137	AEWLQYQYGM PRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGFIRFIAE					
	190	200	210	220	230	240


```

a137.seq
1  ATGATTACCC ATCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCGCG TGGTATGCCG TAAGCTACAT CCTCGGATTT ATTCCTTTTA
101 CTTTCTCGG CAGAAGGCCG ATCGCGCAAG GCTTGTCCGT TTTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGG GTGTAGTTAT TGCCATATGG TTGTTCGGTC GCAAACACGG
351 CATCGGCTTC CTCAAACTGA TGGACACGGT CGAACCGCTC GTTCCACTGG
401 GTCTCGCTTC GGCACGTATG GGCAACTTCA TCCACGCGCA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAC CTGGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CTTCCGAGCT TTATCAGTTT
601 GCACTTGAAG GACATCTGCT GTTCGCCGTC GTTTCGCTGT TCTCTAAAAA
651 ACAGCGGCCG ACCGGACAGA TCGCTCACT CTTCCTCGCG GGCTCGGCA
701 TATTCCGCTT CATTGCCGAA TTGCAACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCCGGT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

a137.pep

1	MITHPQFDPV	LISIGPLAVR	WYALSYILGF	ILFTFLGRRR	IAQGLSVFTK
51	ESLDDEFTWG	ILGVILGGRL	GYVLFYKFS	YLAHPLDIFK	VWEGGMSFHG
101	GFLGVVIAIW	LFGRKHGIGF	LKLMDTVAPL	VPLGLASGRI	GNFINGELWG
151	RVTDINAFWA	MGFPQARYED	LEAAAHNPLW	AEWLQYQYGM	PRHPSQLYQF
201	ALEGICLFAV	WVLFSSKKQRP	TGVQASLFLG	GYGIFRFIAE	FARQPPDYL
251	LLTILGLSMG	WLSVPMIVLG	IQGFVRFGMK	KOH*	

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFTKESLDDFLT	WG			
a137	MITHPQFDPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFTKESLDDFLT	WG			
	10	20	30	40	50	60
	70	80	90	100	110	120
m137.pep	ILGVILGGRGLGYVLFYKFS	DYLAHPLDIFKVVWEGGMSFHGGFLGVVIAIRL	FGRKHGIGF			
a137	ILGVILGGRGLGYVLFYKFS	DYLAHPLDIFKVVWEGGMSFHGGFLGVVIAIW	LFGGRKHGIGF			
	70	80	90	100	110	120
	130	140	150	160	170	180
m137.pep	LKLMDTVAPLPLGLASGRIGNF	INGELWGRVTDINAEWAMGFPQARYEDAEAAAHN	PLW			
a137	LKLMDTVAPLPLGLASGRIGNF	INGELWGRVTDINAEWAMGFPQARYEDLEAAAHN	PLW			
:	130	140	150	160	170	180
	190	200	210	220	230	240
m137.pep	AEWLQQYGMLPRHPSQLYQFA	LEGICLFTVIWLFSSKKORSTGQVASLFLGGYGIF	RFIAE			
a137	AEWLQQYGMLPRHPSQLYQFA	LEGICLFAVVWLFSSKKORPTGQVASLFLGGYGIF	RFIAE			

	190	200	210	220	230	240
	250	260	270	280		
m137.pep	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX					
a137	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

g138.seq

```

1  ATGGAGTTTG AAAACATTAT TTCCGCCGCGc gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACatcc gccgGTTTTT CGGTTGCGTC GCCGTCATCA
101 AGTATGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAGAGAC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGCGACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAAACTT TTGGTCGATA CGCCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCCGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT GGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCcgccgtc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTCGATG ATTTTAGGCA GAGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

g138.pep

```

1  MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVVLKLKLVG IHPVIVHGGG PQINAMLEKV GKGGEFVQGM RVTDKETMDI
101 VBMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LVDTPQNSV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEBLNAEKL LMTNIAQVM DKTGNLLTKL TPKRIDGLIA DGTLYGGMLP
251 KIASAVRAAV NGVKATHIID GRLEPNALLE IFTDAGIGSM ILGRGEDA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

m138.seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGTTTTTC CGGTTGCGTC GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAGAGAGC GATGGATATT
301 GTCGAAATGG TGTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAAACTT TTGATCGATA CGCCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCCGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 : ATGCCGTAT CGGTCGATG ATTTTGGGCG GTGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

m138.pep

```

1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA

```


51 RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKRAMDI
 101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
 151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
 201 LABELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
 251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGGGEDA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 138 shows 98.0% identity over a 298 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

m138/g138

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
g138	MEFENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDKRAMDIVEMVLGGHVNKEIVSMINTY					
g138	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDKETMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
g138	GGHAVGVSGRDDHFIKAKKLLVDTPEQNSVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
g138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDGLIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
g138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGRGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 539>:

a138.seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGTTTTC CGGTTCGGTC GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTGGGCGG GCATGTCAAT AAAGAAATCG TGTGATGAT
351 TAACACATAT GCGCGACACG CGGTCGGCGT AAGCGGACGC GACGACCAT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTGCGTAC GGTGGAAAGC ATCGATACCG GTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACTC ACGCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTGCA AGCCGCCGTC AACGGCGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGGTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGTAT CGGTTGATG ATTTTGGGCG GTGGGGAAGA TGCCTGA

```


This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
  1 MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
 51 RDVVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151 DIGQVGTVES IDTGLVKGLI ERGCIPVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRVPNALLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
a138	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVKKGEFVQGMRTDKEAMDIVEMVLGGHVNKEIVSMINTY					
a138	IHPVIVHGGGPQINAMLEKVKKGEFVQGMRTDKEAMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVAP					
a138	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAEEELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
a138	VGVGEKGEAFNINADLVAGKLAEEELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRPNALLEIFTDAGIGSMILGGGEDAX					
a138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRVPNALLEIFTDAGIGSMILGGGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
  1 ATGCGAACCA CCTCAACCTT CCCTACAAA ACTTTCAAAC CGGCTGCCAT
 51 GCGGTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGgc ggcggcggag
101 gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
151 AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
201 AAAAAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCTGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
301 ATACCGGAGA CTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
351 CCTCAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
401 GTATCGTCGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCCGAACTG
451 TATGCGAGAA AAGAACACGG CTATAACGAA AATTACAAA ACAAAATTACA
501 AAACTATAC GCGTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
  1 MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
 51 NSRATIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
101 IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPPEL
151 YGRKEHGYNE NYKNKLQKLY GVIYABGSA*
```


m139.seq

1	ATGCGAACGA	CCCCAACCTT	CCCTACAAAA	ACTTTCAAAC	CGACTGCCAT
51	GGCGTTAGCT	GTTGCAACAA	CACTTTCTGC	CTGCTTAGGC	GGCGGCGGAG
101	GCGGCACCTC	TGCGCCCGAC	TTCAATGCAG	GCGGTACCGG	TATCGGCAGC
151	AACAGCAGAG	CAACAACAGC	GAAATCAGCA	GCATCTATCT	ACGCCGGTAT
201	CAAGAACGAA	ATGTGCAAA	ACAGAAAGCAT	GCTCTGTGCC	GGTCCGGGATG
251	ACGTTGCGGT	TACAGACAGG	GATGCCAAAA	TCAATGCCCC	CCCCGGAATC
301	TGCATACCGG	AGACTTTCCA	AACCCAAATG	ACGCATTACA	AGAATTTGAT
351	CAACCTCAAA	CCTGCAATTG	AAGCAGGCTA	TACAGGACGC	GGGGTAGAGG
401	TAGGTATCGT	CGACACAGCG	GAGTCCGTAC	CGACCATATC	CTTTCCCGAA
451	CTGTATGGCA	GAAAAGAAC	CAATCTATAC	GAAAATTACG	AAAAACTATA
501	CGCGCTATAT	CGCGAAGGAA	GCGCTCTGA		

m139.pep

1 MRTTPTFPTK TFKPTAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
51 NSRATTAKSA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETPQTQM THYKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSIISFPE
151 LYGRKEHGYN ENYEKLYGVY AEGSA*

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

m139/g139

	10	20	30	40	50	60
m139.pep	MRTTPTFTPKTFKPTAMALAVATTLSACLGGGGGGTSAPDFNAGGTGIGSNSRATTAKSA					
g139	MRTTSTFTPKTFKPAAMALAVATTLSACLGGGGGGTSAPDFNAGGTGIGSNSRATIAESA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGRDDVAVTDTRDAKINAPPRICIPETFQTMTHYKNLNLK					
g139	AVSYAGIKNEMCKDRSMLCAGRDDVAVTDTRDAKIKAP-RICIPETFQTMINIKNMINLK					
	70	80	90	100	110	
	130	140	150	160	170	
m139.pep	PAIEAGYTGREGVEVGIVDTGESVGSISFPPELYGRKEHGYNENY----EKLYGVYAEGSAX					
g139	PAIEAGYTGREGVEVGIVDTGESVGSISFPPELYGRKEHGYNENYKNKLQKLYGVYAEGSAX					
	120	130	140	150	160	170

a139.seq

1	ATGCGAACGA	CCCCAACCTT	CCCTACAAAA	ACTTTCAAAC	CGGCTGCCAT
51	GGCGTTAGCT	GTTGCAACAA	CACTTTCTGC	CTGCTTAGGC	GGCGGCGGAG
101	GCGGCACTTC	TGCGCCCGAC	TTCATGCGAG	GCGGCACCGG	TATCGGCAGC
151	AACAGCAGGG	CAACAACAGC	GAATTCAGCA	GCAATATCTT	ACGCCGGTAT
201	CAAGAACGAA	ATGTGCAAG	ACAGAAAGCAT	GCTCTGTGCC	GGTCGGGATG
251	ACGTTTCCGT	TACAGCAGG	GATGCCAAAA	TCNATGCCCC	CCCCGAATC
301	TGCATACCGG	AGACTTTACA	AACCCAAATG	ACGCAT.ACA	AGAATTTGAT
351	CAACCTCAAA	CCTGCAATTG	AAGCAGGCTA	TACAGGACGC	GGGGTAGAGG
401	TAGGTATCGT	CGACACAGGC	GAATCCGTGC	GCAGCATATC	CTTCCCGGAA
451	CTGTATGGCA	GA AAAAGAAC	CGGCTATAAC	GAAAATTAC.	AAAACTATA
501	CGCGCTATAT	CGCGAAGGAA	CGGCCTGA		

a139.pep

1 MRTTPTEPTK TEKPAAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS

51 NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
 101 CIPETLQTM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSI SFPE
 151 LYGRKEHGYN ENYXKLYGVY AEGSA*

m139/a139 97.1% identity in 175 aa overlap

	10	20	30	40	50	60
m139.pep	MRTTPTFTKTFKPTAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA	
a139	MRTTPTFTKTFKPAAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGR	DDVAVTDR	DAKINAPPRI	CIPETLQTM	THXKNLINLK	
a139	AISYAGIKNEMCKDRSMLCAGR	DDVAVTDR	DAKINAPPRI	CIPETLQTM	THXKNLINLK	
	70	80	90	100	110	120
	130	140	150	160	170	
m139.pep	PAIEAGYTGRGVEVGIVDTG	ESVGSISFPE	LYGRKEHGYN	ENYKLYGVY	AEGSAX	
a139	PAIEAGYTGRGVEVGIVDTG	ESVGSISFPE	LYGRKEHGYN	ENYKLYGVY	AEGSAX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 547>:

g140.seq

1	Atgtcgccac	gCGGCAAGGG	GGCAGgctat	ctcAACAGTA	CCGGACGACa
51	TGTTCCCTTC	CTGAGTGCCG	CCAAAATCGG	GCAGGATTAT	TCTTTCTTCA
101	AAAATATCAA	AACCGACGGC	GGTCTGCTGG	CTTCCCTCGA	CAGCGTCGAA
151	AAAACAGCGG	GCACTGAAGG	CGACACGCGG	TCCTATTATG	TCCGTGCGCG
201	CAATGCGGCA	CGGACTGCTT	CGGCAGCGGC	ACATTCCGCG	CCCGCCGGTC
251	TGAAACACGC	CGTAGAACAG	GGCGGCAGCA	ATCTGGAAAA	CCTGATGGTC
301	GAGCTGGATG	CCTCCGAATC	ATCCGCAACA	CCCGAGACGG	TTGAAACTGC
351	GGTCGCCGAC	CGCACAGATA	TGCCGGGCAT	CCGCCTACGG	CGCACAACTT
401	TCCGCACAGC	GGCAGCCGTA	CAGCATGCGA	ATACCGCCGA	CGCGGTACGc
451	aTCTTcaaCA	GTCTCGCCGC	TaccgTCTat	GccgACAGTG	CCGCCGCCCA
501	TGccgATATG	CAGGGACGCC	GCCTGAAAGC	CGTATCGGAC	GGGTTGGACC
551	ACAACGGTAC	GGGTCTGCGC	GTCATCGCGC	AAACCCAAACA	GGACGGTGGA
601	ACGTGGGAAC	AGGGCGGTGT	CGAAGGCAAA	ATGCGCGGCA	GTACCCAAAC
651	TATCGGCATT	GCCGCGAAAA	CCGGCGAAAA	TACGACAGCA	GCCGCCACAC
701	TGGGCATAGG	ACGCAGCACA	TGGAGCGAAA	ACAGTGCAAA	TGCAAAAACC
751	GACAGCATTa	GTCTGTTTGC	AGGCATACGG	CACGATGTGG	GCGATATCGG
801	CTATCTCAAA	GGCCTGTCTT	CctaCGGACG	CTACAAAAAC	AGCATCAGCC
851	GCAGCACCGG	TGCGGATGAA	TATGCGGAAG	GCAGCGTCAA	CGGCACGCTG
901	ATGCAGCTGG	GCGCACTGGG	TGGTGTCAAC	GTTCCGTTTG	CCGCAACGGG
951	AGATTTGACG	GTTGAAGGCG	GTCTGCGCCA	CGACCTGCTC	AAACAGGATG
1001	CATTTCGCCA	AAAAGGCagt	GCTTTGGGCT	GGAGCGGCAA	CAGCCTCACT
1051	GAAGGCACAC	TGGTCGGACT	CGCGGGTCTG	AAACTGTGCG	AACCCCTTGAG
1101	CGATAAAGCC	GTCTGTCTTG	CGACGGCGGG	CGTGGAACGC	GACCTGAACG
1151	GACGCGACTA	CGCGGTAACG	GGCGGCTTTA	CCGGCCGCGC	TGCAGCAACC
1201	GGCAAGACGG	GTGCACGCAA	TATGCCGCAC	ACCCGCCGGG	TTCGCGGTCT
1251	GGGGGTGGAT	GTGAAATTCG	GCAACGGCTG	GAACGGCTTG	GCACGTTACA
1301	GCTACACCGG	TTCCAAACAG	TACGGCAACC	ACAGCGGACA	AATCGGCGTA
1351	GGCTACCGGT	TCTGA			

This corresponds to the amino acid sequence <SEQ ID 548; ORF 140.ng>:

g140.pep

1	MSARGKGAGY	INSTGRHVPF	LSAAKIGQDY	SFFKNIKTDG	GLLASLDSVE
51	KTAGEGSDTP	SYIVRRGNAA	RTASAAHSA	PAGLKHAVEQ	GGSNLENLMV
101	ELDASESSAT	PETVETAVAD	RTDMPGIRLR	RTTFRTAAAV	QHANTADGVR
151	IFNSLAATVY	ADSAAAHADM	QGRRLKAVSD	GLDHNGTGLR	VIAQTQDGG
201	TWEQGVVEGK	MKGSTQTIGI	AAKTGENTTA	AATLGIGRST	WSENSANAKT

251 DSISLFAGIR HDVGDIGYLK GLFSYGRYKN SISRSTGADE YAEGSVNGTL
 301 MQLGALGGVN VPFAATGDLT VEGGLRHDLL KQDAFAEKGS ALGWSGNSLT
 351 EGTLVGLAGL KLSQPLSDKA VLSATAGVER DLNGRDYAVT GGFTGAAAAT
 401 GKTGARNMPH TRRVAGLGVD VEFNGWNGL ARYSYTGSKQ YGNHSGQIGV
 451 GYRF*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 549>:

m140.seq
 1 ATGTCGGCAC GCGCAAGGG GGCAGGCTAT CTCAACAGTA CCGGACGACG
 51 TGTTCCTTC CTGAGTGCCG CCAAATCGG GCAGGATTAT TCTTTCTTCA
 101 CAAACATCGA AACCGACGGC GGCCTGCTGG CTTCCTCGA CAGCGTCGAA
 151 AAAACAGCGG GCAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
 201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
 251 TGAACACGCG CGTAGAACAG GCGCGCAGCA ATCTGGA AAA CCTGATGGTC
 301 GAACTGGATG CCTCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
 351 GGCAGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTAC GGCGCAACTT
 401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
 451 ATCTTCAACA GTCTGCGCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
 501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
 551 ACAACGGCAC GGGTCTGCGC GTCATCGCGC AAACCAACA GGACGGTGGA
 601 ACGTGGGAAC AGGCGGGTGT TGAAGGCAA ATGCGCGGCA GTACCCAAAC
 651 CGTCGGCATT GCCGCAAAA CCGCGAAAA TACGACAGCA GCCGCCACAC
 701 TGGGCATGGG ACGCAGCACA TGGAGCGAAA ACAGTGCAA TGCAAAAACC
 751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
 801 CTATCTCAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
 851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG
 901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG
 951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
 1001 CATTTCGCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCCTCACT
 1051 GAAGGCACGC TGTCGGACT CGCGGGTCTG AAGCTGTGCG AACCTTGAG
 1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGAACGC GACCTGAACG
 1151 GACGCGACTA CACGGTAACG GCGGCTTTA CCGGCGCGAC TGCAGCAACC
 1201 GGCAAGACGG GGCACGCAA TATGCCGCAC ACCCGTCTGG TTGCCGGCCT
 1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
 1301 GCTACGCCGG TTCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
 1351 GGCTACCGGT TCTGA

This corresponds to the amino acid sequence <SEQ ID 550; ORF 140>:

m140.pep
 1 MSARGKGAGY LNSTGRRVPF LSAAKIGQDY SPFTNIETDG GLLASLDSVE
 51 KTAGSEGDTL SYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
 101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
 151 IFNSLAATVY ADSTAAHADM QGRRLKAVSD GLDHNGTGLR VIAQTQDGG
 201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGRST WSENSANAKT
 251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
 301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSLT
 351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
 401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
 451 GYRF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 140 shows 94.5% identity over a 454 aa overlap with a predicted ORF (ORF 140.ng) from *N. gonorrhoeae*:

m140/g140

	10	20	30	40	50	60
m140.pep	MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSPFTNIETDGGLLASLDSVEKTAGSEGDTL					
g140	MSARGKGAGYLNSTGRHVPFLSAAKIGQDYSPFTNIETDGGLLASLDSVEKTAGSEGDTP					
	10	20	30	40	50	60
	70	80	90	100	110	120

m140 . pep	SYVVRGNAARTASAAAHSAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAAAD
g140	SYVVRGNAARTASAAAHSAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAVAD
	70 80 90 100 110 120
m140 . pep	130 140 150 160 170 180 RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLSLAATVYADSTAHAADMQGRRLKAVSD
g140	RTDMPGIRLRRTTFRATAAVQHANTADGVRIFNLSLAATVYADSAAAHADMQGRRLKAVSD
	130 140 150 160 170 180
m140 . pep	190 200 210 220 230 240 GLDHNGTGLRVIAQTQDDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST
g140	GLDHNGTGLRVIAQTQDDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLIGRST
	190 200 210 220 230 240
m140 . pep	250 260 270 280 290 300 WSENSANAKTDSISLFAIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
g140	WSENSANAKTDSISLFAIRHDVGDIGYLKGLFSYGRYKNSISRSTGADEYAEGSVNGTL
	250 260 270 280 290 300
m140 . pep	310 320 330 340 350 360 MQLGALGGVNVPPAATGDLTVEGGLRDLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
g140	MQLGALGGVNVPPAATGDLTVEGGLRDLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
	310 320 330 340 350 360
m140 . pep	370 380 390 400 410 420 KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD
g140	KLSQPLSDKAVLSATAGVERDLNGRDYAVTGGFTGAAAATGKTGARNMPHTRRVLGLVD
	370 380 390 400 410 420
m140 . pep	430 440 450 VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX
g140	VEFGNGWNLARYSYTGSKQYGNHSGQIGVGYRFX
	430 440 450

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140 . seq
1  ATGTCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCTTC CTGAGTGCCG CCAAAATCGG GCGGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCGGCCGGTC
251 TGAAACACGC CGTAGAACAG GGCGGCAGCA ATCTGGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCCTAC GGCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGCTAC GGGTCTGCGC GTCATCGCGC AAACCCAAAC GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGCAAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGCGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATCGCG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CCGTGTC AAC GTTCCGTTT CCGCAACGGG

```



```

951 AGATTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCATCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGGTCTG AAGCTGTCGC AACCCCTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGAACGC GACCTGAACG
1151 GACGCGACTA CACGGAACG GCGCGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGCCTGG TTGCCGGTCT
1251 GGGCGCGGAT GTCGAATTCT GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACGCCGG TTCCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 552; ORF 140.a>:

```

a140.pep
1 MSAGGKGAGY LNRTGQRVPF LSAKIGRDY SFFTNIETDG GLLASLDSVE
51 KTAGSEDTL SYVVRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNNLAATVY ADSTAAHADM QGRRLLKAVSD GLDHNATGLR VIAQTQDDGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGHST WSENSANAKT
251 DSISLFAIR HDAGDIGYLG GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSIT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

m140/a140 98.2% identity in 454 aa overlap

m140.pep	10	20	30	40	50	60
	MSARGKGAGYLNSTGRRVPFLSAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEDTL					
a140	MSAGGKGAGYLNRTGQRVPFLLSAKIGRDYSFFTNIETDGGLLASLDSVEKTAGSEDTL					
	10	20	30	40	50	60
m140.pep	70	80	90	100	110	120
	SYVVRGNAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
a140	SYVVRGNAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
	70	80	90	100	110	120
m140.pep	130	140	150	160	170	180
	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLSLAATVYADSTAAHADMQGRRLLKAVSD					
a140	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNNLAATVYADSTAAHADMQGRRLLKAVSD					
	130	140	150	160	170	180
m140.pep	190	200	210	220	230	240
	GLDHNGTGLRVIAQTQDDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST					
a140	GLDHNATGLRVIAQTQDDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGHST					
	190	200	210	220	230	240
m140.pep	250	260	270	280	290	300
	WSENSANAKTDSISLFAIRHDAGDIGYLGKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
a140	WSENSANAKTDSISLFAIRHDAGDIGYLGKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
	250	260	270	280	290	300
m140.pep	310	320	330	340	350	360
	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITTEGLTVGLAGL					
a140	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITTEGLTVGLAGL					
	310	320	330	340	350	360
m140.pep	370	380	390	400	410	420
	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					
a140	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					

398

	370	380	390	400	410	420
	430	440	450			
m140.pep	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
a140	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

g141.seq

```

1  atgagcttca aAaccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGCGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATGTC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TCGCGAGACC TTCTTTGGGT
301 CCGGTGTTTCG GCGTGAAAGG CGGCGGGCA GCGCGGGCT ACGCGCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGCGAC TTCCACGCCA
401 TCGGTGCGGC GAATAACCTC CTCGCCGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCAAA CGCGTGCTGT GCGGCGCGT
501 GGTCGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTTga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTGa tggcgGTATT CTGCCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTtt gGCAATATTC TCGTCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAG GCACACGGCG CGATGGCGGC ATTGCTAAAA
751 GATGCGATTA AGCCCAATTT GGTGCAAACC ATCGAAGGCA CTCCGGCCTT
801 TGTAACCGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG TGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCCGCG
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAAC
1051 CTCGAAGCCT TGGCAAAAGG TTTGCCCAAC CTGTTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCCGAC TGCCCGTTCG CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCTT GACCGAAGTG TGGGGCAAAG GCGGCGCGGG
1251 CGGCGCGGAT TTGGCGGCA AAGTCGTCAA TGCCATCGAC AACCAACCTA
1301 ATAACTTCGG TTTCCCTTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTCG ATTTCAGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTAGCGA CAACGCCAAA
1501 CTCTTGGGCT GCCCGAAGG CTTCCGCATC GCCGTACGCG GTATCACTGT
1551 TTCGCGCGC GCGGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGGGCCT GCCGAAAGT CCGCTGCCG AGAAAATCGA TGTGGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

g141.pep

```

1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGA GGYAQVLPD EDINLHFTGD FHAIGAANNL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDH NDRQLRNIID GMGKPVGDVM RPDGFDITVA
201 SEVMAVFCFLA KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGVESVLTVE WKGKGAGGAD LARKVVNAID NQPNNFGPAY DVELGIKDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPGEGFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAEKIDVDE
551 HGVIHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1  ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGGTCA TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGCGGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTCG
251 GCCACATCGG CAAAGATGCC GTGATTGCCC TGC CGGAACC TTCTCTGGGG
301 CCGGTGTTCC GCGTGAAAGG CGGCGCGGCA GGCGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GGCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCCTGTTA CCGCGTGATG CGTCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTCCCTA CGCCAAAGAC GGCAGCCCG
701 TTTACGCCAA AGATTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTCG CCAACATCGC CCACGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCAGAGCA
901 CGCTTCGGCG CGGACTTGCG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCCTTCG
1151 TGTCGACGCG CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACTTCGG TTTGCCTTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCATGTC CCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1  MSFKTDARIA QSSTMRPIGE IAAKGLNAD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFVGKGGAA GGGYAQVLPD EDINLHFTGD FHAIGAANNL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPDGVM RPDGFDITVA
201 SEVMAVFCLA KDIDSLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDADAE LAMIEKACAE
401 HGVEVSLTEV WKGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIAQKVYGA EDVDFSAEAS AETASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAEEKIDVDA
551 EGVINGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

```

          10      20      30      40      50      60
m141.pep  MSFKTDARIAQSSTMRPIGEIAAKGLNADNIEPYGHYKAKINPAEAFKL PQKQGRLLIV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g141       MSFKTDATAQSSTMRPIGEIAAKGLNVDNIEPYGHYKAKINPAEAFKL PQKQGRLLIV
          10      20      30      40      50      60

```


400

	70	80	90	100	110	120
m141.pep	TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGGAAGGGYAQVLP					
g141	TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGGAAGGGYAQVLP					
	70	80	90	100	110	120
m141.pep	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVVDMMNDRQLRNIID					
g141	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVVDMMNDRQLRNIID					
	130	140	150	160	170	180
m141.pep	GMGKPPVDGVMRPDGFDTIVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSVPYAKDLK					
g141	GMGKPPVDGVMRPDGFDTIVASEVMAVFCLAKDISDLKERFGNILVAYAKDGSVPYAKDLK					
	190	200	210	220	230	240
m141.pep	ANGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCSVTATRLAKHLADYAVTEA					
g141	AHGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
g141	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
	310	320	330	340	350	360
m141.pep	LLKHISNLKNVFGLPVVVALNRFVSDADAEALAMIEKACAEHGVESLTVWVGKGGAGGAD					
g141	LLKHISNLKNVFGLPVVVALNRFVSDSDAEALAMIEKACAEHGVESLTVWVGKGGAGGAD					
	370	380	390	400	410	420
m141.pep	LARKVVNAIESQTNNGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
g141	LARKVVNAIDNQPNNGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
g141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
m141.pep	PAAEKIDVDAEGVHGLFX					
g141	PAAEKIDVDEHGVHGLFX					
	550	559				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

a141.seq

```

1  ATGAGTTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAACGT
151 CCGCAAAAAC AGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC

```



```

201 GCGGGGCGAA GGTAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTCC GCGTGAAAGG CGGCGCGGCA GCGGCGCGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GCGGCGCGCT
501 GGTGCGATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTTGA CGGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTCCCTA CGCCAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GCGCCGTTCC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAA
1051 TTAGACGCTT TGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCCTTCG
1151 TGTCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGCGCTT AAGTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTCGG TTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCAAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCGCCGAAGA CTTCCGCATC GCGGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

```

a141.pep
1 MSFKTDAEIA QSSTMRPIGE IAAKGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFVGKGGAA GGGYAQVLP EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVDM NDRQLRNII GMGKPVGVDM RPDGFEDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTFAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WGGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAEKIDVDA
551 EGVHGLF*

```

m141/a141 99.5% identity in 558 aa overlap

```

m141.pep      10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKGLNADNIEPYGHYKAKINPAEAFKLPQKQGRILIV
|||||
a141          10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKGLNVDNIEPYGHYKAKINPAEAFKLPQKQGRILIV
|||||

m141.pep      70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGGAAGGGYAQVLP
|||||
a141          70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGGAAGGGYAQVLP
|||||

m141.pep     130     140     150     160     170     180
EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVDMNDRQLRNII
|||||
a141         130     140     150     160     170     180
EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVDMNDRQLRNII
|||||

```


	190	200	210	220	230	240
m141.pep	GMGKPVGDGVMRPDGFDTVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSFVYAKDLK					
a141	GMGKPVGDGVMRPDGFDTVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSFVYAKDLK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m141.pep	ANGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m141.pep	GFGADLGAEKFCDIKCRLAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGAEKFCDIKCRLAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m141.pep	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAHEGVEVSLTEVWKGKGAGGAD					
a141	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAHEGVEVSLTEVWKGKGAGGAD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m141.pep	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQAQKVYGAEDVDFSAEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQAQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
a141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
	550	559				
m141.pep	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

```

g142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCTGC AGGTGCGCCA
51  ACGCGCCTTC TATTTCAAGT TGTCCCCTTT TGCCGCGATG CCAAATATGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTT
151 GGCAACATCC TGATGTTTCGT CCGCCAGCAT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATcggaATG AttcgCGCAC TCCGGTTTAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCTGTGAT GACATGAACG CCTGCCGCAC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC CGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCC ATGTGCAGCA GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

```

g142.pep
1  MRADPMFADN MPVQVRQRAF YFKLSRFAAM PNMVGKPLFG RQAGQPGKMP
51  GNILMFVRQH IDAAEAVFRQ DRNDSRTVPY AQHHGRRLVG NRRNRRHCNA
101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN RPLYKNAAHK
151 ASPHVQQF*

```


1	ATGCGTGCCG	ATTTCATGTT	TGCCGACAAT	ATGCCCGTGC	AGGTGCGCCA
51	ACGCGCCCTC	TATTTCAAGT	TGTCCCGTTT	TGCCGCGATG	CCAGATGTGG
101	TAGGCAAAAC	GCTCTTCGGG	CGACAGCCCG	GTGAGCCCGG	CAAAATGTTT
151	GGCAACATCC	TGATGTTCGT	CGCGCAGCGT	ATTGTGACG	AGGCTGCCGT
201	TTTCCGACAG	GATCGGAATG	ATTGCGGCAC	TCCGGTTGAT	GACAGACATC
251	ACGGTCGGCG	GCTCGTCGGT	AACCGGCGCG	ACCGCCGTCA	TTGTAATGCC
301	GTAACGCCCT	GCCGCACCGT	CTGTCGTGAT	GACATGAACG	CCTGCCGCGC
351	AAGATGCCAT	CGCATCACGG	AACGAAGTTT	GAAAATTTTT	CTGCAATACC
401	GCCATTTTTT	CCCTTTAAAC	TGTTCCCTAT	ATAAGAATGC	TGCACACAAG
451	GCATCCCCcC	ATGTGCAGCA	GTTTTTGA		

1 MRADFMFADN MPVQVRQRAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
51 GNILMFVRQR IDAAEAVFRQ DRNDSRTVPD AQHHGRRLVG NRRDRRHENA
101 VTPCRTVCRD DMNACRARCH RITERSLKIF LQIRHFSPLN CPLYKNAAHK
151 ASPHVQOF*

m142/g142

```

      10      20      30      40      50      60
m142.pep  MRADFMFADNMPVQVRQRALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFGNILMFVRQR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      MRADFMFADNMPVQVRQRAFYFKLSRFAAMPNMVGKPLFGRQAGQPGKMFGNILMFVRQH
          10      20      30      40      50      60

      70      80      90      100     110     120
m142.pep  IDAEAAVFRQDRNDSRTVPVDAQHHGRRLVGNRRDRRHCAVTPCRTVCRRDDMNACRARCH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      IDAEAAVFRQDRNDSRTVPVYQHHGRRLVGNRRNRHCAVTPCRTVCRRDDMNACRTGCH
          70      80      90      100     110     120

      130     140     150     159
m142.pep  RITERSLKIFLQIRHFSPLNCPLYKNAAHKASPHVQQFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      RITERSLKSFLQIRHFSPLNRPLYKNAAHKASPHVQQFX
          130     140     150

```

1	ATGCGTGCCG	ATTTTCATGTT	TGCCGACAAT	ATGCCCGTGC	AGGTGCGCCA
51	ACGCGCCCTC	TATTTCAAGT	TGTCCCGTTT	TGCCGCGATG	CCAGATGTGG
101	TAGGCAAAAC	GCTCTTCGGG	CGCAGGCCG	GTCAAGCCCG	CAAAATATTT
151	GGCAACATCC	TGATGTTCGT	CCGCCAGCGT	ATTGATGAG	AGAGTGCCGT
201	TTTCCGACAG	GATCGGAATG	ATTCGCGCAC	TCCGTTTGAT	GCACAGCATC
251	ACGGTCGGCG	GCTCGTCCGT	AACCGCGCAT	ACCGCCGTCA	TGTGAATGCC
301	GTAAACGCCCT	GCCGACCCGT	CTGTCGTGTA	GACATGAACG	CCTGCCGCAC
351	AGGATGCCAT	CGCATCACGG	AACGAAGTTT	GAAAGTTTTC	TGCAAAATCC
401	GCCATTTTTT	CCCTTTAAAC	TGTCCTTAT	ATAAGAATGC	TGCACACAAG
451	GCACCCCCCA	TGTCGACGAC	TTCTGATTCA	AAAGCCGTC	GGTCCGAGAT
501	TTCCGCGCGT	TACGCGGTAT	TACGAGTTCA	ACGCATCCTC	GATTTTGGCA
551	AGTTCTGCCA	ACAGGTCTTT	AAGCAGCAGC	ATTTTCTCGC	GCGCCAGCAC
601	TTCCTCGATA	GCTTCGTAAC	GCTCGTCCAC	TTCTTCGCCG	ATTTCTCTCAT
651	ACAGCTTCTC	GCCCTCGGCA	GTCAGCTTCA	GAAAAACACG	TCGTTTGGTC
701	TGTGAAGGTT	TCAGGCGGAC	AACCAAAACC	GCTTTTTTCA	GCGGGTTCAG
751	GATACCGGTC	AGGCTGGGGC	GCAAAATGCA	GCCTGATTCC	GCCAAATCTT

801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC
 851 TGATCGGTAA TATTCGCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG
 901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

a142.pep
 1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVR NRRNRRHCNA
 101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAHK
 151 APPMCSSSDS KSRRSDisAR YGVLVRQIL DFGKFCQVVF KQHFLLAAQH
 201 FLDSVVTLVH FFADEFLIQLL ALGSQLOKNT SLVVGGRFQAD NQTRFFKAGQ
 251 DTGQAGAQNA RLIRQILKVO RAVFRQKTDN PPLLIGNIRL IQNRPELGHQ
 301 GFPCLYQTDI DRRMF*

m142/a142 96.1% identity in 153 aa overlap

	10	20	30	40	50	60
m142.pep	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGROAGQPGKMFNGNILMFVRQR					
a142	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGROAGQPGKMFNGNILMFVRQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m142.pep	IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRHCNAVTPCRTVCRDDMNACRARCH					
a142	IDAEAAVFRQDRNDSRTPVDAQHHGRRLVNRNRRRHCNAVTPCRTVCRDDMNACRTGCH					
	70	80	90	100	110	120
	130	140	150	159		
m142.pep	RITERSLKIFLQIRHFSPLNCPLYKNAAHKASPHVQQFX					
a142	RITERSLKSFQIRHFSPLNCPLYKNAAHKAPPMCSSSDSKSRRSDisARYGVLVRQIL					
	130	140	150	160	170	180
	190	200	210	220	230	240
a142	DFGKFCQVFKQHFLLAAQHFLDSVVTLVHFFADEFLIQLLALGSQLOKNTSLVVGGRFQAD					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

g143.seq
 1 ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAAG
 51 CTCGCAGATG AGCCGCATT TCAAAACGCT AGGCGCAGAC CCGCACAAAT
 101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTTCAGCCG
 151 ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCCG
 201 CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCCTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTCGTCGAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGATATG GTCAACGAGG
 401 AGCAGAAAAG CTACGCCTAC GGGATCAAA GTTTCTTAGC GAATACGGAC
 451 GCGGTTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC
 501 GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCGTGGTC GTAGCATTCT
 551 ATGTGGGTGC GCGGTTACTG ATTATTACCA GTGCGTTCAC AATCTCCAAA
 601 GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACGCGCG
 701 CTAAAGTGT TTGGACGGTT ACTCCGGTAC AGTTTTCTG CTGGTTCGCC
 751 TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGCAG AAAACGCTGT
 801 GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCAACCGGT
 851 ACGCGGTTTT GGCGCGGGT TAGTCGGTTG CGGCGGTGAT TTGTTCTGTT
 901 ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGCGGGGTT ATTTCTGGCTG
 951 TTTGGCTTTG GGCGCGCTCG GTTCTTCTC TATCTTCTC ATCTACAATC
 1001 AATACGCACT CATCCTGTCT TATATCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGGCC AACGCTTTGT CGGGCAAAAC
 1101 CATGGATACT TATTGGGCC TGTttaacg ctctgtCTGT ATGCGgcaaa
 1151 tcgTcgctTC GctgttgAGT TTCGTGCTTT TCCCGATGCT GGGCGGCCAT

1201 CAGGCAACCA TGTCTTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT
1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep
1 MLSFGYLGVO TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
51 IVGYSDRTW KPRLGRRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA
101 ALSFALMIA LLDVSSNMAM QPFKMMVGDV VNEEQKSYAY GIQSFLANTD
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSAFTISK
201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFWTV TPVQFFCWFA
251 FRYMWTYSAG AIAENVWHTT DASSVGHQEA GNRYGVLAAY *SVAAVICSF
301 ILAKVPNKYH KAGYFGCLAL GALGFFSIFV IYNQYALILS YILIGIAWAG
351 IITYPLTIVA NALSGKHMGT YLGLFNGSVC MPQIVASLLS FVLFPMLGGH
401 QATMFLVAGA VLLLAGAFSVC LIKEIHGGV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq
1 ATGCTCAGTT TCGGCTTCTT CCGCGTTCAG ACGGCCTTTA CCCTGCAAAG
51 CTCGCAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAATT
101 TGGGCTGTTT TTTCATCTCG CCGCCGCTGG CCGGGATGCT GGTGCAGCCG
151 ATTGTCGGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG
201 CCGTCTGCCG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA
251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
301 GCTTTGTCTG TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCTGCAAA
351 TATGGCGATG CAGCCGTTTA AGATGATGGT CCGCGACATG GTCAACGAGG
401 AGCAGAAAGG CTACGCCTAC GGGATTCAAA GTTCTTAGC AAATACGGGC
451 GCGGTCGTGG CCGCGATTCT GCCGTTTGTG TTGCGTATA TCGGTTTGGC
501 GAACACCGCC GAGAAGGCG TTGTGCCGCA GACCGTGGTC GTGGCGTTTT
551 ATGTGGGTGC GCGTTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA
601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCGC
701 CTAAGGCGTT TTGGACGTTT ACTTTGGTGC AATTCTTCTG CTGGTTTCGCC
751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGCTCG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGTT
851 ACGGCGTTTT GCGCGCGGTG CAGTCGGTTG CCGCGGTGAT TTGTTCTGTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTCGGCTG
951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CCGGCAAGCA
1101 TATGGGCACT TACTTGGGCT TGTTTAACGG CTCTATCTGT ATGCCTCAAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGCGGTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CCGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep
1 MLSFGFLGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
51 IVGHYSRTW KPRLGRRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA
101 ALSFALMIA LLDVSSNMAM QPFKMMVGDV VNEEQKSYAY GIQSFLANTG
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FQYMWYTSAG AIAENVWHTT DASSVGYQEA GNWYGVLAAY QSVAAVICSF
301 VLAQVPNKYH KAGYFGCLAL GALGFFSVFF IYNQYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGH
401 QATMFLVGGV VLLLAGAFSVF LIKEITHGGV*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10 20 30 40 50 60

m143.pep	MLSEFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
g143	MLSEGYLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGYYSDRTW
	10 20 30 40 50 60
m143.pep	70 80 90 100 110 120
	KPRLGGRRLPYLLYGTLLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
g143	KPRLGGRRLPYLLYGTLLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
	70 80 90 100 110 120
m143.pep	130 140 150 160 170 180
	QPFKMMVGDVNEEQKGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGVVPQTVV
g143	QPFKMMVGDVNEEQKSYAYGIQSFLANTDAVVAAILPFVFAYIGLANTAEGVVPQTVV
	130 140 150 160 170 180
m143.pep	190 200 210 220 230 240
	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV
g143	VAFYVGAALLIITSFTISKVKEYDPETYARYHGIDVAANQEKANWFELLKTAPKVFWTV
	190 200 210 220 230 240
m143.pep	250 260 270 280 290 300
	TLVQFFCWFAFQYMWYTSAGAIAENVWHTTDASSVGQYQAGNWWYGVLAQVQSVAAVICSF
g143	TPVQFFCWFAFRYMWYTSAGAIAENVWHTTDASSVGHQAGNRYGVLAQVXSVAVICSF
	250 260 270 280 290 300
m143.pep	310 320 330 340 350 360
	VLAQVQSVAAVICSFVLAQVQSVAAVICSFVLAQVQSVAAVICSFVLAQVQSVAAVICSF
g143	ILAKVPNKYHKAGYFGCLALGALGFFSIFFIYNYQALILSYILIGIAWAGIITYPLTIVA
	310 320 330 340 350 360
m143.pep	370 380 390 400 410 420
	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVLLLGAFSVC
g143	NALSGKHMGTYLGLFNGSVCMPQIVASLLSFVLPMLGHHQATMFLVAGAVLLLGAFSVC
	370 380 390 400 410 420
m143.pep	430
	LIKETHGGVX
g143	LIKEIHGGVX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 569>:

a143.seq

1	ATGCTCAGTT	TCGGCTTTCT	CGGCGTTCAG	ACGGCCTTTA	CCCTGCAAAG
51	CTCGCAGATG	AGCCGCATCT	TCCAGACGCT	CGGTGCCGAT	CCGCACAGCC
101	TCGGCTGGTT	CTTTATCCTG	CCGCCGCTGG	CGGGGATGCT	GGTGCAGCCG
151	ATTGTCGGCC	ATTACTCCGA	CCGCACTTGG	AAGCCGCGTT	TGGCGCGCCG
201	CCGTCTGCCG	TATCTGCTTT	ATGGCACGCT	GATTGCGGTT	ATTGTGATGA
251	TTTTGATGCC	GAATCGGGC	AGCTTCGGTT	TCGGCTATGC	GTCGCTGGCG
301	GCTTTGTCGT	TCGGCGCGCT	GATGATTGCG	CTGTTAGACG	TGTCGTCAAA
351	TATGGCGATG	CAGCCGTTTA	AGATGATGGT	CGGCGACATG	GTCACAGAGG
401	AGCAGAAAGG	CTACGCCTAC	GGGATTCAAA	GTTTCTTAGC	GAATACGGGC
451	GCGGTCGTGG	CGGCGATTCT	GCCGTTTGTC	TTTGCGTATA	TCGGTTTGGC
501	GAACACCGCC	GAGAAAGGCG	TTGTGCCGCA	GACCGTGGTC	GTGGCGTTTT
551	ATGTGGGTGC	GGCGTTGCTG	GTGATTACCA	GCGCGTTCAC	GATTTTCAAA
601	GTGAAGGAAT	ACAATCCGGA	AACCTACGCC	CGTTACCACG	GCATCGATGT
651	CGCCGCGAAT	CAGGAAAAAG	CCAACTGGAT	CGAACTCTTG	AAAACCGCGC
701	CTAAGCGGTT	TTGGACGGTT	ACTTTGGTGC	AATTCTTCTG	CTGGTTCGCC


```

751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCGT
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGTGT
851 ACGGCGTTTT GCGCGCGGTG CAGTCGGTTG CCGCGGTGAT TTGTTCTGTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTCCGCTG
951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTTAACGG CTCTATCTGT ATGCCGCAAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGCGGTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTC CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
  1  MLSFGFLGVQ TAFTLQSSQM SRIFQTLGAD PHSIGWFFIL PPLAGMLVQP
 51  IVGHYSDRTW KPRLGGRRLP YLLYGTLIIV IVMILMENSG SFGFGYASLA
101  ALSFGALMIA LLDVSSNMAM QPFKMMVGDV VNEEQKGYAY GIQSFLANTG
151  AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201  VKEYNPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251  FQYMWTSYAG AIAENVWHTT DASSVGYQEA GNWYGVLA AVQSVAVICSF
301  VLAQVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
351  IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGL
401  QATMFLVGGV VLLGAFSVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

	10	20	30	40	50	60
m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
a143	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m143.pep	KPRLGGRRLPYLLYGTLIIVIMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
a143						
	70	80	90	100	110	120
	130	140	150	160	170	180
m143.pep	QPFKMMVGDVNEEQKGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTA EKGVPQTVV					
a143						
	130	140	150	160	170	180
	190	200	210	220	230	240
m143.pep	VAFYVGAALLVITSAFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
a143						
	190	200	210	220	230	240
	250	260	270	280	290	300
m143.pep	TLVQFFCWFAFQYMWTSYAG AIAENVWHTTDASSVGYQEA GNWYGVLA AVQSVAVICSF					
a143						
	250	260	270	280	290	300
	310	320	330	340	350	360
m143.pep	VLAQVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT					
a143						
	310	320	330	340	350	360
	370	380	390	400	410	420
m143.pep	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMLGGLQATMFLVGGVVLLGAFSVF					

408

```

a143      |||||
          NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVVLLLGAFSVF
          370      380      390      400      410      420

          430
m143.pep  LIKETHGGVX
          |||||
a143      LIKETHGGVX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTTCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTTGGC AGACGGCGTG
151 GCGGAAAACC CCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGTAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CCGTTCGCAC GGGCTGGCCG TTACCcgtTT
351 CAACGCGGTG GCGGCAGACG GccgacggTt atCCCAACGA TTTGGatatT
401 TCctaccgCT TGGACGAGGA CGGCCGGCTT ACCGTtacct ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGGCGGACAT
551 ATTCCGCGCG ATGCCGAAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFSVLADGV
51  RENPVVSFDD AASYADNPFO INKQIGRVAG RIRGAAFDIN GR TYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FG YFLPLGRG RPAYRYLSRH
151 RARRHGVRPD AAHLLAAGRG PARCGSAYSA GR TYSGRCRK TARLNGFRRP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTTGGC AGACGGCGTG
151 GCGGAAAACC TCGTGGTGTC GTTCGATGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CCGTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTCCGT GGTGCTGCGC AGCCGCCTGg
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGGA ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TA cCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFSVLADGV
51  RENLVVSFDD AASYADNPFO INKQIGRVAG RIRGAAFDIN GR TYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRL SQRFGFYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAHLL AAGRGPARGC SAYSAGR TYA
201 GRCKRTARLN GFRRPRSI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFVSLADGVRENLVVSFDD					
g144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEFVSLADGVRENPVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
g144	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m144.pep	AADGRSVVLRSLATVGRRLSQRFGFGYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL					
g144	AAD-----GRRLSQRFG--YFLPLGRGRPAYRYSRHRARRHGVRPDAHLL					
		130	140	150	160	
	190	200	210	219		
m144.pep	AAGRGPARGSAYSAGRTYAGRCRKRTARLNGFRPRPSIX					
g144	AAGRGPARGSAYSAGRTYSGRCRKRTARLNGFRPRPSIX					
	170	180	190	200		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

a144.seq

1	ATGAGCGATA	CCCCGCTAC	CCGCGATTTC	GGCCTGATCG	ACGGGCGTGC
51	CGTAACCGGC	TATGTGCTGT	CCAACCGGCG	TGGTACGCGT	GTCTGCGTGC
101	TGGACTTGGG	CGGATTGTG	CAGGAATTTT	CCGTTTGGC	AGACGGCGTG
151	CGCGAAAACC	TCGTGGTGTC	GTTGACGAT	GCGGCTTCCT	ATGCGGACAA
201	TCCGTTTCAG	ATTAACAAGC	AGATAGGGCG	CGTGGCCGGA	CGCATCCGCG
251	GTGCGGCGTT	CGACATCAAC	GGCAGGACTT	ACCGCGTGGA	GGCCAACGAA
301	GGCAGGAACG	CGCTGCACGG	CGGTTCCGAC	GGGCTGGCCG	TTACCCGTTT
351	CAACGCGGTG	GCGGCAGACG	GCCGTTCCGT	GGTGTGCGC	AGCCGCGTG.
401	CAACAGTCGG	CCGACGGTTA	TCCCAACGAT	TTGGATTGG	ATATTTCCTA
451	CCGCTTGGAC	GAGGACGACC	GGCTTACCGT	TACCTATCGC	GCCACCGCGC
501	TCGGCGACAC	GGTGTTCGAC	CCGACGCTGC	ACATTTACTG	GCGGCTGGAC
551	GCGGGCCTGC	ACGATGCGGT	TCTGCATATT	CCGCAGGGCG	GACATATTCC
601	GGCCGATGCC	GAAAACTGC	CCGTCTCAAC	GGTTTCAGAC	GACCTCGAAG
651	TATTTGA				

This corresponds to the amino acid sequence <SEQ ID 576; ORF 144.a>:

a144.pep

1	MSDTPATRDF	GLIDGRAVTG	YVLSNRRGTR	VCVLDLGGIV	QEFVSLADGV
51	RENLVVSFDD	AASYADNPFQ	INKQIGRVAG	RIRGAAFDIN	GRTYRVEANE
101	GRNALHGGSH	GLAVTRFNAV	AADGRSVVLR	SRLXTVGRRL	SQRFGFGYFL
151	PLGRGRPAYR	YLSRHRARRH	GVRPDAHLL	AAGRGPARGC	SAYSAGRTYS
201	GRCRKRTARLN	GFRRPRSI*			

m144/a144 99.1% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFVSLADGVRENLVVSFDD					
a144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFVSLADGVRENLVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					


```

|||||
a144      AASYADNPFQINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
              70          80          90          100          110          120

              130          140          150          160          170          180
m144.pep  AADGRSVVLRSLATVGRRLSQRFGFGYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL
|||||
a144      AADGRSVVLRSLXTVGRRLSQRFGFGYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL
              130          140          150          160          170          180

              190          200          210          219
m144.pep  AAGRGPARGCSAYSAGRTYAGRCRKRTARLNGFRRPRSIX
|||||
a144      AAGRGPARGCSAYSAGRTYSGRCRKRTARLNGFRRPRSIX
              190          200          210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

g146.seq
1  ATGAAGCAAA TCCCCCTCCG CCTTCTCCAG GTCGTCATTG ACCACGACAA
51 AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAa ctTCCCGACT GTCCGTCCCG CGCcttTGA GGCGCGCGGC
151 AAGCACGTCG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCCGGCA
201 GCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGCTCTG CGTATTCCAA AAAAGCTTCC TGCGCGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTATGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGGAC ACCCTATTTT
601 ATATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

g146.pep
1  MKQIPLRLQ VVIDHDKVEQ YGLDFMPCL RQPPLDNFPT VRPAPEARG
51 KHVERRRQDK DTDSFRQVA NLRALNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCVFQ KSLLRDKRFK LFFGNKVIMY AVCFATFTRA RMRHGNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1  ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51 AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA CTCCCGACT GTCCGTCCCG CGTCCGTTGA GGCGCGCGGC
151 AAGTACGTCG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCGTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGCTCG CGTATTCCAA AAAAGCTTCC TGCGCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTGTGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.pep
1  MAQILLRSRQ VVIDHDKVKQ YGLDFMPCL RQPPLDNFPT VRPASVEARG
51 KYVERRRQDK DADGFGQVA NLRALNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYGVVFQ KSFLRDKRLK LFFGNKVIMY AVCFATFTRA RVRHGNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```


Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

	10	20	30	40	50	60
m146.pep	MAQILLRSRQVVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
g146	MKQIPLRLQVVVIDHDKVEQYGLDFMPCLRQPPLDNFPTVRPAPFEARGKHVERRRQDK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m146.pep	DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK					
	:					
g146	DTDSFRQRVANLRRALNVDFQNHVIACRRQRIHALRACAVIVAEYVCVFQKSLLRDKRKF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m146.pep	LFFGNKVIMYAVCFATRRARRVRHGNATVMVCQPPRHQRFARAGSGRNDKDVAFSIS					
g146	LFFGNKVIMYAVCFATRRARRMRHGNATVMVCQPPRHQRFARAGSGRNDKDVAFSIS					
	130	140	150	160	170	180
	190	200	210			
m146.pep	GHIFYLYIFQPIVSQWTPSFLFADAHILPLLEFX					
g146	GHIFYLYIFQPIVSQRTPYFIFADAHILPLLEFX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

```

a146.seq
1  ATGGCGCAAA TCCTCCTCCG CCCGCGCCAA GTCATCAT TG ACCACGACAA
51  AATCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCC TT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTCCGTCCCG CGTCCGTTGA GACGCGCAGC
151 AAGCACATCG AAAGACGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCATCTCG AACCTGAGCC GCGCCCTGAA CGTCGATTTC CAAAATCAGC
251 TCATAACCTG CCGCCGCCAA CGCATTCA CA CCTCCGCGC TTGTGCCGTA
301 ATAGTTGCCG AACACGTCCG CGTATTCCAA AAAAGCCTCC TCGCGGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGACG CGTCGTGTGC GACACGGA AA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTT TG CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAACGGAC ACCCGGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

a146.pep	1	MAQILLRPRQ VIIDHDKIEQ YGLDFMPCL RQPPLDNFPT VRPASVETR				
	51	KHIERRRQDK DADGFGQRIS NLSRALNVDF QNHVITCRRQ RIHTLRACAV				
	101	IVAHEVRVFEQ KSLLRDKRLK LFFGNKVIMY AVCFATRRRT RVRHGNAT				
	151	VMVCQPPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPGF				
	201	LFADAHILPL LF*				
m146/a146	90.6% identity in 212 aa overlap					
	10	20	30	40	50	60
m146.pep	MAQILLRSRQVVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
a146	MAQILLRPRQVIIDHDKIEQYGLDFMPCLRQPPLDNFPTVRPASVETR SKHIERRRQDK					
	10	20	30	40	50	60
	70	80	90	100	110	120

412

```

m146.pep    DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK
              |||||::|| |||||::|||::|||::|||::|||::|||::|||::|||::|||
a146        DADGFGQRISNLSRALNVDFQNHVITCRRQRIHTLRACAVIVA EHV RVFQKSLLRDKRLK
              70          80          90          100         110         120

              130          140          150          160          170          180
m146.pep    LFFGNKVIMYAVCFATRRARRVRHGNAQTVMVCQQRHQRGFARAGSGRNDKDVAFSIS
              |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
a146        LFFGNKVIMYAVCFATRRARRVRHGNAQTVMVCQQRHQRGFARAGSGRNDKDVAFSIS
              130          140          150          160          170          180

              190          200          210
m146.pep    GHIFYLYIFQPIVSQWTPSFLFADAHILPLLFX
              |||||::|||::|||::|||::|||::|||::|||::|||
a146        GHIFYLYIFQPIVSQRTPGFLFADAHILPLLFX
              190          200          210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```

g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC AACTCAAAC CCATTGTTTT
51 ATCAATCTTT TTAATCAACA CACCCCTCCT CGCCCAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCGG
151 CGCGCGACTT CGGGGCTGCT GCACACTTCG ACCGCCTCCG ACAAAATCAT
201 CTCCGGCGAT ACTTTGCGCC AAAAAGCCGT CAACTTGGGC GACGCTTTGG
251 ACGGCGTACC GGGCATCCAC GCTTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAAGTAT TGAACCATCA
351 CGGCGAAACG GCGGATATGG CGGACTTTTC TCCCGATCAC GCCATTATGG
401 TAGATACCGC CTGTGCGCAA CAGGTTGAAA TCCTGCGCGG GCCGGTTACG
451 CTCTTGTA CA GCTCGGcaa tgtggccgGG GCTGGtcaat gttgccgatg
501 gAAAAAtccc ccaaaaAAtg cc..

```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```

g147.pep (partial)
1  ..MRREAKMAQI TLKPIVLSIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51 RATSGLLHTS TASDKIISGD TLROKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHGET GDMADFS PDH AIMVDTALSQ QVEILRGFVT
151 LLYSSGNVAG AGQCCRWNKP PKNA..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

```

m147.seq (partial)
1  ..CCGCATAAAA CTGAGCAATC GGTGGATTG GAAACGGTCA GCGTCGTCGG
51 CAAAAGCCGT CCGCGCGCCA CGTCGGGGCT GTTGACACT TCGACCGCCT
101 CCGACAAAAT CATCTCCGGC GATACCTTGC GCCAAAAAGC CGTCAACTTG
151 GGCGACGCTT TAGACGGCGT ACCGGGCATC CACGCTTCGC AATACGGCGG
201 CGGCGCGTCT GCTCCCGTCA TTCGCGGTCA AACAGGCAGG CGGATTAAAG
251 TGTTGAAACA TCACGGCGAA ACAGGCGATA TGGCGGATT TTCGCCCGAT
301 CACGCCATTA TGGTAGATAC CGCCTTGTG CAACAGGTCG AAATCCTGCG
351 CGGGCCCGTT ACGCTCTTGT ACAGCTCGGG CAATGTGGCG GGGCTGGTCG
401 ATGTTGCCGA TGGCAAAATC CCCGAAAAA TGCTGAAAA CGGCGTATCG
451 GGCGAACTCG GATTGCGTTT GAGCAGCGGC AATCTGGAAA AACTCACGTC
501 CGGCGGCATC AATATCGGTT TGGGCAAAAA CTTTGTATTG CACACGGAAg
551 GGCTGTACCG CAAATCGGGG GATTACGCG TACCGCGTTA CCGCAATCTG
601 AAACGCCTGC CCGACAGCCA CGCCGATTTC CAAACGGGCA GCATCGGGCT
651 GTCTTGGGTT GGCGAAAAAG GTTTTATCGG CGTAGCGTAC AGCGACCGTC
701 GCGACCAATA TGGTCTGCCT GCCACAGCC ACGAATACGA TGATTGCCAC
751 GCCGACATCA TCTGGCAAAA GAGCTTGATT AACAAACGCT ATTTACAGCT
801 TTATCCGCAC CTGTTGACCG AAGAAGACAT CGATTACGAC AATCCGGGCT
851 TGAGCTGCGG CTTCCACGAC GACGATAATG CACACGCACA CACCCACAGC
901 GCGAGACCGT GGATAGACCT GCGCAACAAA CGCTACGAAC TCGGTGCCGA
951 ATGGAAGCAA CCGTTCCCGG GTTTTGAAGC CCTGCGCGTA CACCTGAACC
1001 GCAACGACTA CCGCCACGAC GAAAAAGCAG GCGATGCAGT CGAAAACTTT
1051 TTTAACAAAC AAACGCAAAA CGCCCGCATC GAGTTGCGCC ACCAACCCAT

```



```

1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACCGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCGACC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACGCG CACAACACAA ACTCAGCCTG ACCGCCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCCTTCG GTAACATACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGCGCG CGACTTCTAC GCGCGGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCCGTCT GAAAAACCTG CCTTCCCTAC CCGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGTGACC
1951 GACCGTATCG ATGCCAATTT GGACTACTAC CGCGTGTTCG CCCAAACCAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCCGG ACACCATATG CTCAACCTCG
2051 GCGCAAACCTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACA GCAGCTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGCGGCG GTGAACGTGA
2201 AGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

m147.pep (partial)

```

1 ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51 GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLKNFVL HTEGLYRKSQ DYAVPRYRNL
201 KRLPDSHADS QTSIGLSWV GEKGFIVGAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301 GRPWIDLRNK RYELRAEWKQ PFPGFALRV HLNRRNDYRHD EKAGDAVENF
351 FNNQTQNAIR ELRHQPIGR LKSGWVQYLQ QKSSALS AIS EAVKQPMLLD
401 NKVQHYSFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IDRENYNHP
451 LPDLGAHRQT ARSFALSGNW YFTPOHKL SL TASHQERLPS TQELYAHGKH
501 VATNTFEVGN KHLNKRSSNN IELALGYEGD RWQYNLALYR NRGNYIYIAQ
551 TLNDGRGPKS IEDDSEMCLV RYNQSGADFY GAEGEYIFKP TPRYRIGVSG
601 DYVRGRLKNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNK LAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

m147.pep                                10      20      30
                                PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
g147                                1:||||| ||||| ||||| ||||| |||||
                                10      20      30      40      50      60
m147.pep                                40      50      60      70      80      90
                                TASDKIISGD TLRQKAVNL GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
g147                                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
                                TASDKIISGD TLRQKAVNL GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
                                70      80      90      100     110     120
m147.pep                                100     110     120     130     140     150
                                GDMADFSPD HAIMVDTALS QQVEILRGPV TLLYSSGNVAGLVDVADGKI PEKMPENGVS
g147                                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
                                GDMADFSPD HAIMVDTALS QQVEILRGPV TLLYSSGNVAGAGQCCRWNPPKNA

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

```

a147.seq
1  ATGCGACGAG AAGCCAAAT GGCACAACT ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCCAGCG CATGGAACGT
101 AGCAATCAGT GGGCTTGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGGAC AAAAAGCCGT CAACTTGGGT GATGCTTAG
251 ACGGCGTACC GGGCATTCAT GCCTCGCAAT ACGGCGGCG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAGTGT TGAACCATCA
351 CGGGGAAACG GGCACATGG CGGACTTCTC TCCAGACCAT GCAATCATGG
401 TGCACAGCGC CTTGTGCAA CAGGTCGAAA TCCTGCGCGG TCCGGTTACG
451 TCTTTGTACA GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGCCGATGG
501 CAAATCCCC GAAAAATGC CTGAAACGG CGTATCGGGC GAACTCGGAT
551 TCGCTTTGAG CAGCGGCAAT CTGGAACAA TCACGTCCGG CGGCATCAAT
601 ATCGGTTTGG GCAAAACTT TGTATTGCAC ACGGAAGGGC TGTACGCCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTGCAA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATACAGC GACCGTCGCG ACCAATATGG
801 TCTGCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAA CCGGGCTTGA GTCGCGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGA
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCCGGTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACTTTTTT AACAACCAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCATGCT GCTTGACAA AAAGTGCAAC
1301 ATTACAGCTT TTTGGGTGTA GAACAGGCAA ACTGGGACAA CTTACAGCTT
1351 GAAGGCGGCG TACGCGTGA AAAACAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGA AACTACTACA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAACCGCC CGCTCATTCG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAACT CAGCCTGACC GCCTCCCATC AGGAACGCCT
1551 TCCGTCAAAC CAAGAGCTGT ACGCACACGG CAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAAACGACG
1751 GACGCGGCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CCGCGCTACC GCATCGGCGT TTCGGCGGAC TATGTACGAG
1901 GCGGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACCGCCAC TCATTGCCA AGCCGACCAA AACGCCCTC GCGTTCCGGC
2001 TCGCGGCTC GCGTCCACC TGAAGCCTC GCTGACCGC CGCATCGATG
2051 CCAATTTGGA CTACTACCGC GTGTTGCCCC AAAACAACT CGCCGCTAC
2101 GAAACGCGCA CGCCGGACA CCATATGCTC AACCTCGGCG CAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGAATTG GTACGTCAA GCCGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGTTTAC CGGCGCGTG AACGTGAAGT TTTAA

```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

```

a147.pep
1  MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFS PDH AIMVDSALSQ QVEILRGPT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVS ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKS GD HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEEDIDYDN PGLSCGFHDD DDAHAHANG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNAIE LRHQPIGRK
401 GSWGQVYLGQ KSSALSATSE AVKQPMLLDN KVQHSFFGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYNHNPL PDLGAHRQTA RSFALSGNWX
501 FTPQHKLST ASHQRLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR

```


601 YNQSGADFYG AEGEIYFKPT PRYRIGVSGD YVRGRLKNLP SLPGREDAYG
 651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLDYYR VFAQNKLARY
 701 ETRTPGHHML NLGANYRRNT RYGEWNWYVK ADNLLNQSVY AHSSFLSDTP
 751 QMGRSFTGGV NVKF*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLETVS	VVGKSRPRATSGLLHTS
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHTS					
	10	20	30	40	50	60
m147.pep		40	50	60	70	80
		TASDKIISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET				
a147	TASDKIISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET					
	70	80	90	100	110	120
m147.pep		100	110	120	130	140
		GDMADFS	PDHAIMVDTALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
a147	GDMADFS	PDHAIMVDSALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPEKMPENGVS				
	130	140	150	160	170	180
m147.pep		160	170	180	190	200
		ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQ				
a147	ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQ					
	190	200	210	220	230	240
m147.pep		220	230	240	250	260
		TGSIGLSWVGEGKFIGVAYS	DRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHL			
a147	TGSIGLSWVGEGKFIGAAYS	DRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHL				
	250	260	270	280	290	300
m147.pep		280	290	300	310	320
		LTEEDIDYDNPGLSCGFHDDNAHAH	THSGRPWIDLNRNKRYELRAEWKQFPFGFEALRVH			
a147	LTEEDIDYDNPGLSCGFHDDDAHAHAH	NGKFPWIDLNRNKRYELRAEWKQFPFGFEALRVH				
	310	320	330	340	350	360
m147.pep		340	350	360	370	380
		LNRNDYRHDEKAGDAVENFFNNQ	TQNARIELRHQPIGRLKGSWGVQYLQKSSALSATSE			
a147	LNRNDYRHDEKAGDAVENFFNNQ	TQNARIELRHQPIGRLKGSWGVQYLQKSSALSATSE				
	370	380	390	400	410	420
m147.pep		400	410	420	430	440
		AVKQPMLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASI	QYDKALIDRENYNHNPL			
a147	AVKQPMLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASI	RYDKALIDRENYNHNPL				
	430	440	450	460	470	480
m147.pep		460	470	480	490	500
		PDLGAHRQTARSFALSGNWFYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
a147	PDLGAHRQTARSFALSGNWFYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK					
	490	500	510	520	530	540
m147.pep		520	530	540	550	560
		HLNKERSNNIELALGYEGDRWQYNLALYRNRF	GNYYAQTINDGRGPKSIEDDSEMKLVR			
a147	HLNKERSNNIELALGYEGDRWQYNLALYRNRF	GNYYAQTINDGRGPKSIEDDSEMKLVR				

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	550	560	570	580	590	600
	580	590	600	610	620	630
m147.pep	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPPIAQDDQ					
a147	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQ					
	610	620	630	640	650	660
	640	650	660	670	680	690
m147.pep	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNKLYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIDANLDYYRVFAQNKLYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
	700	710	720	730		
m147.pep	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1  ATGGCGTTAA AAACATCAAA CTGGAACAC GCAATGctgg ttcaTCCCGA
51  AgctATgagt gtcggcgcGC TTGccgAcaa AATCCGCAAA AtcgaAAact
101 gGCCGCAAAA AGgcaTCTTA TTCCACGACA TCACGCCCGT CCTGCAAAAGT
151 GCGGAATACT TCCGCCTTTT GGTGATTTG CTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGCTTGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCAaCGtcg gctTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTAcg cgcTCGAATA
351 CGGGGAAGCT GCGGTGGAAA TCCACACCGa tgccgTCAAA CCCGTTCCG
401 GCGTCCTGCT GGTGATGAT TTGGTTGCCA CGGGCGGCAC AATGCTTGCC
451 GGGCTGGAAC TGATCCGCAA ACTCGGCGGG GAAATTGTCT AAgccgcccG
501 CATTTTGGAA TTTACCGACC TTCAAGGCGG CAAGAATATC CGCGCAAGTG
551 GCGCGCCCTT ATTTACCCTG CTTCAAAACG AAGGCTGCAT GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148.pep
1  MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKGIL FHDITPVLQS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPIRK
101 KKKLPFETVS QSYALEYGEA AVEIHDAVK PGRVLLVDD LVATGGTMLA
151 GLELIRKLG EIVEAAAILE FTDLQGGKNI RASGAPLETL LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1  ATGGCGTTAA AAACATCAAA CTGGAACAC GCAATGCTGG TTCATCCCGA
51  AGCTATGAGT GTCGGCGCGC TTGCCGACAA AATCCGCAAA ATCGAAAAGT
101 GGCCGCAAAA AGGCATCTTA TTCCACGACA TCACGCCCGT CCTTCAAAGC
151 GCGGAATACT TCCGCCTTTT GGTGATTTA TTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGTTTGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCAACGTCG GTTTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTACG CGCTCGAATA
351 CGGGGAAGCT GCGGTGGAAA TCCACACCGA TGCCGTCAAA CTCGGTTCCG
401 GCGTCCTGCT GGTGATGAT TTGATTGCCA CGGGCGGCAC GATGCTTGCC
451 GGAAGTGAAC TGATCCGCAA ACTCGGCGGA GAAATTGTCT AAGCCGCCGC
501 CATTTTGGAA TTTACCGACC TTCAAGGCGG CAAGAATATC CGTGCAAGCG
551 GCGCGCCCTT ATTTACCCTG CTTCAAAACG AAGGCTGTAT GAAGGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1  MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKGIL FHDITPVLQS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPIRK

```


101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDL VATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTCGGTGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAACT
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCGT	CCTGCAAAGC
151	GCGGAATACT	TCCGACTTTT	GGTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGTTTGA	CGCGCGCGGC	TTCATTATCG
251	GCGCGCACT	CGCCTACCAG	CTCAACGTCG	GTTCGTCC	CATCCGCAAA
301	AAAGCAAGC	TGCCTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGA	TCCACACCGA	TGCCGTCAA	CTCGGTTCCG
401	GCGTGCTGCT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGACTGGAGC	TGATCCGCAA	ACTCGCGGG	GAAATTGTCG	AAGCCGCCGC
501	CATTTTGGA	TTTACCGACC	TTCAAGGCGG	CAAGAATATC	CGTGCAAGCG
551	GCGCGCCTT	ATTTACCCTG	CTTCAAAACG	AAGGCTGTAT	GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDQKI	DIVAGLDARG	FIIGAALAYQ	LVNGFVPIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	LGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m148.pep  LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSVALEYGEA
|||||
a148      LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSVALEYGEA
              70      80      90      100     110     120

              130      140      150      160      170      180
m148.pep  AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
|||||
a148      AVEIHTDAVKLGSRVLLVDDLVATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
              130      140      150      160      170      180

              190      200
m148.pep  RASGAPLFTLLQNEGCMKGX
|||||
a148      RASGAPLFTLLQNEGCMKGX
              190      200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

g149.seq

```

1  ATGTTGATTG ACAACAAATGT CCGCCATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGA AAAAAC
101  AAAAAAGCCTC CATCCGGTAC GACAAAGCAT TGATTGATCG AGAAACTAC
151  TACAACCAGC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201  GTTCGCACTT TCGGGCAACT GGTATTTCAC GCCACACCAC AAACCTCAGCC
251  TGACCGCCTC CCATCAGGAA cgCCTGCCGT CAACGCAaga actGtACgca
301  cacggcAAGC ACGtcgccac CAACACCTTT GAagtcggca acaaACACCT
351  CAACAAAGaG Cgttccaaca atatcgAACT CGCGCTGGgc tAcaaaggcg
401  accGCTGGCA ATACAATCTG GCAGCCTACC GCAACCGATt CGGCAACTAC
451  ATTTACGCCC AAACCTTAaa cgaaggacgc GGCCCCAAAT CCATCgaaga
501  cgacagcgaa ATGaagcTCG TGCGCTACAA CCAATCCGGT GCCGACTTCT
551  ACGgcgcgga aggcgaaatc tACTTcaaac CGAcACCGCG CTACCGCATC
601  GGTGTTTCCG GCGACTatgt acgaggccgT CTGAAAAACC TGCCGTCCCT
651  ACCCGGCAGG gaagatccCT AcggcAAACG TCccttcaTC GCACAAGCCG
701  ACCAAAACGC CCCCCGCATT cgggctGCGC GCCTCGGCTT CCACCTGAAA
751  ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801  CGCCCAAAAC AAACCTCGCCC GCTACGAAAC GCGTACGCCC GGACACCATA
851  TGCTCAACCT CCGTGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901  AATTGGTACG TCAAAGCCGA CAACCTGctc aACcaatCcg tTTACGCCCa
951  cAGCAGCTTC CTCTCTGATA CGCCGCAAAat gGGCCGCAGC TtgccgGCg
1001 gcgtAACGT GaAGTTttaA

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

g149.pep

```

1  MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSPAL SGNWYFTPHH KLSLTASHQE RLPSTQELYA
101  HGKHVATNTF EVGNKHLNKE RSNNIELALG YKGRWQYNL AAYRNRFGNY
151  IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201  GVSQDYVRGR LKNLPSLPGR EDPYGKRPFi AQADQNAPRI PAARLGFHLK
251  TSLTDRIDAN LDYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301  NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

m149.seq

```

1  ATGCTGCTTG .ACAACAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAACCTG GACAACTTCA CGCTTGAAGG AGGCGTACGC GTGGA AAAAAC
101  AAAAAAGCCTC CATTCACTAC GACAAAGCAT TGATTGATCG GGA AAACCTAC
151  TACAACCACC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201  ATTCGCACTT TCGGGCAACT GGTATTTCAC GCCACAACAC AAACCTCAGCC
251  TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301  CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
351  CAACAAAGAG CGTTCACAA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401  ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CCGTAACTAC

```



```

451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
501 CGACAGCGAA ATGAAGCTCG TCGCTACAA CCAATCCGGC GCCGACTTCT
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601 GGCGTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
651 ACCCGGCAGA GAAGATGCCT ACGGCAACCG TCCTTTCATC GCACAGGACG
701 ACCAAAATGC CCCCGTGT TCGGCTGCGC GCCTCGGCTT CCACCTGAAA
751 GCCTCGCTGA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCCGGTGTT
801 CGCCCCAAAC AAACCTCGCCC GCTACGAAAC GCGCAGCCCC GGACACCATA
851 TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA
951 CAGCAGCTTT CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACGGCG
1001 GCGTGAACCT GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 598; ORF 149>:

m149.pep

```

1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIY DKALIDRENY
51 YNHPLPDLGA HRQTARSPAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
101 HCKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSVDYVRGR LKNLPSLPGR EDAYGNRPFI AQDDQNAPRV PAARLGPHLK
251 ASLTDRIAN LDYYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKFX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 149 shows 95.9% identity over a 339 aa overlap with a predicted ORF (ORF 149.ng) from *N. gonorrhoeae*:

m149/g149

m149.pep	10	20	30	40	50	60
	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYYNHPLPDLGA					
g149	MLIDNNVRHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNQPLPDLGA					
	10	20	30	40	50	60
m149.pep	70	80	90	100	110	120
	HRQTARSPALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
g149	HRQTARSPALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	130	140	150	160	170	180
	RSNNIELALGYEGDRWQYNLALYRNRFNGYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
g149	RSNNIELALGYKGRWQYNLAAYRNRFNGYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
	130	140	150	160	170	180
m149.pep	190	200	210	220	230	240
	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGR LKNLPSLPGREDAYGNRPFI AQDDQNAPRV					
g149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGR LKNLPSLPGREDPYKRPFI AQADQNAPRI					
	190	200	210	220	230	240
m149.pep	250	260	270	280	290	300
	PAARLGPHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHMLNLGAN YRRNTRYGEW					
g149	PAARLGPHLKSLTDRIANLDYYRVFAQNKLARYETRTPGHMLNLGAN YRRNTRYGEW					
	250	260	270	280	290	300
m149.pep	310	320	330	340		
	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX
310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq
1 ATGCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTTCG GTGTAGAACA
51 GGCAAACTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAAACTAC
151 TACAACCATC CCCTGCCCCG CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTCAC GCCACAACAC AAACCTCAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGCAACTAC
451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
501 CGACAGCGAA ATGAAGCTCG TGCCTACAA CCAATCCGGT GCGGACTTCT
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601 GCGCTTTCGG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
651 ACCCGCAGG GAAGACGCCT ACGGCAACCG CCCACTCATT GCCCAAGCCG
701 ACCAAAACGC CCCTCGCGTT CCGGCTGCGC GCCTCGGCGT CCACCTGAAA
751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCCAAAAC AAACCTCGCCC GCTACGAAAC GCGCACGCCC GGACACCATA
851 TGCTCAACCT CGGCGCAAAC TACCGCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTACGCCCA
951 CAGCAGCTTC CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACCGGCG
1001 GCGTGAACGT GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep
1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51 YNHPLPDLGA HRQTARSFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSVDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV PAARLGVHLK
251 ASLTDRIAN LDYRVFAQN KLARYETRTP GHMMLNLGAN YRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

m149/a149 98.8% identity in 339 aa overlap

	10	20	30	40	50	60
m149.pep	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYQYDKALIDRENYYNHPLPDLGA					
a149	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYYNHPLPDLGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m149.pep	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m149.pep	RSNNIELALGYEGDRWQYNLALYRNRFNGYIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG					
a149	RSNNIELALGYEGDRWQYNLALYRNRFNGYIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m149.pep	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRKLNLPGLPREDAYGNRPFFIAQDDQNAPRV					
a149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRKLNLPGLPREDAYGNRPLIAQADQNAPRV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m149.pep	PAARLGPHLKASLTDRIANLDYRVFAQNKLARYETRTPGHMMLNLGAN YRNTRYGEW					

q149-1.seq

1	ATGGCACAAA	TCACACTCAA	ACCCATTGTT	TTATCAATTC	TTTTAATCAA
51	CACACCCCTC	CTCGCCCAAG	CGCATGAAAC	TGAGCAATCG	GTGGGGCTGG
101	AAACGGCTAG	CGTCGTGCGC	AAAAGCCCGT	CGCGCGCGAC	TTCCGGGGCTG
151	CTGCACGCTT	CGACCGCCTC	CGACAAAATC	ATCTCCGGCG	ATATCTTTGCG
201	CCAAAAAGCC	GTCAACTTGG	GGCAGCCTTT	GGACGGCGTA	CCGGGCATCC
251	ACGCTTCGCA	ATACGGCGGC	GGCGCATCCG	CTCCCGTTAT	TCGGCGGTCAA
301	ACGGGCACAG	GGATTAAAGT	ATTGAACCAT	CACGGCGAAA	CGGCGGATAT
351	GGCGGACTTT	TCTCCCGATC	ACGCCATTAT	GGTAGATACC	GCCTTGTCG
401	AACAGGTTGA	AATCTCGCCG	GGGCGGGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GCGTGTGCTG	TGTTGCCGAT	GGAAAAATCC	CCGAAAAATC
501	GCCTGAAAAC	GGCGTATCGG	GCGAagccgG	ATTGCGTTTG	AGCAGCGCGCA
551	ATTTTGAAAA	ACTGACATCC	GCAGGCATCA	ATATCGGACT	GGGCAAAAC
601	TTCGTGCTGC	ATACCGAAGC	CTTGTCACCG	AAATCGGGCG	ATTACGCCGT
651	ACCGCGTTAC	CGCAATCTGA	AACGCCGTGC	GCACAGCCAT	CCCGGATTCCG
701	AAACGGGCAG	CATCGGGCTG	TCTTGGGTGG	GCGAAAAAGG	CTTTATCGGC
751	GCAGCATACA	GCGACCGTGC	CGACCGCTAC	GGCCTGCCTG	CCGATGACCA
801	CGAATACGAT	GATTGCCACG	CCGACATCAT	CTGGCAAAAG	AGTTTGATCA
851	ACAAACGCTA	TTTGCAGCTT	TATCCGCACT	TGTTGACCGA	AGAAGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTGCGCG	TTCACCGACG	CGCAGCGTGC
951	ACACGCAACAC	ACCCACAACG	CGAAACCGTG	GATAGACCTG	GCGACAACAC
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGC	CATTCCCCCG	TTTTGAAGCC
1051	CTCGCGCTAT	ATCTGAACCG	CAATGACTAC	CACCACGACG	AAAAAGCAGG
1101	CGATGCAGTA	GAATAATCTT	TCAACACAA	AACACACAAC	CGCCGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGCGACCTG	GGGCGTGCAA
1201	TATTTGGGAC	ATAATTCAGC	CGCGCTTTCC	GCCATTTCGG	AAACCGTCCA
1251	ACAAACCGAT	TTGATTGACA	ACAATGTCCG	CCATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAATTGGGAC	AACTTCACGC	TGGAAGCGGG	CTGTACGGCTG
1351	AAAAAACAAA	AAGCCTCCAT	CCGGTAGCAG	AAAGCATTGA	TTGATCGAGA
1401	AACTACTACT	AACCAGCCCC	TGCCCGACCT	CGGCGCGCAC	CGCCAAACCG
1451	CCCGCTCGTT	CGCACTTTCG	GGCAACTGTT	ATTTCACGCC	ACACCCACAA
1501	CTCAGCTCAG	CCGCGTCCCA	TCGAGCAACG	CTGCCGTCAA	CGCAAGAACT
1551	GTACGCCACG	GGCAAGCAGC	TGCCCAACCA	CACCTTTGAA	GTCCGCAACA
1601	AACACCTCAA	CAAGAAGCGT	TCCAACAATA	TCCAATCTCG	CTGTGGGTAC
1651	GAAGCGGACC	GCTGGCAATA	CAATCTGGCA	GCCTACCGCA	ACCGATTCCG
1701	CAACTACATT	TACGCGCCAA	CTTFAAACCA	CGGACGCGCG	CCCAAAATCCA
1751	TCGAAGACGA	CAGCGAAATG	AAGCTCTGCG	GTCAACAACG	ATCCGTTGCC
1801	GACTTCTACG	GCGCGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCCGCGCTA
1851	CCGCACTCGT	TTTCCGGCG	ACTATGTACG	AGGCCGTCTG	AAAAAAGCTG
1901	CGTCCCTATC	CGGCAGGGAA	GATCCCTACG	GCAAAACGTC	CTTCATCGCA
1951	CAAGCCGACC	AAAACGGCCC	CGGCAATTCC	TCTGGCGGCC	TCGGGTTCCA
2001	CTGAAAAACG	TCGCTAACC	ACCGTATCGA	TGCCAAATTG	GACTACTACC
2051	GCGTGTTTCG	CCAAACACAA	CTCGCCCGCT	ACGAAACCTG	TACGCCCGGA
2101	ACCATATATG	TCACACTTCG	TGCAAACTAC	CGCGGCAATA	CGCGTATATG
2151	CGAGTGGAA	TGCTACGTCA	AAGCCGACAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCCCACG	CAGCTTCTCT	TCTGATACCG	CGCAANTGGG	CCGCGAGCTT
2251	ACCGCGGGCG	TAAACGTGAA	GTTTTTAA		

g149-1.pep

1	MAQITLKPIV	LSILLINTPL	LAQAHETEQS	VGLETVSUVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQA	VNLGDALDGV	PGIHASQYGG	GASAPVIRGG
101	TGRIKVLNKH	HGETGMDADF	SPDHAMNDVT	ALSQOQVEILR	GPVTLTYLSSG
151	NVAGLVDVAD	GKIPEKMPEN	GVSGEAGLRL	SSGNLEKITS	AGINTGLGN
201	FVLHTEGLYR	KSGDYAVPRY	RNLKRLPDSH	ADSQTKSIGL	SWVGEGKFIG
251	AAYSRRDRYD	GLPAHSYHD	DCHADRIQWK	SLINKRYLQL	YPHLLTEEDI
301	DDYDNPGLSCG	FHDGDGAHH	THNGKPWIDL	RNRKYELRAE	WKOPPPFGFA


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351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AIPETVQOPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA AYRNRFNGYI YAQTLNDRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSPLEGRE DPGKRPFFIA
651 QADQNAAPRI AARLGFHLKT SLTDRIDANL DYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

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1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGCG
101 AAACCGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGCG GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GGCGGATTIT TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTGTGA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGCGCGAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAACG GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGGAATA ACTCACGTCC GCGGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCCGGTTAC CGCAATCTGA AACGCGTGCC CGACAGCCAC GCCGATTTCG
701 AAACGGGCAG CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAACGCTA TTTACAGCTT TATCCGCACC TGTTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GCTACGAACCT CCGTGCCGAA TGGAAACAAAC CGTTCCCGGG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTC GAAAACTTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCCGCA CCAACCCATA GGTCTGTCTA AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTTAA
1251 ACAACCGATG CTGCTTGACA ACAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAACCTGGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTAC AACCAACCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCGCTCATTT CGCACTTTTC GGCAACTGGT ATTTACAGCC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCGGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAAAACAG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGCGGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTACATT TACGCCCCAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGCGCC
1801 GACTTCTACG CCGCGGAAGG CGAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTCCCGGCG ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGAGAA GATGCCTACG GCAACCGTCC TTTCATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCGAAAGGCC TCGCTGACCG ACCGTATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAA TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTTCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGCGCGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

```

1 MAQTTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLTYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLTG GGINIGLGN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDH ADSQTGSIGL SWVGEKGFIG
251 VAYSDDRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPLGLSCG FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQPFPGFEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTN ARIELRHQPI GRLKGSWGVQ
401 YLQKSSALS AISEAVKQPM LLDNKVQHSY FFGVEQANWD NFTLEGGVRV
451 EKQKASIYQD KALIDRENY NHPPLDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

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551 EGDWQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
 601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSPGREG DAYGNRPFFIA
 651 QDDQNAPRVP AARLGPHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
 701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
 751 TGGVNVKF*

m149-1/g149-1 96.2% identity in 758 aa overlap

	10	20	30	40	50	60
m149-1.pep	MAQTTLKPIVLSILLINTPLLAQAHE	TEQSV	DLET	VS	VVGKSRPRATSGLLHTSTASDKI	
g149-1	MAQTTLKPIVLSILLINTPLLAQAHE	TEQSV	GLET	VS	VVGKSRPRATSGLLHTSTASDKI	
	10	20	30	40	50	60
m149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
g149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
m149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
g149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
m149-1.pep	SPDHAIMVDTALSQQVEILRGPV	VTLLYS	SGNVAGLVDVADGKI	PEKMPENGVS	GELGLRL	
g149-1	SPDHAIMVDTALSQQVEILRGPV	VTLLYS	SGNVAGLVDVADGKI	PEKMPENGVS	GELGLRL	
	130	140	150	160	170	180
m149-1.pep	SPDHAIMVDTALSQQVEILRGPV	VTLLYS	SGNVAGLVDVADGKI	PEKMPENGVS	GELGLRL	
g149-1	SPDHAIMVDTALSQQVEILRGPV	VTLLYS	SGNVAGLVDVADGKI	PEKMPENGVS	GELGLRL	
	130	140	150	160	170	180
m149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
g149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
	190	200	210	220	230	240
m149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
g149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
	190	200	210	220	230	240
m149-1.pep	SWVGEKGFIVGAYSDDRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI					
g149-1	SWVGEKGFIVGAYSDDRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
m149-1.pep	SWVGEKGFIVGAYSDDRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI					
g149-1	SWVGEKGFIVGAYSDDRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
m149-1.pep	DYDNPLGSCGFHDDDNAHAH	THSGRPWIDLRNKRYELRAEWKQ	FFPGFEALRVHLNRNDY			
g149-1	DYDNPLGSCGFHDDDNAHAH	THSGRPWIDLRNKRYELRAEWKQ	FFPGFEALRVHLNRNDY			
	310	320	330	340	350	360
m149-1.pep	DYDNPLGSCGFHDDDNAHAH	THSGRPWIDLRNKRYELRAEWKQ	FFPGFEALRVHLNRNDY			
g149-1	DYDNPLGSCGFHDDDNAHAH	THSGRPWIDLRNKRYELRAEWKQ	FFPGFEALRVHLNRNDY			
	310	320	330	340	350	360
m149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQYLGKSSALSASEAVKQPM					
g149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQYLGKSSALSASEAVKQPM					
	370	380	390	400	410	420
m149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQYLGKSSALSASEAVKQPM					
g149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQYLGKSSALSASEAVKQPM					
	370	380	390	400	410	420
m149-1.pep	LLDNKQVHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYNHPDPLGAH					
g149-1	LLDNKQVHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYNHPDPLGAH					
	430	440	450	460	470	480
m149-1.pep	LLDNKQVHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYNHPDPLGAH					
g149-1	LLDNKQVHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYNHPDPLGAH					
	430	440	450	460	470	480
m149-1.pep	RQTARSFALSGNWFYTPQHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
g149-1	RQTARSFALSGNWFYTPQHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
	490	500	510	520	530	540
m149-1.pep	RQTARSFALSGNWFYTPQHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
g149-1	RQTARSFALSGNWFYTPQHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
	490	500	510	520	530	540
m149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA					
g149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA					
	550	560	570	580	590	600
m149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA					
g149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA					
	550	560	570	580	590	600
m149-1.pep	DFYGAEGEII FKPTPRYRIGVSGDYVRGRLKNLPSPGREGDAYGNRPFFIAQDDQNAPRVP					
g149-1	DFYGAEGEII FKPTPRYRIGVSGDYVRGRLKNLPSPGREGDAYGNRPFFIAQDDQNAPRVP					
	610	620	630	640	650	660
m149-1.pep	DFYGAEGEII FKPTPRYRIGVSGDYVRGRLKNLPSPGREGDAYGNRPFFIAQDDQNAPRVP					
g149-1	DFYGAEGEII FKPTPRYRIGVSGDYVRGRLKNLPSPGREGDAYGNRPFFIAQDDQNAPRVP					
	610	620	630	640	650	660

424

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      670      680      690      700      710      720
m149-1.pep  AARLGPHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
|||||:|||||
g149-1      AARLGPHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
      670      680      690      700      710      720

      730      740      750      759
m149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
|||||
g149-1      WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
      730      740      750

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

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a149-1.seq
1  ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51  CACACCCCTC CTCTCCCAAG CGCATGGAAC TGAGCAATCA GTGGGCTTGG
101 AAACGGTCAG CGTCGTGGC AAAAGCCGTC CGCGGCCAC TTCGGGGCTG
151 CTGCACACTT CTACCGCCTC CGACAAAATC ATCAGCGGCG ACACCTTGCG
201 ACAAAGAGCC GTCAACTTGG GTGATGCTTT AGACGGCGTA CCGGGCATTG
251 ATGCCTCGCA ATACGGCGGC GCGCATCCG CTCCGTTAT TCAGCGTCAA
301 ACAGGCAGAC GGATTAAAGT GTTGAACCAT CACGGCGAAA CGGGCGACAT
351 GCGCGACTTC TCTCCAGACC ATGCAATCAT GGTGGACAGC GCCTTGTCGC
401 AACAGGTCGA AATCTGCGC GGTCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGCGCAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAC GCGTATCGG GCGAATCGG ATTGCGTTG AGCAGCGGCA
551 ATCTGAAAA ACTCAGTCC GCGGCGATCA ATATCGGTTT GGGCAAAAAA
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGG ATTACGCCGT
651 ACCGCGTTAC CGCAATCTGA AACGCTGCC CGACAGCCAC GCCGATTGCG
701 AAACGGGCG CATCGGGCTG TCTTGGGTTG GCGAAAAAGG CTTTATCGGC
751 GCAGCATACA GCGACGCTCG CGACCAATAT GGTCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGTTTGATTA
851 ACAACGCTA TTTGAGCTT TATCCGACCC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTTACGAGC ACGATGATGC
951 ACACGCCCAT GCCACAACG GCAAACCTTG GATAGACCTG CGCAACAAAC
1001 GCTAGGAAC CCGCGCCGAA TGGAAACAAC CGTTCGCCG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGAGC AAAAAGCAGG
1101 CGATGCAGTA GAAAACCTTT TAAACAACCA AACGCAAAAC GCCCGTATCG
1151 AGTTGCGCCA CCAACCCATA GGCGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTGGGAG AAAATCCAG TGCTTTATCT GCCACATCCG AAGCGGTCAA
1251 ACAACCGATG CTGCTTGACA ATAAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATGGGAC AACTTCACGC TTGAAGGCGG CGTACGCGTG
1351 GAAAAACAAA AAGCTCCAT CCGCTACGAC AAAGCATTGA TTGATCGGGA
1401 AAACCTACTA AACCATCCCC TGCCCGACCT CGCGCGCAC CGCCAAACCG
1451 CCCGCTCATT CGCACTTTTC GGCAACTGGT ATTTACGCGC ACAACACAAA
1501 CTCAGCCTGA CCGCTCCCA TCAGGAACGC CTGCCGTCAG CGCAAGAGCT
1551 GTACGCAAC GGCAAACACG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 CAATACATT TACGCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGCTGCG
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTCCGGCG ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGGGAA GACGCTACG GCAACCGCCC ACTCATTGCC
1951 CAAGCCGACC AAAACGCCCC TCGCTTCCG GCTGCGCGCC TCGGCGTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGCATCGA TGCCAATTTG GACTACTACC
2051 GCGTGTTCG CCAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAA TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGGCGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

```

a149-1.pep
1  MAQTTLKPIV LSILLINTPL LSQAHGTEQS VGLTVSVVG KSRPRATSGI
51  LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDS ALSQVEILR GPVTLIYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSGLGLRL SSGNLEKLT SGINIGLGRN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 AAYSDDRDQY GLPAHSHEYD DCHADIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPGLSG FHDDDDAHAA AHNGKPWIDL RNKRYELRAE WKQFPFGFEA

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351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRKLGSGWVQ
 401 YLGQSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
 451 EKQKASIRYD KALIDRENY NHPPLDLGAH RQTARSFALS GNWYFTPOHK
 501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
 551 EGDWQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
 601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSPFGRE DAYGNREPLIA
 651 QADQNAPRVP AARLGVHLKA SLTDRIDANL DYRVFAQNK LARYETRTPG
 701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
 751 TGGVNVKF*

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
m149-1	MAQTTLKPIVLSILLINTPLLAQAHETEQSVDLTVSVVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a149-1.pep	SPDHAIMVDSALSQQVEILRGPVTLTYSSGNVAGLVVDVADGKIPEKMPENGVSSELGLRL					
m149-1	SPDHAIMVDTALSQQVEILRGPVTLTYSSGNVAGLVVDVADGKIPEKMPENGVSSELGLRL					
	130	140	150	160	170	180
	190	200	210	220	230	240
a149-1.pep	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSQDYAVPRYRNLKRLPDSHADSTGSGIGL					
m149-1	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSQDYAVPRYRNLKRLPDSHADSTGSGIGL					
	190	200	210	220	230	240
	250	260	270	280	290	300
a149-1.pep	SWVGEKGFIGAAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
m149-1	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a149-1.pep	DYDNPGLSCGFHDDDDAHAHNGKPWDLRNKRYELRAEWKQPPFGFEALRVHLNRNDY					
m149-1	DYDNPGLSCGFHDDDDAHAHNGKPWDLRNKRYELRAEWKQPPFGFEALRVHLNRNDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
a149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRKLGSGWVQYLGQSSALSATSEAVKQPM					
m149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRKLGSGWVQYLGQSSALSATSEAVKQPM					
	370	380	390	400	410	420
	430	440	450	460	470	480
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPPLDLGAH					
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYNHPPLDLGAH					
	430	440	450	460	470	480
	490	500	510	520	530	540
a149-1.pep	RQTARSFALSGNWFYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
m149-1	RQTARSFALSGNWFYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
	490	500	510	520	530	540
	550	560	570	580	590	600
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660


```

a149-1.pep  DFIGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQNAFPRVP
|||||
m149-1      DFIGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQNAFPRVP
          610      620      630      640      650      660

          670      680      690      700      710      720
a149-1.pep  AARLGVHLKASLTDRIDANLDYYRVFAONKLARYETRTPGHHMLNLGANYRRNTRYGEWN
|||||
m149-1      AARLGVHLKASLTDRIDANLDYYRVFAONKLARYETRTPGHHMLNLGANYRRNTRYGEWN
          670      680      690      700      710      720

          730      740      750      759
a149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
|||||
m149-1      WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
          730      740      750

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

g150.seq (partial)

```

1  ..TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGTA
101 GCGGTTTCGA TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCTTGCCG GTTGCCTCCG
251 CACTGTATAT CCATTTGCGA CTCACGCAA ACACCCCGCG CTTTGTCAAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCCGGCAAAA CTGACGCGCG AACAAATCGC CGGCCTGCTG
451 CGCCCGCTTG CGCCGCGCCT GTATTCGATT TCCTCGTCGC AGCGCGAAGC
501 GGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCCTTTC GAACACGAAG
551 GGCGCGCCAG GCGGGCGCGC GCATCGGTT TCTTTGCCGA CCGGCTGGAA
601 GAGGACGGCA CGGTGCGCGT GTTTGCGGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGGCG
701 TCGCACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA
751 GGCAGAAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGCGAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCGCG AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC
951 GCATATCTAT GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GAAGTGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGCGG GCATTTCGGA CGAAGACGGC
1051 GCAGAAGGAT ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

g150.pep (partial)

```

1  ..YCKADFFPAA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAGGKTLV VASALLSHFE LTONTAPFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLLVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLPED SRKPIVMIGS GTGVAPFRAF VQORAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDF LHRDYFAWSR DQEEKIYVQD
301 KIREQAEGLW QWLQEGAHY VCGDAAKMAK EVEAALLDVI IGAGHSDEDEG
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

m150.seq

```

1  ATGCAGAACAA CAAATCCGCC ATTACCGCCT CTGCCGCCCG AAATCAGCA
51  GCTCCTGTGCG GGGCTGGACG CGGCACAATG GCGGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CCGCCTTCAG
151 ACGGCATTGC CGGCGGCGA ACCTTTTTC GTAACCGTCC TTTCCGCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGCG GACAGCCTGG
251 AAGCCGCGCG CATCCAAGTC AGTCGCGCG AACTGAAAGA CTATAAGGCG
301 AAAACATCG CCGCGGAAAC CCGCCTGCTG CTGGTTACCT CCACCCAAGG
351 CGAAGGCGAA CCGCGGAAAG AAGCCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAGC CCCGAAATTG GACAACTCC AATTGCGGT ACTGGGTTTG

```



```

451  GGCGACAGTT CCTATCCGAA TTTCTGTCAG GCAGGTAAAG ATTTGACCG
501  GCGTTTTGAA GAATTGGGCG CAAAACGGCT GCTCGAACGC GTTGATGCGG
551  ATTTGGACTT TACCGCCTCC GCAAACGCCT GGACAGATAA TATCGCCGCA
601  CTCTTAAAG AAGAAGCCGC AAAAAACCGG GCAACGCCCC CGCCGCAGAC
651  AACGCCCCC GCGGCGCTTC AGACGGCACC GGATGGCAGG TACTGCAAGG
701  CAGCCCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT CACCGCCCGC
751  CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTTGA GCGGTTCCGA
801  TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT GACAACGATC
851  CGGCACTGGT CAGGGAAATC CTAGACCTGC TCGGCATCGA TCCGGCAACG
901  GAAATACAGG CGGGCGGAAA GATGATGCCG GTTGGCGCGG CACTTTCATC
951  TCATTTCGAA CTCACGCAAA AACTCCGGC TTTCTGCAAA GGCTATGCCG
1001 CGTTCGCCCA TTATGAAGAA CTCGATAAAA TCATTGCCGA TAACGCCGTT
1051 TTGCAGGATT TCGTGCAAAA CACGCCTATT GTCGATGTGC TGCACCGCTT
1101 CCCGCAAGC CTGACGGCAG AACAAATTCAT CCGTTACTG CGTCCGCTTG
1151 CACCCCGTTT GTATTGATT TCTTCAGCAC AGGCGGAAGT GGGCGATGAA
1201 GTGCATTTAA CTGTCGGCGT GGTTCTGTTT GAACACGAAG GCCGCGCCAG
1251 AACGGGCGGC GCATCGGGTT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
1301 CCGTGCGCGT GTTGTGGAA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
1351 AGCCGCAAGC CGATTGTGAT GATCGGCTCG GGCACCGGCG TCGCACCGTT
1401 CCGCGCTTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA GGCAAAACT
1451 GGCTGATTTT CGCAATCCG CATTTTGCCC GTGATTTTCT CTATCAAACC
1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGGT ACGATTTCGC
1551 CTGGTCCCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
1601 AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
1651 GTGTGCGGCG ATCGGGCAAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT
1701 GGATGTGATT ATCGGGGCAG GACATTTGGA CGAAGAGGGC GCAGAAGAAT
1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTATTATGA

```

This corresponds to the amino acid sequence <SEQ ID 610; ORF 150>:

m150.pep

```

1  MQNTNPPLPP LPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
51  TALPAABPFS VTVLSASQTG NAKSVADKAA DSLEAGIQV SRAELKDYKA
101 KNIAGERLL LVTSTQGEGE PPKEAVVLHK LLNGKKAPKL DKLQFAVLGL
151 GDSSYPNFCQ AGKDFDRRFE ELGAKRLLER VDADLDFTAS ANAWTDNIAA
201 LLKEEAAKNR ATPAQTTTPP AGLQTAPDGR YCKAAPFPAA LLANQKITAR
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDPAT
301 EIQAGGKMMP VARALSSHFE LTQNTPAFVK GYAFAHYEE LDKIIDNAV
351 LQDFVQNTPI VDLHRFPAS LTAEQFIRLL RPLAPRLYSI SSAQAEVGDE
401 VHLTVGVVRF EHEGRARTGG ASGFLADRLE EDGTVRVFVE RNDGFRLLPED
451 SRKPIVMIGS GTGVAPFRAF VQRAAENAE GKNWLIFGNP HFARDFLYQT
501 EWQQFAKDFG LHRYDFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHY
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

```

                210      220      230      240      250      260
m150.pep  LLKEEAAKNRATPA PQTTFPAGLQTAPDGRYCKAAPFPAA LLANQKITARQSDKDVRHIE
g150                      YCKADFPFAALLANQKITARQSDKDVRHIE
                                10      20      30

                270      280      290      300      310      320
m150.pep  IDLSGSDLHYLP GDALGVWFDNDPALVREILDLLGIDPATEIQAGGKMMPVARALSSHFE
g150      IDLSGSDLHYLP GDALGVWFDNDPALVGEILDLLGINPATEIQAGGKTLPVASALLSHFE
                                40      50      60      70      80      90

                330      340      350      360      370      380
m150.pep  LTQNTPAFVKGYAFAHYEELDKIIDNAV LQDFVQNTPIVDVLRFPASLTAEQFIRLL

```


a150.seq

```

a150.seq
1    ATGCAGAACA CAAATCCGCC ATTACCGCCT ATGCCGCCCG AAATCACGCA
51   GCTCTGTGTC GGGCTGGACG CGGCACAATG GGCCTGGCTG TCCGGCTACG
101  CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGATCGCC CGCGCTTACG
151  ACGGCATTGC CGACGGCAGA ACCTTTTTTC GTAACCGTCC TTTCGGCTC
201  GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251  AAGCCGCCGG CTCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301  AAAAACATCG CCGGCGAAGC CGCGCTGCTG CTGTTTACCT CCACCCAAGG
351  CGAAGGCGAA CCGCGGAAG AAGCCGTCGT GTGCACAAA CTGCTGAACG
401  GCAAAAAGC CCCGAAATTG GACAAACTCC AATTTGCCGT ACTGGGTTTG
451  GCGCAGACGT CCTATCCGAA TTTCTGCGCG GCGGGCAAAG ATTTCCACAA
501  ACGTTTTGAA GAATTGGCGG CAAAACGCCT GCTCGAACGC GTTGATGCGG
551  ATTTGGACTT TGCCGCCGCC GCAGACGGAT GGACAGATAA TATCGCCGCA
601  CTCTTAAAG AAGAAGCCGC AAAAAACCGG GCAACGCCCG CGCCGCAGAC
651  AACGCCCCCC GCGGCCTTC AGACGGCACC GGATGCGAGG TACTGCAAGG
701  CAGACCCCTT TCCCGCCGCG CTGCTGGCCA ATCAGAAAAT CACCGCCCGC
751  CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTTGA GCGGTTCCGA
801  TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGTTTT GACAACGATC
851  CGGCACTAGT CAGGAAATC CTAGACCTGC TCGGCATCGA TCAGGCAACG
901  GAAATACAGG CGGCGGAAAC AACCTGCGCG GTTGCTCCCG CACTGTTATC
951  CCATTTTGAA CTCACGCAA ACACCCCGCG CTTTGTCAAA GGCTATGCCC
1001 CGTTCGCCGA TGTATACGAA CTCGACCGTA TTGCTGCCGA CAACCGCGTT
1051 TTGCAAGGCT TTGTGCAAG CACGCCGATT GCCGATGTGC TGCACCGCTT
1101 CCCGGCAAAA CTGACAGCGG AACAAATTCG CCGGCTACTG CGCCCCGTTG
1151 CGCCGCGCCT GTATTGCAAT TCCTCGTTCG AGGCGGAAGT .GGGGGACGAA
1201 GTGCACCTGA CCGTCCGGCG GGTGCGTTTC GAACGCAAGG GGGCGGCGAG
1251 GGCGGGCGGC GCATCGGGTT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
1301 CGGTGCGCGT GTTTGTGGAA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
1351 AACCGCAAGC CGATTGTGAT GATCGGCTCG GGCACCGGCG TCGCACCGTT
1401 CCGCGCTTTT GCCTCAACAC GATCCGCGAG ATGCGCGGAA GGCACAAACT
1451 GGCTGTTTTT CGGCAATCCG CATTTTGCCC GTGATTTTCT CTATCAAACT
1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT ACGATTTTCG
1551 CTGGTCGCCG GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
1601 AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
1651 GTGTGCGCGC ATGCGGCAAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT

```



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a150.pep
1  MQNTNPPLPK MPPEITQLLS GLDAAQQAWL SGYAWAKAGN GASAGLPALQ
51  TALPTAEPPS VTVLSASQGT NAKSVADKAA DSLEAAGIQV SRAELKDYKA
101 KNIAGERRL LVTSTQGEGE PPEEAVVLHK LLNGKKAPKL DKLQFAVLGL
151 GDSSYPNFCR AGKDFDKRFE ELGAKRLER VDADLDFAAA ADGWTDNIAA
201 LLKEEAAKNR ATPAPQTPP AGLQAPDGR YCKADFPFAA LLANQKITAR
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLKGIDAT
301 EIQAGGKTLF VASALLSHE LTQNTPAFVK GYAPFDADDE LDRIAADNAV
351 LQGFGQSTPI ADVLHRFPK LTAEQFAGLL RPLAPRLYSI SSSQAEVGDE
401 VHLTVGAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLEPD
451 SRKPIVMIGS GTGVAPFRAF VQORAENEA GKNWLFFGNP HFARDFLYQT
501 EWQGFADKGF LHRYPFAWSR DQEEKIYVD KIREQAEGLW QWLQEGAHYI
551 VCGDLAKMAK DVEAELLDVI IGAGHLEDEG AEAYLDMLRE EKRYQRDVY*

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	10	20	30	40	50	60
m150.pep	MQNTNPPLPPLPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQTALPAAEFFS					
a150	MQNTNPPLPMPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQTALPTAEFFS					
	10	20	30	40	50	60
m150.pep	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRaelKDYKAKNIAGERRLLVLTSTQGEGE					
a150	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRaelKDYKAKNIAGERRLLVLTSTQGEGE					
	70	80	90	100	110	120
m150.pep	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRaelKDYKAKNIAGERRLLVLTSTQGEGE					
a150	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRaelKDYKAKNIAGERRLLVLTSTQGEGE					
	70	80	90	100	110	120
m150.pep	PPKEAVVLHKLlNGKKAPKLDKlQFAVLGLGDSSYPNFCQAGKDFDRRFEELGAKRLLER					
a150	PPKEAVVLHKLlNGKKAPKLDKlQFAVLGLGDSSYPNFCRAGKDFDKRFEELGAKRLLER					
	130	140	150	160	170	180
m150.pep	PPKEAVVLHKLlNGKKAPKLDKlQFAVLGLGDSSYPNFCQAGKDFDRRFEELGAKRLLER					
a150	PPKEAVVLHKLlNGKKAPKLDKlQFAVLGLGDSSYPNFCRAGKDFDKRFEELGAKRLLER					
	130	140	150	160	170	180
m150.pep	VDADLDFTASANAWTDNIAALLKEEAakNRATPApQTTPPAGLQTAPDGRYCKAAFFPAA					
a150	VDADLDFAAAADGWTDNIAALLKEEAakNRATPApQTTPPAGLQTAPDGRYCKADFFPAA					
	190	200	210	220	230	240
m150.pep	VDADLDFTASANAWTDNIAALLKEEAakNRATPApQTTPPAGLQTAPDGRYCKAAFFPAA					
a150	VDADLDFAAAADGWTDNIAALLKEEAakNRATPApQTTPPAGLQTAPDGRYCKADFFPAA					
	190	200	210	220	230	240
m150.pep	LLANQKITARQSDKDVrHIEIDLsgSDLHYLPGDALGVWFDNDPALVREILDLLGIDPAT					
a150	LLANQKITARQSDKDVrHIEIDLsgSDLHYLPGDALGVWFDNDPALVREILDLLGIDQAT					
	250	260	270	280	290	300
m150.pep	LLANQKITARQSDKDVrHIEIDLsgSDLHYLPGDALGVWFDNDPALVREILDLLGIDPAT					
a150	LLANQKITARQSDKDVrHIEIDLsgSDLHYLPGDALGVWFDNDPALVREILDLLGIDQAT					
	250	260	270	280	290	300
m150.pep	EIQAGGKMPFVARALSSHFELTQNTPAFVKGYAAFAHYEELDKIADNAVLDQFVQNTPI					
a150	EIQAGGKTLFVASALLSHFELTQNTPAFVKGYAPFADDELDRIAADNAVLDQFVQSTPI					
	310	320	330	340	350	360
m150.pep	EIQAGGKMPFVARALSSHFELTQNTPAFVKGYAAFAHYEELDKIADNAVLDQFVQNTPI					
a150	EIQAGGKTLFVASALLSHFELTQNTPAFVKGYAPFADDELDRIAADNAVLDQFVQSTPI					
	310	320	330	340	350	360
m150.pep	VDVLHrFPASLTAEQfIRLLRPLAPrLYSISSAQAEVGDEVHlTVGVrFEHEGRARTGG					
a150	ADVHLrFPAKLTAEQfAGLLRPLAPrLYSISSAQAEVGDEVHlTVGAVrFEHEGRARAGC					
	370	380	390	400	410	420
m150.pep	VDVLHrFPASLTAEQfIRLLRPLAPrLYSISSAQAEVGDEVHlTVGVrFEHEGRARTGG					
a150	ADVHLrFPAKLTAEQfAGLLRPLAPrLYSISSAQAEVGDEVHlTVGAVrFEHEGRARAGC					
	370	380	390	400	410	420
m150.pep	ASGFLADrLEEDGTvrVfVERNDGfRLPEDSRKPIVMIGSGTGVAPfRAfVQqRAAENa					
a150	ASGFLADrLEEDGTvrVfVERNDGfRLPEDSRKPIVMIGSGTGVAPfRAfVQqRAAENa					
	430	440	450	460	470	480
m150.pep	ASGFLADrLEEDGTvrVfVERNDGfRLPEDSRKPIVMIGSGTGVAPfRAfVQqRAAENa					
a150	ASGFLADrLEEDGTvrVfVERNDGfRLPEDSRKPIVMIGSGTGVAPfRAfVQqRAAENa					
	430	440	450	460	470	480
m150.pep	GKNWLIFGNPHfARDfLYQTewQQfAKDGLHrYDFAWSRDQEEKIYVQDKIREQAeGL					
a150	GKNWLIFGNPHfARDfLYQTewQQfAKDGLHrYDFAWSRDQEEKIYVQDKIREQAeGL					
	490	500	510	520	530	540

430

```

a150      GKNWLFPGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQDKIREQAEGWL
           490      500      510      520      530      540

m150.pep  QWLQEGAHYVCGDAAKMAKDVEAALLDVIIIGAGHLDEEGAEYLDMLREEKRYQRDVYX
           550      560      570      580      590      600
           |||
a150      QWLQEGAHYVCGDAAKMAKDVEAALLDVIIIGAGHLDEEGAEYLDMLREEKRYQRDVYX
           550      560      570      580      590      600

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 613>:

g151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCACACGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGA AAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTG
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGCGCGAAG
251 TGGAGCGCGT TTTGGGGATG GTGGATTGCG TCGTCTTGTT GGTGGACGCA
301 CAGGAAGGTC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCCTCATCAA CAAAATCGAC AAACCGTCCG
401 CCCGTCGAG CTGGGTTATC GACCAGACTT TCGAGTTGTT CGACAACCTG
451 GGTGCGACCG ACGAGCAGTT GGATTTCCTG ATTGTTTACG CTTAGGTTT
501 GAGCGGCTTT GCCAAGCTGG AAGAAAccga CGAGAGCAGC GATATGCGCC
551 CGCtggttegA CACCATCCTA AAATACacgc ctgCACCGAG CCGCAGCGCG
601 GACGAGCGCG TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTGATGAAC CACGAGCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGCTTGGA CGCGTGCCG TTGAAGAAGC
801 CGAAGCCGCG GACATTGTGA TTATTTCCGG TATCGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGCCTGACC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGAATTT ATGGTAAACA CCAGCCCGCT
951 CGCAGGTACA GAAGGCAAT TCGTGACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTTGCC TGCGCGTGA AGACACCGCC
1051 GatgCCGACG TGTTCGCGT ATCcgGGCG GCGGAAGTGC ACCTGACGAT
1101 TTTGCTGGAA AATATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAGC
1151 CGCGCGTCGT GTACCGAGAC ATCGACGGTC AAAAATGCGA ACCTTATGAA
1201 AACCTGACTG TGGACGTACC cgacgacAAC CAAGCGCGCG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACCAA TATGGAAAGC GACGGCAACG
1301 GacgCACCGC CCTCGAATAC CATATTCCAG CGCGCGCTT GATCGGTTT
1351 CAAGGCGAAT TCATGACCCT GACGCGCGGC GTCGGGCTGA TGAgccacGT
1401 GTTcgacgac tacgcgcccg tcaAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTactggt GtcccaAGAG CAGGCGGAGG CGGTTGCTTA CGCCTTGTTG
1501 AATCTTGAAG ACCGCGGCGG TATGTTGTA TCGCCCAACG ACAAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGCCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTCACCAATA TCCGTGCCAG CCGTACCGAC
1651 GAAGCGGTGC GCCTGACCAC GCCGATCAAA CTGAcgcTGG AAGGCGCGGT
1701 CGAGTTTATC GACGATGACG AGCTGGTGA AATCACGCCG CAAtccatcc
1751 gcctgcgcat gcgttacctG AGCGaattgg aacgcgcgcg tcaTTTTAAA
1801 AagctgGATT AA

```

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

g151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGCHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESS DMRPLFDITL KYTPAPSGSA
201 DEPLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HEQQAQGR
251 NQLLPGKLE RVPLEFAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW

```


501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMYL SELERRRHFK
 601 KLD*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq

```

1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCG ACCACGGCAA
51 AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAGCCGTCCG
401 CTCGTCCGAG CTGGGTATC GACCAAACTT TCGAGCTGTT CGACAATTG
451 GGCGCGACCG ACGAGCAGTT GGATTTCCTG ATTGTTTACG CTTCAGGGTT
501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATCGGTC
551 CGCTGTTTGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGCCCGCCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTGGA CCGTGCCGC TGAAGAAGC
801 CGAAGCCGGC GACATCGTGA TTATTCCGG TATCGAAGAC ATCGGTATCG
851 GCGTAACCAT CACCGACAAA GACAATCCCA AAGGCCTACC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGCT
951 GGCGGGTACG GAAGGCAAAT TCGTAACCA CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TGCGCGTGA AGATACCGCC
1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GCGAGCTGC ACCTGACCAT
1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
1201 AACCTGACCG TGGATGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGAAAGC GACGGCAACG
1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TTATGACCTT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTTG
1501 AATCTGGAAG ACCGCGGCCG TATGTTGTA TCGCCCAACG ACAAAATCTA
1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCCGTTT GCCTGACCAC GCCAATCAAG CTGACGCTGG AAGGTGCGGT
1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCACTTTAAA
1801 AAGCTGGATT GA

```

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep

```

1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HDQQIAQGRI
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DGNRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVFDG YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
601 KLD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng)
from *N. gonorrhoeae*:

m151/g151

m151.pep	10	20	30	40	50	60
	MKQIRNIAIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
g151	10	20	30	40	50	60
	MKQIRNIAIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
m151.pep	70	80	90	100	110	120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	70	80	90	100	110	120
	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
m151.pep	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN					
g151	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
m151.pep	190	200	210	220	230	240
	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
g151	190	200	210	220	230	240
	DMRPLFDITILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
m151.pep	250	260	270	280	290	300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
g151	250	260	270	280	290	300
	HEQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
m151.pep	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
g151	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
m151.pep	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVYRDIQKCEPYENLTVDPDDNQAVMEELGR					
g151	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVYRDIQKCEPYENLTVDPDDNQAVMEELGR					
m151.pep	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG					
g151	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG					
m151.pep	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGKK					
g151	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGKK					
m151.pep	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					

m151.pep KLDX
 ||||
 g151 KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

a151.seq
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCACGTCG ACCACGGCAA
 51 AACACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGCGGAAG
 251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
 301 CAGGAAGGCC CGATGCCGCA AACCCTTTC GTGACCAAAA AAGCCTTGGC
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAATCGAC AAACCGTCCG
 401 CCCGTCCGAG CTGGGTCATC GACCAAATT TCGAGCTGTT CGACAACTTG
 451 GCGCGACCGC ACAGCAGTT GGATTTCCTG ATTGTTTATG CTTCCGGTCT
 501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
 551 CGCTGTTTCA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
 601 GACGAAACGC TGCAACTGCA AATTTCCTAA CTCGACTACG ACAACTACAC
 651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC
 701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGCATC
 751 AACCTGACTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCCG TTGAAGAAGC
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATTGAAGAC ATCGGCATCG
 851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCTGCC GATGTGAGC
 901 GTGACGAAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGTT
 951 GGCAGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TGCGCGTGGG AGATACCGCC
 1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GCGAGCTGC ACCTGACCAT
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
 1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
 1251 ACTCGGCCGC CGCGTGCGC AACTGACTAA TATGGAAGC GACGGCAACG
 1301 GACGCACCGC CCTCGAATAC CATATCCAG CGCGCGGCTT GATCGGCTTC
 1351 CAAGGCGAAT TTATGACCCT GACGCGCGGG GTCCGGCTGA TGAGCCACGT
 1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCTGGC CGCCACAACG
 1451 GCGTGCTGGT GTCCAAGAG CAGGCGGAGG CAGTCGCTTA CGCCTTGTTG
 1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGA TCGCCCAACG ACAAATCTA
 1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
 1651 GAAGCCGTTT GCCTGACCAC GCCGATTAAG CTGACGCTGG AAGGTGCGGT
 1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC
 1751 GTCTGCGCAA GCGTACTTGG AGCGAATTGG AACGCCGCCG CCATTTCAAA
 1801 AAGCTAGATT GA

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

a151.pep
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVVLVDA
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQAQGGRI
 251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
 301 VDEPTLTMDF MVNTSELAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
 351 DADVERVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
 401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
 451 QGEFMTLTRG VGLMSHVFDG YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
 501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
 601 KLD*

m151/a151 99.8% identity in 603 aa overlap

10 20 30 40 50 60

m151.pep	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
a151	
	10 20 30 40 50 60
m151.pep	70 80 90 100 110 120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
a151	
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
	70 80 90 100 110 120
m151.pep	130 140 150 160 170 180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
a151	
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
	130 140 150 160 170 180
m151.pep	190 200 210 220 230 240
	DMRPLFDTILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
a151	
	DMRPLFDTILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
	190 200 210 220 230 240
m151.pep	250 260 270 280 290 300
	HDQQAQGRINQLLGFKGLERVPLEEAEGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
a151	
	HDQQAQGRINQLLGFKGLERVPLEEAEGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
	250 260 270 280 290 300
m151.pep	310 320 330 340 350 360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLRQKELLTNVALRVEDTADADVFRVSGR
a151	
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLRQKELLTNVALRVEDTADADVFRVSGR
	310 320 330 340 350 360
m151.pep	370 380 390 400 410 420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQAVMEELGR
a151	
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQAVMEELGR
	370 380 390 400 410 420
m151.pep	430 440 450 460 470 480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG
a151	
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG
	430 440 450 460 470 480
m151.pep	490 500 510 520 530 540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGHSRDNLDVNNPLKGKK
a151	
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGHSRDNLDVNNPLKGKK
	490 500 510 520 530 540
m151.pep	550 560 570 580 590 600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
a151	
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
	550 560 570 580 590 600
m151.pep	KLDX
a151	KLDX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAAaca aaACCaaagt ctgGGacttc cCaccgcc ttTTCactG
51  GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGCTCG GGCTGCTCGT CCTTTCTCTG

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435

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151 CTCGTATTCC GCCTCTGCTG GGGCATTGTT GGCAGcgATA CCGCCCGTTT
201 CTCccgTtTC GTCCGAGGTT GGGCAGGTAT ACGCGGCTAT CTGAAAAAcg
251 gCATTCCCGA ACAtatcCAG CCCGACACA ACCCCTTGGG CGCACTgatg
301 gtcGTTGCGC TTTTGgcccgc cgtcTCATTT CAagtccgca CGGGGCTTTT
351 Tgcccgaat gaaaacacct tcagcaCCaA cggctacctc aaccatttgg
401 tttccgaaca tacgGGCAGC CTTATACGGA AAATCCACCT CAACTTTTTTC
451 AAGCTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCATATTC AAAAAGAAAA ACCTCGTCCG CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 620; ORF 152.ng>:

g152.pep

```

1 MKNKTKVWDF PTRLFWLLA ASLPFMWYSA KAGGDMQWH TRVGLLVFL
51 LVFRLCWGIW GSDTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAN ENTFTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVFSAVH IAAVAAYRIF KKKNLVRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

m152.seq

```

1 ATGAAAAACA AAACCAAGT CTGGGACCTC CCCACCCGCC TTTTCCACTG
51 GCTGCTTGCC GCGTCCCTGC CCTTTATGTG GTATAGCGCG AAAGCCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTCTG CTTTTTCCTG
151 CTCGTATTTC GCCTCTGCTG GGGCATTGTT GGCAGCGATA CCGCCCGTTT
201 TTCCCGTTTC GTCCAAGGCT GGGCAGGCAT ACGCGGCTAT CTGAAAAACG
251 GTATTCCCGA ACACATCCAG CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGCCCGC CGTGTCTTTC CAAGTCGGCA CCGGGCTTTT
351 TGCCGCCGAT GAAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGTTG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCACCT CAACTTTTTTC
451 AAGCTGCTCG CCGTTTTTTC TGCAATCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCGTATTC AAAAAGAAAA ACCTCATCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCAGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CTCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 622; ORF 152>:

m152.pep

```

1 MKNKTKVWDL PTRLFWLLA ASLPFMWYSA KAGGDMQWH TRVGLFVFL
51 LVFRLCWGIW GSDTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD ENTFTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAIH IAAVAAYRVF KKKNLILPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVASLA AAAILLLS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng)

from *N. gonorrhoeae*:

m152/g152

```

          10      20      30      40      50      60
m152.pep  MKNKTKVWDL PTRLFWLLA ASLPFMWYSA KAGGDMQWH TRVGLFVFL LVFRLCWGIW
          ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g152      MKNKTKVWDF PTRLFWLLA ASLPFMWYSA KAGGDMQWH TRVGLLVFL LVFRLCWGIW
          10      20      30      40      50      60

          70      80      90     100     110     120
m152.pep  GSDTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM VVALLAAVSF QVGTGLFAAD
          ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g152      GSDTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM VVALLAAVSF QVGTGLFAAN
          70      80      90     100     110     120

```


436

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAIHIAA VAAAYRVFKKKNLILPMI					
	: : : : :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAA VAAAYRIFKKNLVRPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLLSX			
	: : :			
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```

a152.seq
1  ATGAAAAACA AAACCAAAGT CTGGGACTTC CCCACCCGCC TTTTCCACTG
51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCCTG
151 CTCGTATTCC GCCTCTGCTG GGGCATTGCG GGCAGCGATA CCGCCCGTTT
201 CTCCCGTTTC GTCCGCGGAT GGTCCGGTAT CAGAGAGTAT ATGAAAAACG
251 GTATTCCTCG ACACGTCCAA CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGCCGCG CGTGTGCTTC CAAGTCGGCA CAGGGCTTTT
351 TGCCGCCGAT GTAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCATCT CAACTTTTTC
451 AAATGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501 CCGCGTGTTC AAAAAGAAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
1  MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFILEL
51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAVH IAXVAAAYRVF KKKNLVLEPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLS*

```

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLFLLVFRLCWGIW					
	: : : : :					
a152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKTGGDMLQWHTRVGLFILELLVFRLCWGIW					
	10	20	30	40	50	60

	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	: : : : :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAIHIAA VAAAYRVFKKKNLILPMI					
	: : : : :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAVHIAA VAAAYRVFKKKNLVRPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLLSX			
	: : :			
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```
g153.seq
1  atgggggtttg cttacAgatg gacgtatatc gaggtCGGga taccggaggc
51  ggcacccgctc ctttCgctGC CCGAGATgat ggcctgatG GTGTTtCagg
101 attATGGTTT TttggcCGAA GTGATGTTTG TgctgaCTTT cGGCGcgcCG
151 GTTCTGTTtC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTTCG TTCGGGCCGG CGTTTTATCT
351 GATGTTCCGG CTGTCCGTTA TGCTGATTCG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTCCAA ATCGGGCGGC TGACGGGGAA TAATGCGGTT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTTCcg
501 cgacAGTgcc gaatccCCCT GCGGGGTGTg cgCGCGggaA CTgtacggcg
551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCtgac ggcggcggtT
601 GTTTTGTATT TCCctgCcaa TATCctgceg attatGAttt cgtccaATCc
651 tgccgccacg GAGGcCAACA CCATCTTTAG CCGCATCGCT TATATGTGGG
701 ACGagggcgA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CCGCGGCACG
801 GTTCGCTTTG CCGGCGGGCG CAAAGAAATT GTCCGACCTC tacCGCATCA
851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCCaCaC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CCGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```
g153.pep
1  MGFAYSMTYI EVGIPEAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRVN VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR FGPAPYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGNNAV
151 QTASEGKTCC SRCLYFRDSA BSPCGVCGAE LYGGRPKSLs ISSAFLTAaV
201 VLYFFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIAAARFAL PAGAKKLSHL YRITEAVGRW SMIDIFVII
301 LMCSFHTYAA RVIPGSAaVY FCLVVILTML SAYYFDPRLL WDKRASDGLA
351 FNETBKVD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```
m153.seq
1  ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTCGGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CCGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTTCG TTCGGGCCGG CGTTTTATCT
351 GATGTTCCGG CTGTCCGTTA TGCTGATTCG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCGG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTCTGTCG CGTTTCTGAC GGCGGCGGTT
601 ATTTTGTATT TCCCTGCCAA TATCCTGCCG ATTATGATTT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CCGCATCGCT TATATGTGGG
701 ACGAGGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCG
801 CTTTCGCTTTG CCAACGGGTG CAAAGAAATT GTCCGACCTC TACCGCATCA
851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CgTTCCACaC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CCGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```
m153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRVN VRLRQAMMVD VFFVSTLVAY
```


101 IKLSSVAEVR FGPAPYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNAV
 151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSLs ISSAFLTAAY
 201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
 251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
 301 LMCSFHYYAA RVIPGSAAVY FCLVVILTML SAYYFDPRLI WDKRASDGIA
 351 FNTEKHDX*

m153 / g153 96.1% identity in 358 aa overlap

m153.pep	10	20	30	40	50	60
	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLEAVMFVLTFGAPVLFLLCLYV					
g153	10	20	30	40	50	60
	MGFAYSMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLEAVMFVLTFGAPVLFLLCLYV					
m153.pep	70	80	90	100	110	120
	YAALIRKQAYPALRLATRVMLRQAMMVDVFPVSTLVAYIKLSSVAEVRFGPAPYLMFA					
g153	70	80	90	100	110	120
	YAALIRKQAYPALRLATRVMLRQAMMVDVFPVSTLVAYIKLSSVAKVRFGPAPYLMFA					
m153.pep	130	140	150	160	170	180
	LSVMLIRTSVSVPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
g153	130	140	150	160	170	180
	LSVMLIRTSVSVPQHWVYFQIGRLTGNNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
m153.pep	190	200	210	220	230	240
	LYRRRPKSLsISSAFLTAAYVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
g153	190	200	210	220	230	240
	LYGGRPKSLsISSAFLTAAYVILYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI					
m153.pep	250	260	270	280	290	300
	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
g153	250	260	270	280	290	300
	AAVIFSASILVPVLKIAAMSVLIAARFALPAGAKKLSHL YRITEAVGRWSMIDIFVIII					
m153.pep	310	320	330	340	350	359
	LMCSFHYYAARVIPGSAAVYFCLVVILTML SAYYFDPRLI WDKRASDGIAFNTEKHDX					
g153	310	320	330	340	350	
	LMCSFHYYAARVIPGSAAVYFCLVVILTML SAYYFDPRLI WDKRASDGIAFNTEKYDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 629>:

a153.seq

1	ATGGCGTTTG	CTTACGGTAT	GACGTATATC	GAGGTCGGGA	TACCGGGTGC
51	GGCATCCGTC	CTTTCGCTGC	CCGAGATGAT	GCGCCTGATG	GTGTTTCAGG
101	ATTATGGTTT	TTTGCCCGAA	GTGATGTTTG	TGCTGACCTT	CGGCGCGCCG
151	GTTCTGTTTC	TGCTGCTGTG	CCTGTATGTC	TATGCCGCGC	TGATACGGAA
201	ACAGGCGTAT	CCTGCGCTGC	GTTTGCAAC	GCGTGTGATG	GTGCGCTTGA
251	GACAGGCGAT	GATGGTGGAT	GTGTTTTTGG	TTTCCACTTT	GSTGGCGTAT
301	ATCAAGCTCT	CGTCTGTGGC	AGAGGTCGCG	TTCCGGATCGG	CGTTTTATCT
351	GATGTTCCGC	CTGTCGGTTA	TGCTGATTCG	GACTTCGGTA	TGGGTTCCCC
401	AGCATTGGGT	GTATTTTCAA	ATCGGGCGGC	TGACGGGGGA	TAATGCGGTT
451	CAGACGGCAT	CGGAAGGTAA	AACCTGTTGC	AGCCGCTGCC	TGTATTCCCG
501	CGACAGTGCC	GAATCCCCCT	GCGGCGTGTG	CGGTGCGGAA	CTGTACCGCC
551	GACGGCCGAA	AAGTCTGAGT	ATTTCTGTCG	CGTTTCTGAC	GGCGGCGGTT
601	ATTTTGTATT	TCCCTGCCAA	TATCTGCGCG	ATTATGATT	CGTCCAATCC
651	TGCCGCCACG	GAGGTCAATA	CCATCCTTAA	CGGCATCGCT	TATATGTGGG
701	ACGAGGGCGA	CAGGCTGATT	GCGGCGGTTA	TTTTCAGCGC	GAGTATTTTG
751	GTGCGGGTAC	TGAAGATTGC	GGCAATGTCG	GTTTTGATTG	CGTCCGCCCC
801	CTTCGCTTTG	CCAACGGGTG	CAAAGAAATT	GTCGCACCTC	TACCGCATCA

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851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGAAGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAEVR FGSAYFLMFA LSVMLIRTSV SVPOHWVYFQ IGRITGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL SISAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGI
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMRLMVFQDYGFLAEVMFVLTFGAPVLFLLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMRLMVFQDYGFLAEVMFVLTFGAPVLFLLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVPOHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSVSVPOHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSLSISAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
a153	LMCSFHTYAAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
51  CAAAAACAAC accttctct CCGCGTCTG GCTGGTCCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCAATTAAG GTATTGAGCA TCGATGTCGG ACGGTTACC CGAATCAAAC
251 TCGCGGACGA CCAAAAAGGC GTGGAAGTTA CTGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtaa CCGGTTTGGG TACGCTGCTT TCGGTTTCGT

```



```

401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCCGCCCGT TACGCCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTGTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcccg
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAATCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTGAGGCG CGATTTTATT TGATTCGCCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCCT GTCgaATACA AAGGGctga
951 TGTcggCATG GTTTCGGATG TCCCTTATTT TGACCGCAAT gacagCCTGC
1001 ACCTgtTTGA aaacggctgg aTTcccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAACAACA
1101 ATTCCAGACG GCCTTAAACA AAGGCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCGGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GGGGGTTTGG ATGACTTGCA GGTCAAATTG CCGGATTTCG
1301 TCGACaaatT CAACAATCTG CCATTggata aaACCGTTCG CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaaTCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACTCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGagacgta caAAATAcgc tgCaAAGTTT
1551 GGACAAAACC TTAaaagacg TtcaACCGT CATTAACACT TTGaaAGAAa
1601 aacCCaaCgc actGATTtTc aacaACAGCA GCAAAGAccc tATCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

g154.pep

```

1 MTDNSPPFNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKIERNRGP
51 VVTLLMDSAB GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FVVVKPRIDQ SGVTGLGTL LSGSYIAFTPG KSGEAKDVPQ
151 VQDIPPVTAI GQSGRLRLNI GKNDRIILNVN SPVLYENFMV QQIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLN SAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSPTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIBPS
351 RLEINADREQS KEHWKQFQT ALNKGLTATI SSNNLLTGK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLIDKFNML PLDKTVARLN
451 GSLAEKLSAL KSANAALSSI DKLVGNPQTQ NIPNELNQT LKRLITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKFNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

m154.seq

```

1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51 CAAAAACAAC ACCTTCCTCT CTGCCGCTCG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCAATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCTG
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCCGCCCGT TACGCCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTGTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGLCCAPA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAATCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTGCGGCG CGATTTTATT TGATTCGCCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTCCGCC GTGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCGACG TCCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAGC AAAGAACATT GGAACAACA
1101 ATTTACAGAC GCCTTAAACA AAGGCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

```


1201 TCACCTAAGC TGCACCCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTTGCA GGTCAAATG GCGGATTGTC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCCACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCACACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCGCAAT CGCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAACT TTAAGAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

m154.pep

1 MTDNSPPENG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51 VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTL LSGSYIAFTPG KSDEAKDVFQ
151 VQDIPPVTAI QSGRLRLNLI GKNDRIILNVN SPVLYENFMV QVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLINADEQS KEHWKQFPQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVARLN
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT LKELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

m154 / g154 97.8% identity in 553 aa overlap

	10	20	30	40	50	60
m154.pep	MTDNSPPPPNGHAQARVRKNNNTFLSAVWLVP LIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
g154	MTDNSPPPPNGHAQARVRKNNNTFLSAVWLVP LIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m154.pep	GIEVNNTVIKVL SIDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
g154	GIEVNNTVIKVL SIDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m154.pep	SGVTGLGTL LSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
g154	SGVTGLGTL LSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m154.pep	SPVLYENFMVGVQVESAHFDP SDQSVHYTIFIQSPNDKLIH SASRFWLESG INIETTGSGI					
g154	SPVLYENFMVGVQVESAHFDP SDQSVHYTIFIQSPNDKLIH SASRFWLESG INIETTGSGI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m154.pep	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYYTAFKQ					
g154	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEIANLPDDRSLYYTAFKQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m154.pep	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLINADEQS					
g154	SVRGLTVGSPVEYKGLNVGMVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLINADEQS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m154.pep	KEHWKQFPQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
g154	KEHWKQFPQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATRG					

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154 . pep	GGLDDLQVKLADLLDKFDKLPDKTVAEIINGSLAEIKSTLKSANAALSSIDKLVGKPQTQ					
	: : : : :					
g154	GGLDDLQVKLADLLDKFNNLPDKTVAEIINGSLAEIKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154 . pep	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	: : : : :					
g154	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154 . pep	NSSSKDPIPKGSRX					
	:					
g154	NSSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154 . seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCAATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCAGCAGCA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCTT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAAT CCGCCCCTCT GCCTGCCCTG
751 CTGTCCGGCG CGATTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACCGCGTT TTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTGCGCT GTCGAGTACA AAGGGCTGAA
951 TGTCCGCGTG GTTTCGGATG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTCAAGAC GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGCAGCCGA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATG GCGGATTGCG
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCTTGG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAAAC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAACC TTAAAAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCCAAACG GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154 . pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ

```



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151 VQDIPPVTAI QSGSLRLNLI GKNDRIILNVN SPVLYENFMV QVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAEIN
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT LKELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154/a154 100.0% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPFNHQAQARVRKNNTFLSAVWLVPLIALIAGGWLWVKEIRNRGPVVTLMLDSAE					
a154	MTDNSPPFNHQAQARVRKNNTFLSAVWLVPLIALIAGGWLWVKEIRNRGPVVTLMLDSAE					
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
a154	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVQVQDIPPVTAIGQSGSLRLNLIGKNDRIILNVN					
a154	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVQVQDIPPVTAIGQSGSLRLNLIGKNDRIILNVN					
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTGSGI					
a154	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTGSGI					
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSPKTKNSKNVKSSEDFTLYDSRSEVANLPDDRSLYYTAFFKQ					
a154	KLNSAPLPALLSGAISFDSPKTKNSKNVKSSEDFTLYDSRSEVANLPDDRSLYYTAFFKQ					
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
a154	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
a154	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
	370	380	390	400	410	420
m154.pep	430	440	450	460	470	480
	GGLDDLQVKLADLLDKFDKPLDKTVAEINLSLAELKSTLKSANAALSSIDKLVGKPTQ					
a154	GGLDDLQVKLADLLDKFDKPLDKTVAEINLSLAELKSTLKSANAALSSIDKLVGKPTQ					
	430	440	450	460	470	480
m154.pep	490	500	510	520	530	540
	NIPNELNQT LKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
a154	NIPNELNQT LKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540

444

```

                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1  atGAAaatcg GtateCCACG CGAGTCatta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gCCACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CCGTGCaggt TTGGCGGCAA GTTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGCGCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCTCCG ATTTCCCGCG CTCAGGCCTT GGACGCTTGT TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATAACCG CTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GGGCGCAGCG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTTG CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CTCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGCGGCG AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGGCGT GAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgaATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGgagcg gcgaaATCAC
1101 CTTCCCGCCT CCGcgaTTc aggtTTCgcg ccggccgCAG CAAAcgcgct
1151 ctgaAAAaag cgcGCCTGCC GCCAagcccg AgccGaaacc tghtCCcctg
1201 tggaAAAaac tcgGCCCGCG CGCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcacccgcag CATCTTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCTGCGT CATCGGCTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGatgtcggt aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAAATCG GTCAGGGcaa cggcttcgtT TCgctGCTGT
1451 CGTTTGTGTC CATCTGATT GCCGCGATCA ATATCTTCGG CGGCTTGGCG
1501 GTTACACGGC GTATGCTGAA TATGTTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDVPR ISRAQALDAL SSANISGYR AVIEAANAFG
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDLQES GSGGDYAKV MSDEFIAEM KLFQAEQAVEV
251 DIIITTAIP GKPAKPLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTGNVVKII GYTDMANRLA QSSQLYATN LVNLTKLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFP PPIQVSARPO QTPSEKAAPA AKPEKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAAEFNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAI LQIGQGNFV SLLSEVAILI AGINIFGGFA
501 VTRRMLNMEK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1  ATGAAAATCG GTATCCCACG CGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CCGTGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAACTG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```



```

301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GGCGGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GGCGACGGGC GGCAACTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGGAAAA AACTCGCGCC CGCCGTCATC GCCGCCGTCT TGGTACTGTG
1251 GGTCGGCGCG GTCGCACCCG CAGCATTCCT GAACCACTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCTTTGT TGCCATCTG ATTGCCGCA TCAACATCT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWVCLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDVPR ISRAQALDAL SSANISGYR AVIEAANAFG
151 RFFTQGITAA GKVPQAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAEM KLFAEQAKEV
251 DIIITTAAP GKPAKLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QQTPSEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVLVVGA VAPAAFLNHF IVFVLACVIG YVYVWNVSHS
451 LHTPLMSVTN AISGIIIVGA LLOIGQNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRMLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||||||
g155           MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m155.pep      AAVWVCLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDVPR
              |||:|||||
g155           AAVWACPLIYKVNAPSEGELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDVPR
              70      80      90      100     110     120

              130     140     150     160     170     180
m155.pep      ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQGITAAAGKVPPAQVLVIGAGVAGLAA
              |||||||
g155           ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQGITAAAGKVPPAQVLVIGAGVAGLAA

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446

	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAIPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAIPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPIQVSAQPQPTPSEKAVPAAKEPEPKPVPLWKKLAPAVIAAVLVLVWVGA					
g155	VTRDGEITFPPIQVSARPPQPTPSEKAAPAAKEPEPKPVPLWKKLAPAAIAAVLVLVWVGA					
	360	370	380	390	400	410
m155.pep	430	440	450	460	470	480
	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
g155	VAPAAFLNHFIVFVLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
	420	430	440	450	460	470
m155.pep	490	500	510			
	VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAATCG GTATCCACG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGCATACCC
201 TTTAATTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGCTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGCTCGAAG CCTTGCCGCG CAAGAAAGTG AACCGCTGG CAATGGACAT
351 GGTGCCCGCG ATTTCCGCGC CGCAGGCTTT GGACGNTTG TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCG CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GCGGCAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTGT CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGACGGGC GGCAACTGCG AACTCACCAA ACAGGGCGAA
901 TTGTTCTGTA CCGGCAACGG CGTGAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGCTGGAC
1051 TTCGAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTT CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCAAGC CCGAACCGAA ACCCGTTCCC

```



```
1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTCGGCGCG GTGCGACCCG CAGCATTCTT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAA TCGGTCAGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```
a155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIY SFLWPRQNEA
101 LVEALRAKKV NALAMDMVPR ISRAQALDXL SXMANISGYR AVIEAANAFG
151 RXFTGQITAA GKVPAPQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFFQES GGSGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAAP GKPAKXXXX EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LFVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLWVGA VAPAAFLNHF IVFVLACVIG YVVVWNVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIGQGNF VSLLSFVAIL IASINIFGGF
501 FVTRRLNMF RKG*
```

m155/a155 95.3% identity in 513 aa overlap

```
10      20      30      40      50      60
m155.pep MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
|||||
a155      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK
10      20      30      40      50      60

70      80      90      100     110     120
m155.pep AAVWVCPLIYKVNAPSEQLPLLNEGQTIYSFLWPRQNEALVEALRAKKVNALAMDMVPR
||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
a155      AAVWAYPLIYKVNAPSEDELPLLKEGQTIYSFLWPRQNEALVEALRAKKVNALAMDMVPR
70      80      90      100     110     120

130     140     150     160     170     180
m155.pep ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGQITAAGKVPPAQVLVIGAGVAGLAA
||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a155      ISRAQALDXLSXMANISGYRAVIEAANAFGRXFTGQITAAGKVPPAQVLVIGAGVAGLAA
130     140     150     160     170     180

190     200     210     220     230     240
m155.pep IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDFFQESGGSGDGYAKVMSDEFIAAEM
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a155      IGTANSLGAVVRFDTLXVAEQLESMGGKFLKLDFFQESGGSGDGYAKVMSDEFIAAEM
190     200     210     220     230     240

250     260     270     280     290     300
m155.pep KLFAEQAKEVDIIITTAAPGKPAKKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a155      KLFAEQAKEVDIIITTAAPGKPAKPKXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE
250     260     270     280     290     300

310     320     330     340     350     360
m155.pep LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a155      LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT
310     320     330     340     350     360

370     380     390     400     410     420
m155.pep VTHDGEITFPPPIQVSAQPQQTPEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLWVGA
||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a155      VTRDGEITFPPPIQVSAQPQQTPEKAAPAAKPEPKPVPLWKKLAPAXIAAVLVLWVGA
370     380     390     400     410     420
```


448

```

          430      440      450      460      470      480
m155.pep  VAPAAFLNHFIVFVLACVIGYVVVWVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF
          |||||
a155      VAPAAFLNHFIVFVLACVIGYVVVWVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF
          430      440      450      460      470      480

          490      500      510
m155.pep  VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX
          |||||
a155      VSLLSFVAILIASINIFGGFFVTRRLNMFRRGX
          490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
  1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
 51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101  ACAATCCTCG CGGTTTCTCG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151  CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCACCGT TTGCCGCCGC
201  CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251  CGCTTGCCGG ATTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301  ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTTCG
351  CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
  1  MTFAYWCILI ACLKPLFCAA YAKKAGGERF KDNHNPRGFL AHTQGAAARA
 51  HAAQQNGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLEI LFRLAFIWCY
101  IADKAALRSL MWAGGFACTV GLEVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
  1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
 51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101  ACAATCCGCG CGGTTTCTTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151  CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCACCGT TTGCCGCCGC
201  CGTTTTGACG GCACACGCAA CCGGCAATGC GCGCAATCG ACCATCAACA
251  CGCTTGCCCTG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAT
301  ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTTCG
351  CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
  1  MTFAYWCILI ACLKPLFCAA YAKKAGGERF KDNHNPRGFL AHTQGAAARA
 51  HAAQQNGFEA FAPFAAAVLT AHATGNAAQS TINTLACLEI LFRLAFIWCY
101  IADKAAMRSL MWAGGFACTV GLEVAAA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

```

          10      20      30      40      50      60
m156.pep  MTFAYWCILIACLKPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
          |||||
g156      MTFAYWCILIACLKPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
          10      20      30      40      50      60

          70      80      90      100     110     120
m156.pep  FAPFAAAVLTAAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV
          |||||

```



```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWAGGFACTV
              70      80      90      100      110      120

m156.pep  GLFVAAAX
            |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTGAAGCC TTTGCACCGT TTGCAGCCGC
201 CGTTTGTACG GCACACGCAA CCGCAATGC CGGACAAGCA ACCGTCAACA
251 CGTTGCGCGC CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTGTG
351 CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
51  HAAQONGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LFRFAFIWCY
101 IADKAALRSL MWVGGFVCTV GLFVAA*

m156/a156  90.6% identity in 127 aa overlap

              10      20      30      40      50      60
m156.pep    MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
              |||||
a156        MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAAQONGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep    FAPFAAAVLTAHATGNAAQSTINTLACLFI LFRFAFIWCYIADKAAMRSLMWAGGFACTV
              |||||
a156        FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWVGGFVCTV
              70      80      90      100     110     120

m156.pep    GLFVAAAX
              |||||
a156        GLFVAAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgccctgcgc cgcgaattgC gCgGgcggcg
51  ttgcgCAATg GGgcgagacg tGCGggCGGC GGCGgCgatA Aaaatcaacc
101 gcctgctcaa aCGTtataac AAGCGCggtc gGaAaatcgG CGTGTATTgg
151 cCGATGGGCA AGGAATTGcg TTTGGGCGGc tTgtcCGCG CGGCGCAAAA
201 ACGCgCGGCA AAactctatc tgccttATAT CGAACCgCAC ACgCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACgCAAGCGC
301 GGtagggCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAAG
401 GCTACCGTTT GGGCAGGCA GCGGCTATT ACgATGCGAC GCTTTCGGCG
451 ATGAAATACC GTTTCAGGC GAAAACCGTG GCGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACGTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```


This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
51  PMGKELRLGG FVRAAQKRG A KLYLPYIEPH TRRMWFTYP ERGMERERKR
101 GRAKLHVPOF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
1  ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
51  TTGCGCAAATG GGGCGGGACG TCGGGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGGC GAAAATCGG CGTGATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACCTCTACC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTCCGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GCGGCTATT ACGATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTTCAGGC AAAAACCCTG GCGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTGCCG TCGAGGCGCA CGACCGGTCT TTGGACGGT
551 TTGTGTCGGA GCGGGGATA TTGTGTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLKRYI KKGRKIGVYW
51  PMGKELRLDG FVRAAQKRG A ELYLPYIEPR SRRMWFTYP ADGVKQERKR
101 GRAKLHVPOF AGRKKRVHDL NLLVPPVGM DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

m157.pep	10	20	30	40	50	60
	MRNEEKRALR	RELGRRSQM	GRDVRAAATV	KINHLKRYI	KKGRKIGVYW	PMGKELRLDG
g157	10	20	30	40	50	60
	MRNEEKRALR	RELGRRSQM	GRDVRAAAAI	KINRLKRYI	KRGRKIGVYW	PMGKELRLGG
m157.pep	70	80	90	100	110	120
	FVRAAQKRG	AELYPYIEPR	SRRMWFTYP	PADGVKQERK	GRAKLHVPOF	FAGRKKRVHDL
g157	70	80	90	100	110	120
	FVRAAQKRG	AKLYLPYIEPH	TRRMWFTYP	PERGMERERK	GRAKLHVPOF	FAGRKIRVHGL
m157.pep	130	140	150	160	170	180
	NLLVPPVGM	DRLGYRLGQ	AGGYDATLSA	MKYRLQAKTV	GVGFACQLVD	RLPVEAHDRS
g157	130	140	150	160	170	180
	SVLLVPLVG	IDREGYRLG	QAGGYDATLSA	MKYRLQAKTV	GVGFACQLVD	RLPREAHDL
m157.pep	190					
	LDGFVSEAGI	LCFX				
g157	190					
	LDGFVSEAGI	LCFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
1  ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCG
51  CGCGCAGATG GGCATCAAG GCGGTTGCG GCGGGGCAA ACGATTAACC
```


451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACTTTATC TGCCTTATAT CGAACC GCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCCGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

```

a157.pep
  1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
 51 PMGKELRLDG FVRAAQKRG A KLYLPYIEPR SRRMWFTYP ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELRRRSQMGRDVRAAATVKINHLLKRYIKRGRKIGVYWPMGKELRLDG					
a157	MRNEEKHALRRELRRARAQMGHQGRLAAGQTINRLLKRYIKRGRKIGVYWPMGKELRLDG					
	10	20	30	40	50	60
m157.pep	FVRAAQKRGAEYLPLPYIEPRSRMWFTYPADGVKQERKGRAKLHVQFAGRKRVHDL					
a157	FVRAAQKRGAKLYLPYIEPRSRMWFTYPESGMEERERIRGRAKLNVPQFAGRKIRVHGL					
	70	80	90	100	110	120
m157.pep	NLLLVFVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
a157	SVLLVPLVGIDREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL					
	130	140	150	160	170	180
m157.pep	LDGFVSEAGILCFX					
a157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

```

g158.seq
  1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGAAAG
 51 CCGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGCGGT GAAcCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTCGCGGT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCgaC TTTGCTCGT TTCTTCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TCGTGCACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCTT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGatgC GCAGGGAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```


452

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
851 TATTTTGGGA TTTTATTAGT AAGGAACTGG GAAAAAATAT GAATAGAACG
901 AATACCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

```

g158.pep
  1 MKTNSEELTV FVQVVEGSGF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFRRA QRILQEMAAA ETEMLAVHEV PQGVLRVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR
301 NTK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

```

m158.seq
  1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTTGAGCGT GGATTCCGCG
301 ATGCCGATGG TGCTGCATCT GCTGCGCGCG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCCGAC TTTGCTCGT TTCTTCCGAA GGCTATATCA
401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCCCG AGAATTGGAC
451 GATTCCGGGC TCGGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
501 CGCCAGTCTT GAATACCTGG CAAACACGCG CACGCCGCAA TCTACAGAAG
551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGATGC GCAGGGAAT CCCTATAAGA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT
701 GCGGTATTGT TTGCTTATCA GATTTTGTG TTGACAACGA CATCGCTGAA
751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
851 TATTTTGGGA TTTTATTAGT GAGGAACTGG GAAACAATCT CTGTGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

```

m158.pep
  1 MKTNSEELTV FVQVVEGSGF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFRRA QRILQEMAAA ETEMLAVHEI PQGVLSVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
251 GKLIPLLAEQ TSKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

```

          10      20      30      40      50      60
m158.pep MKTNSEELTVFVQVVEGSGFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT
          |||
g158      MKTNSEELTVFVQVVEGSGFSRAAEQLEMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT
          10      20      30      40      50      60

          70      80      90     100     110     120
m158.pep EEGAQYFRRAQRILQEMAAAEETEMLAHVHEIPQGVLSVDSAMPMVLHLLAPLAAKFNERYP
          |||
g158      EEGAQYFRRAQRILQEMAAAEETEMLAHVHEVPQGVLRVDSAMPMVLHLLAPLAAKFNERYP
          70      80      90     100     110     120

```


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	130	140	150	160	170	180
m158.pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLSLSCGCGIVCLS					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLSLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNRLRLRVFLDFLVEELGNNLCGX					
g158	DFLVDNDITEGKLIPLFAEQTSNKTHPFNAVYYSDKAVNRLRLRVFLDFLVKELGKMNRT					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAACCA	ATTCAGAAGA	ACTGACCCTA	TTTGTTCAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCGCG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGACAG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCCG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGGAAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTGTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTGGGA	TTTTTTAGTG	GAGGAAGTGG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVEGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRR	QRILQEMAAA	ETEMLAHVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQ	LGFTPEGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLS	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYYSKAVN	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
a158	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRQRILQEMAAAEETEMLAHVHEIPQGVLSVDSAMPVHLHLLAPLAAKFNERYP					
a158	EEGAQYFRRQRILQEMAAAEETEMLAHVHEIPQGVLRVDSAMPVHLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSKTHPFFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GGCGAAACTT  CCCCgcGTCC  GGTCGGCAGC  GGCgATATTG  TATTTTCCC
201 GCGCGGCTTG  GGTcATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATACGACAA  AACGgcACAT  TTATGGTCAA  ACAGTcCGGC
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351 CGCCGATTTG  ATGAACGGGC  TGCCGGAAC  CGTTTTCTG  AACATTGCCC
401 ATCCAAGTTT  GCAGTATGTG  GTTTCAATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTcCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAActCT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGTGATAG  ACAAAccGGA  AGACGAATGG  AATATTGACA  AAATGTTGTC
651 CGCCGCCAAT  ATGTCGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGcACGCC  TTTGTGAACC  ATATCCGCCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAAC  CCCGgATTcG  GTTTTGGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAaA  CGCATTTcGG  CAAGGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAa  TACCGGAaAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTVSUVN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAaAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKKT PDS  VLEVALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTcGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACCGCA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CGGCTATCTC
151 TGcATCGACG  GCGAAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTTCcCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTcCGGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCgCCC  GTTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGTTTTC  ATGGTCAACG  CATTGTcGTC

```



```

501 CGTCCTGCTG GTGCTTATCC TCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAATCTC GGGCGTATTG AAAGGTGGC AGGACAAACG TTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTCTGGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

m160.pep	10	20	30	40	50	60
	MDILDKLVDF	AQLTGSVDVQ	CLLGGQWSVR	HETLQREGLV	HIVTSGSGYL	CIDGETSPRP
g160	MDILDKLVDL	AQLTGSADVQ	CLLGGQW---	HETLQREGLV	HIVTAGSGYL	CIDGETSPRP
	10	20	30	40	50	
m160.pep	70	80	90	100	110	120
	VSTGDIVFFP	RGLGHVLSHD	GKGESLQPD	MRQHGAFTVK	QCGNGQDMSL	FCARFRYDTH
g160	VGTGDIVFFP	RGLGHVLSHD	GKYGESLQPD	IRQNGTFMV	KQCGNGLDMS	LFARFRYDTH
	60	70	80	90	100	110
m160.pep	130	140	150	160	170	180
	ADLMNGLPET	VFLNIAHPSL	QYVVSMLQLE	SKKPLTGTVS	MVNALSSVLL	VLILRAYLEQ
g160	ADLMNGLPET	VFLNIAHPSL	QYVVSMLQLE	SEKPLTGTVS	VVNALPSVLL	VLILRAYLEQ
	120	130	140	150	160	170
m160.pep	190	200	210	220	230	240
	DKDVELSGVL	KGWQDKRLGH	LIQKVIDKPE	DEWNVDMVA	AAANMSRAQL	MRRFKSRVGLS
g160	DKDVELSGVL	KGWQDKRLGH	LIQKVIDKPE	DEWNVDMVA	AAANMSRAQL	MRRFKSQVGLS
	180	190	200	210	220	230
m160.pep	250	260	270	280	290	300
	PHAFVNHIRL	QKGALLLKKN	PDSVLSVALS	VGFQSETHFG	KAFKRQYHVS	PGQYRKEGGQ
g160	PHAFVNHIRL	QKGALLLKKP	DSVLEVALSV	GFGQSETHFG	KAFKRQYHVS	PGQYRKEGGQ
	240	250	260	270	280	290
m160.pep	KX					
g160	KX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
1 ATGGACATTC TGGACAACT GGTGATTTC GCCCAATTGA CGGGCAGTGT
51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```



```

101 TGCAACGCGA AGGATTGGTA CACATTGTTA CATCGGGCAG CGGCTATCTC
151 TGCAATCGACG GCGAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTCCCG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCAGCA ACGGACAGGA TATGAGCCTG TTTTGCGCCG GTTCCGCTA
351 CGACACCCAC GCCGATTGTA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATGTGCTC
501 CGTCTGCTG GTGCTTATCC TGCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCTT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTGCGGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGTCATAT ACCGGAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLEPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||||
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||||
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          70      80      90      100     110     120

          130     140     150     160     170     180
m160.pep ADLMNGLEPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTVS MVNALSSVLL VLILRAYLEQ
          |||||
a160      ADLMNGLEPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTVS MVNALSSVLL VLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS
          |||||
a160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKQYHVS PGQYRKEGGQ
          |||||
a160      PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKQYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep KX
          ||
a160      KX

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGCC
51  GCGGCGCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGCGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGTGCTG CTCCTTGCTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAGGAA
451 CCGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAAGTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GCGGTGGCGA TGTCTGCGgt ttgggcgacg
601 Ctgaccggct ggCACaccT GTCCTTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCCCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTTTCTg ggcgaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCCAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVTLGAAAVL RRDTRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPFSRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAFFEL GEELFWQEIL GMCIIILSGI LSSIRPIAFK ORLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGCC
51  GCGGCGCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGCG CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGTGCTG CTCCTTGCTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAAGTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCTGCGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCTTTTCCA TCGGCAGTTT ATCTGTCTGT
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCGC TTTCTATATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTTTCTG GCGGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVALGAAAVL RRDXTFTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPFSRSGQE

```



```

151 TAALAGLAGG AMGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSEFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	: : : :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLSTVTLGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMVGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	: : : :					
g161	RRDTFRTPHWKNHLNRSVMVGTGAMLLLFYAVTHLPLTTGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFAVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	: : : :					
g161	RISVYTQAVLLLGFAVLLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSEFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT					
	: : : :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSEFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSAALSAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	: : : :					
g161	VASLSYMTVVFSAALSAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	X					
g161	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

```

a161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGCGCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCACT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTGTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGCGTGCTG CTCTTGGTT
401 TTGCCGCGGT GGTATTGCTG CTTAATCCCT CGTTCGCAG CGGTCAAGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAAGTGT CTTGGCGGG CGAACCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTATCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCTT GTCCTTTCCA TCGGCAGTTT ATCTGTCGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCACT GTCGATGACG CGGCCTACA
701 AAGTCGCGCA CAAATTCACG GTTGCCCTCG TTTCTATAT GACCGTCGTT
751 TTTTCGCTC TGTCTGCGC ATTTTCTCTG GCCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA

```


851 TCCGCCCCAC TGCCTTCAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLES
51 TVALGAAAVL RRDFTERTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLIKE RISVYTQAVL LLGFAGVLL LNPFSRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAFFL AEELFWQEL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFERTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTYTSSIFLAVFSFLIKE					
a161	RRDTFERTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTYTSSIFLAVFSFLIKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGAFAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGAFAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAFFLGEELFWQELGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAFFLAEELFWQELGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTTAACGTT TTCCATTTTt
151 ctgGGTTTtc tgctGATACT CTCGGTCAGC GGTGGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTCCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCCTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTGA TGCATTATT TTCGGACATT ACGGTCGGCG CGCCGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCAGC
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTGGCTTA TTTGGTTTC


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451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACTG
751 GGCCTTGCGT TTTTGTGCT GTTTTGTGTT TTGGCGGCGG ACCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGGCCCT CAGTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCCGGGTT TTGCTCATCC CCGGCTGTT CGGCGTTTTCG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTAA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGCTCATTT CCCTGTTTTT TGTAACTTCT GCCGACTCCG GGATTATATG
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGCTGGC
1301 AGGCGGTTAT GTGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCTGA TTGTTTCCCT
1401 GCGGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GAGCGAGGAG CAGGATATT TAAATTCCT CAAACATACC GCATCGCCCC
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTGCTCAT
1701 TCGGAAAGAG ACATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTGTTGG ATGATGTCGG TCAGGAACTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1  MVILTTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPALARS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFESWTVLYW AWCWSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTS
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELOR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTYYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1  ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACG
401 CTGGTTCGGT GTACGGTACG ATTGCATTGG CTTGGCTTA TTTGCGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

```



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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACTAC CTCGGAAATC
851 TGGTGGCGCT CAGTTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTCG
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACTTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTAT GTGGGGCGTG CTGATGCTCG CCGTGGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGGC CTGCTGATGC TGATAATGTG TTTAGCCTG TGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCTT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTTGG ATGATGTCGG TCAGGAAGT
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
  1 MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51 LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSEK TYAYEREHKP
301 WFEWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLML
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

	10	20	30	40	50	60
m163.pep	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
g163	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m163.pep	SLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	:					
g163	GLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITVGAPHRQQ					
	70	80	90	100	110	120
	130	140	150	160	170	180

462

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFGVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	GVKVLSENLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSEKTYAYEREHKP
g163	GVKVLSENLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSEKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	WFESWTVLYWAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQLKFLKQTASPAHMLQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVRIMSQTQEQLKFLKHTASPAHMLQR
	490 500 510 520 530 540
m163.pep	ELSEEYGLSVRVDMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

a163.seq	1	ATGGTTATTT	TGACGACTTT	GTTTTTTGTG	TGTGTTTTGG	TGGTATTGGT
	51	TTTAACCGTG	CCGGATCAGG	TGCAGATGTG	GCTCGATCGG	GCAAAAGAAG
	101	TCATTTTAC	CGAGTTCAGC	TGGTTTTATG	TTTAACGTT	TTCCATTTTT
	151	CTGGGTTTCC	TGCTGATACT	CTCGGTCAGC	AGTTTGGGAA	ACATCAGGCT


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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCCTGTCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGCCT TTTTGCTGCT GTTTTTTGTG TTGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAATTC
851 TGGTGCGCCT CAGTTTAAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCCGGGTT TTGCTCATCC CCGGCCGTGT CGGCGTTTTC
1051 TGGTTTACCG TCTTCGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTAA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGCGGTG CTGATGCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGAT
1451 TGATGCGGGA TAAGAAATAT TTTGAGACCC GGGTTAACC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGAGCA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAAC TG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLEAAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSEK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCESL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFESIFLGFLILSVS
          |||
a163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFESIFLGFLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLEAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

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|||||
a163      SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
              70      80      90      100     110     120

              130     140     150     160     170     180
m163.pep  QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
              |||||
a163      QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
              130     140     150     160     170     180

              190     200     210     220     230     240
m163.pep  MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
              |||||
a163      MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
              190     200     210     220     230     240

              250     260     270     280     290     300
m163.pep  GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              |||||
a163      GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              250     260     270     280     290     300

              310     320     330     340     350     360
m163.pep  WFESWTVLYWAWWCSWAPFVGLFIARISKGRITIREFVFGVLLIPGLFGLVWFTVFGNTAI
              |||||
a163      WFESWTVLYWAWWCSWAPFVGLFIARISKGRITIREFVFGVLLIPGLFGLVWFTVFGNTAI
              310     320     330     340     350     360

              370     380     390     400     410     420
m163.pep  WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              |||||
a163      WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              370     380     390     400     410     420

              430     440     450     460     470     480
m163.pep  ITSRDKGLSAPRWQAVMWGVLMSSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
              |||||
a163      ITSRDKGLSAPRWQAVMWGVLMSSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
              430     440     450     460     470     480

              490     500     510     520     530     540
m163.pep  WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKQTASAMHELQR
              |||||
a163      WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKHTASAMHELQR
              490     500     510     520     530     540

              550     560     570     580     590     600
m163.pep  ELSEEYGLSVRVDMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              |||||
a163      ELSEEYGLSVRVDMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              550     560     570     580     590     600

              610     620     630     640     650     660
m163.pep  HQTTYKPYAYFFDGRVGVDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
              |||||
a163      HQTTYKPYAYFFDGRVGVDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
              610     620     630     640     650     660

m163.pep  X
          |
a163      X
```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGCGC TTCCTGTTCC CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAACGCCCC GTCGAAAAAA TCATTTGGAC GGACAAAAGC
151 CGGCCGCGCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCCG CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTcctg ccgatgTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCCC ttttccaacG TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTcAGATG GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGCGCGCCTT TTGGCGGAAC AAACATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCGTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751 GCCCGCAGCG TCGGCATCCC CTGCGCCGGT TTGGAAGCCA AAGCCGTGCA
801 TGAAGAATTG GTCGAAGTGC CGCGCGCGCA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTC GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGCGTG GTTGAaaACG GGCgATTTCG TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GCGGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGG
1151 GCGAGGACGA aatccgccc caccTGCgTA CCGTGTGGC AAATTTCAAA
1201 ATCCCAAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDLGRQPR INDLAHIYT SGTGTGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVFP FSNVLQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKRD LIISKQNVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACCGA AACGGCACGG CAGTGTTCGA CGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTTCGGCA CACGGTCGCG CTGGCGGTTT CCAATTCAC
201 AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTCGCG
251 TACCGATGAA CACATTTTGG AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAA CGCCCGTCGA AAAATCATT TGGACGGACA
401 AAAGCCGTC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCGCT TCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCC CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTC CAACGTTTTC
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATTTC CCGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA

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951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCTGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTGAT
1251 TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTV A LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WDKSRPTGE TAEGDAFFED
151 VRRFPEKPD L GRQPRINDLA HIIYTSGTTG HPGKALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQTLKLRATV FLGVPAIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVELIVRG GSVMRGYLMN PAATDETIVN GWLKTGDFVT
401 IDEDFGFI FV DRKKDLIISK QONVYPREIE EEIYKLDAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGVKLKRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100     110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      MNTFLKNSEYAYILNDCKARFLFASAGLSK
          10      20      30

          120     130     140     150     160     170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT
          40      50      60      70      80      90

          180     190     200     210     220     230
m164.pep  SGTTHGHPKGALISYANLFANLNGIERIFKISKRDRFIVFLPMFHSFTLTAMVLLPIYMAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      SGTTHGHPKGALISYANLFANLNGIERIFKISKRDRFIVFLPMFHSFTLTAMVLLPIYMAC
          100     110     120     130     140     150

          240     250     260     270     280     290
m164.pep  SIILVKSVPFSPNVLKQTLKLRATVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAP
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      SIILVKSVPFSPNVLKQALLKLRATVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAP
          160     170     180     190     200     210

          300     310     320     330     340     350
m164.pep  LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEEL
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEEL
          220     230     240     250     260     270

          360     370     380     390     400     410

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m164.pep    VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164        VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
             280      290      300      310      320      330

             420      430      440      450      460      470
m164.pep    LIISKGQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
g164        LIISKGQNVYPREIEEEIHKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
             340      350      360      370      380      390

             480      490      500      510
m164.pep    HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
             |||||||||||||||||||||||||||||||||||||||||||||||||
g164        HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
             400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1   ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCTATT TCGCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTGG AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCTCG GCCGGCCTGT CAAAAGAATT
351 GGGCGGCTTG AAGCGCGAAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTGGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCC CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTTC
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCTGCG CCGGTTTGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCTGTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCGC TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1   MNRTYANFYE MLTAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFEKPDLD GRQPRINDLA HIIYTSGTTG HPGKALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQALLKRATV FLGVPAIYTA MSKTIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLVKA
351 VDEELVEVPR GEVGEIVRGG SVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDEGFIFIV DRKKDLIISK QNVYPREIE EEIYKLDAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHLRTV LANFKIPKQI HFKDGLPRNA

```


501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNGNGTAVFDGKEKTAYRALKQAEAEVAAYLQNIQVKGFDTV					
a164	MNRTYANFYEMLTAAACRKNGNGTAVFDGKEKTAYRALKQAEAEVAAYLQNIQVKGFDTV					
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETT					
a164	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETT					
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKDRDFIVFLPMFHSFTLTAMVLLPIYMACSIIIV					
a164	HPKGALISYANLFANLNGIERIFKISKDRDFIVFLPMFHSFTLTAMVLLPIYMACSIIIV					
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKSRATVFLGVPPIYATAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	KSVFPFSNVLKQALLKSRATVFLGVPPIYATAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPPLGLEKAVDEELVEVPR					
a164	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPPLGLEKAVDEELVEVPR					
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
a164	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
	430	440	450	460	470	480
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq

1 ATGGCTGAAG CGACAGACGT TGTCTGGTG GCGGCGGCA TTATGAGCGC


```

51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTc CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCCG GGAAGGCAAG
301 TTGGAagaCA ATTCCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAA ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCTCTT CCTCGCGCGG GCGGCGCGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCCCGC CGATGTCCGT CCCGCACCTC
901 GACACAGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CcTGCTGGgC gAaTTGcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLOK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAEQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTc CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGCGCGG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCCG GGAAGGCAAG
301 TTGGAAGACA ATTCCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAAACT TTTTGAAAA ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCTCTT CCTCGCGCGG GCGGCGGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACAGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMRGR RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF

```


Homology with a predicted ORF from *N. gonorrhoeae*

m165.pep	MAEATDVLVGGGIMSATLGVL	KELEPSWEITLIERLEDVALE	SSNAWNNAGTGH	SALC
g165	MAEATDVLVGGGIMSATLGVL	KELEPSWEITLIERLEDVALE	SSNAWNNAGTGH	SALC
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED			
g165	ELNYAPLGADGVINPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED			
m165.pep	HCSYLOKRYDAFKTQKL	FENMEFSTDRNKISDWAPLMRGRDENQPVAANYSAEGTDVDF		
g165	HCRYLOKRYDVFKTQKL	FENMEFSTDRNKISDWAPLIMRGRDENQPVAANYSAEGTDVDF		
m165.pep	GRLTRQMVKYLOQKGVKTEFN	RHVEDIKRESDGAWVLK	TADTRNPDGQTL	LRTRFLFLGA
g165	GRLTRQMVKYLOQKGVKTEFN	RHVEDIKRESDGAWVLK	TADTRNPDWQTL	LRTRFLFLGA
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYGGASVGAPPM			
g165	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAEQHNAKVYGGASVGAPPM			
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGS	LMDLPLSIHMDNLYPMLCAGWANMPLTK		
g165	DTRNVDGKRHLMFGPYAGFRSNFLKQGS	FMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG		
g165	ELRX			

```

a165.seq
1  ATGGCTGAAG  CGACAGACGT  TGTC'TTGGTG  GGC'GCGCGCA  TTATGAGCGC
51  GACTTTGGGC  GTT'TTGCTA  AAGA'ACT'CGA  ACCGT'CTTGG  GAAAT'CACCC
101 TGATTGAACG  CTTTGAAGCA  GTGGCGTTGG  AATCGTCAA  CGCGT'GGAAC
151 AACGCCGGCA  CGGGGCATTC  CGCGCTGTGC  GAATTGAAC  ATT'GCGCGTT
201 GGGT'GCAAAT  GGGATTATCG  ATCCGGCGCG  CGCCCTCAAT  ATT'GCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGCGA  CGTTGGT'CGC  GGAAGGCAAG
301 TTGGAAGACA  ATTCCTTCAT  CAATGCCGTG  CCGCATATGT  CTTTGGT'GAT
351 GAATGAAGAC  CATTGT'TCTT  ATCTTCAAAA  AGCTTATGAC  CGTTT'AAAAA
401 CCCAAAAACT  TTTTGA AAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CTC'CGCTGAT  GATGCGCGGG  CGGGACGAAA  ACCA'ACCCGT
501 CGCGGCCAACT  TACTCCGCGT  AAGGCACGGA  TGTCGATTTC  GGACGGCTGA
551 CGCGCCAAAT  GGTGAAATAT  TTGCAGGCGA  AGGCGGTAAA  AACCGAGTTT

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601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGGCGGCG CGCTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCT GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACCTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATAA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCGA AACCCCGACG
1151 ACTGGGAACT CATACCCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CACACGCTCG CTCGCGCAT TGCTGGGCGC GTGCGCGGCG GCATCGACCG
1301 CCGTGCCTCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGACCC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

a165.pep

```

1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPGKGYG GFPVSGLFRR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYPEA NPDDWELITA QORVQIIKDD
401 SEKGGLVQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAQVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

m165.pep	10	20	30	40	50	60
	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
a165	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
	10	20	30	40	50	60
m165.pep	70	80	90	100	110	120
	ELNYAPLGANGIIDPARALNIAEQFHSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
a165	ELNYAPLGANGIIDPARALNIAEQFHSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
m165.pep	130	140	150	160	170	180
	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAGTDVDF					
a165	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAGTDVDF					
	130	140	150	160	170	180
m165.pep	190	200	210	220	230	240
	GRLTRQMKYKYLQKGKVKTEFNHVEDIKRESGAWVLKTADTRNPDGQLTLRTRFLFLGA					
a165	GRLTRQMKYKYLQKGKVKTEFNHVEDIKRESGAWVLKTADTRNPDGQLTLRTRFLFLGA					
	190	200	210	220	230	240
m165.pep	250	260	270	280	290	300
	GGGALTLLQKSGIPGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGGAPPMSVPHL					
a165	GGGALTLLQKSGIPGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGGAPPMSVPHL					
	250	260	270	280	290	300

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	310	320	330	340	350
m165.pep	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK				
a165	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG				
	310	320	330	340	350
					360
a165	ELRKTKEERFASLLEYYPEANPDDWELITAGQVRVQIIKKDSEKGGVLQFGTEIVAHADGS				
	370	380	390	400	410
					420

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTCTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cCGGTGGAAC
151 AACGcCGca CGGGGCATTc CGcGCTGTGc GAATTGAACT AtgcgcCGT
201 GGGtgccgac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctggTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAACGAAGAC CACTGCCGTT ACCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TATTCGCCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACC GCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCTCTT CCTCGCGCGC GCGGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCGGCCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAATTCC TCAAGCAAGG CTCGTTTATG GATTGCGCG
1001 TGTCCATCCA TATGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTt gCCTCCCTGC TGgaatacta cccGaggcag acccGACGac
1151 tggctactcat acgcaggnc acGCGTcata tcattanata tgactCgaaa
1201 ctgcgcgtgc tgcagttgta cgagattgtg ccaCGCGacg ctcgctcgcg
1251 cattctggag cgtcgcggcg catcacgctn tgcgctgata tccgctgatg
1301 acactgctcc gaGCGcgccc gtcttggaag gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCRYLQKRYD VFKTQRLFEN MEFSTDNRNI
151 SDWAPLIMRG RDENPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPGKGKYG GLPVSGLFER NSNPETAQEH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPLMRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPKQ TRRLVLITQX TRHIIYDSK
401 LRVLQLYEIV PRDARSRIE RRGASRXALI SADDTAPSAP VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTCTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CCGGTGGAAC
151 AACGCCGCA CGGGGCATTc CGCGCTGTGc GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCCG GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAACCT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCGCCG AAGGTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACC GCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGCG GCAGCTCACC CTCCGTACCC
701 GCTTCTCTT CCTCGCGCGC GCGCGCGCGC CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCGGCCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG

```



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851 TGTACGGGCA GGCTTCCGTC GCGCGCCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTGTCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```

1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMRGR RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTFLFLGA GGGALTLLQK
251 SGIPEGKGYG GPPVSGLFFR NSNPETAQH NAKVYGQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA QQRVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLGVLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
g165-1	MAEATDVVLVGGGIMSATLGVLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165-1	ELNYAPLGADGVINPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDNQPVAAANYSAEGTDVDF					
g165-1	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLMRGRDNQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165-1	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSVPHL					
g165-1	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m165-1.pep	DTRNVDGKRHLMFPGYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG					
g165-1	DTRNVDGKRHLMFPGYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKIDSEKGGVLQFGTEIVAHADGS					
g165-1	ELRKTKEERFASLLEYPR-QTRRLVLTQXTR-HIIXYDS-KLRVLQLYEIVPRDARSR					
	370	380	390	400	410	
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNNPERADEIIA
 : |||
 g165-1 ILERRGASRXALISADDTAPSPVLESVX
 420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq

```

1  ATGCGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGCA CCGGGCATTG CCGCGTGTGC GAATTGAACT ATGCGCCGTT
201 GGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATGTCTT ATCTTCAAAA ACCTTATGAC CGCTTTAAAA
401 CCCAAAAACT TTTTGAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCGCGCG CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCG AAGGCACGGA TGTGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGCG CGTGGGTGCT
651 CAAAACCGCC GATACCGCA ACCCGACGG GCAGCTCACC CTCGGTACCC
701 GCTTCTCTCT CCTCGGCGCG GCGGCGCGCG CGTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGCAA AGGCTACGGT GGCTTCCCG TGTCGGGCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACACAC AACGCCAAAG
851 TGTACGGGCA GGTCTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACAGCA ACCTGGACGG CAAACGCCAC CTTATGTTG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAG CTCACCTATG GATTGCGCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGCTGGGC GAATGCGTA AAACCAAGA
1101 AGAAGCTTTC GCCTCCCTGC TGGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATCCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVFTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTFLFLGA GGGALTLQK
251 SGIPEGKGYG GFFVSGLFFR NSNPETAQEH NAKVYGOASV GAPPMSPVPHL
301 DTRNVGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMRLAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GORVQIIKID
401 SERGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLNE NPERADEIIA YTAKVLDI*

```

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
m165-1	MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
a165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165-1	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDNQPVAAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDNQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDNQPVAAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDNQPVAAANYSAEGTDVDF					
	190	200	210	220	230	240

475

a165-1.pep GRLTRQMVKYLGKGVKTEFNHRHVEDIKRES DGAWVLKTADTRNPDGQLTLRTRFLFLGA
|||||
m165-1 GRLTRQMVKYLGKGVKTEFNHRHVEDIKRES DGAWVLKTADTRNPDGQLTLRTRFLFLGA
190 200 210 220 230 240

250 260 270 280 290 300
a165-1.pep GGGALTL LQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQGASVGAPPMSVPHL
|||||
m165-1 GGGALTL LQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQGASVGAPPMSVPHL
250 260 270 280 290 300

310 320 330 340 350 360
a165-1.pep DTRNVDGKRHLMFPGPYAGFRSNFLKQGS LMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
|||||
m165-1 DTRNVDGKRHLMFPGPYAGFRSNFLKQGS LMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
310 320 330 340 350 360

370 380 390 400 410 420
a165-1.pep ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
|||||
m165-1 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
370 380 390 400 410 420

430 440 450 460 470 480
a165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
|||||
m165-1 LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
430 440 450 460 470 480

489
a165-1.pep YTAKVLDIX
|||||
m165-1 YTAKVLDIX

a165-1/p33940

sp|P33940|YOJH_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF_ID:o372#5; similar to [SwissProt Accession Number
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical
to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct
identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

Query: 3 EATDVVLVGGGIMSATLGVL LKLEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30 QETDVL LIGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63 NYAPL GANGIIDPARALNIAEQFHVS RQFWATLVAEGKLED-NSFINAVPHMSLV MNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90 NYTPQ NADGSISIEKAVAIN EAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQ KRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAANYSAEGTDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150 VNFLRARYAALQQSSLFRGMRYSEDHAQIK EWA PLVMEGRDPQQKVAATRTEIGTDVNYG 209

Query: 182 RLTRQMV KYLGKGVKTEFNHRHVEDIKRES DGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210 EITRQLIASLQKKS NFSLQLSSEVRALKRNDNTWTVTVADLKNGT AQ-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQGASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVNVNHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVDGKRHLMFPGPYAGFRSNFLKQGS LMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329 DTRVLDGKR VVLFGEFATFSTKFLKNGSLWDLMSSTTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389 QVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDAEKGGVLR LGTEVVS DQQT 448

Query: 421 XXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLEKVFGRVSSPQWQATLKAIVPSYGRKLNQDVAATERE 508

Query: 479 IAYTAKVLDI 488
 + YT++VL +

Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq

```

1   atggcgggcgg cggaaataaa acgccccctc gctgtcgatt tccagcacat
51  agcgtccgtt ctgcacggcg gcatagccgc ttttgccctg ctgatatggg
101 tgcagggcgg aatgcgaaat caggtaatca gtcagtttgc cgcggtcttc
151 ggcgatattg cccaccagtt tggcaaacaa ggtatggcac acgcggtttt
201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
251 acgacggcct ccaagtcggt gggatgcttt ccggtcagcc ggacggcggt
301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt
351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
401 ttgtcgatgt atttgacttt gaaaaccggt ttcggcgcg cttgtgccgc
451 attttgcggc tggtccgccc tattttcgga ttgcccagc gcggcaagca
501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
551 tgatggtttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg
601 aggttcggac ggcattgggt ttatttcaac ggcgggatgc cgaccgcac
651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgt ttttgcgcgc
701 ctgctgcaa aatctcttcg atttgcgaag gattagaggt caatgcgttg
751 tag

```

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep

```

1   MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
51  GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQV V GMLSGQPDGV
101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDF ENRFRRALCR
151 ILRLFRRIFG FAAGGKQQA AOHGKRYFQH SALLMVSKCR LKCRLLKRGRR
201 RFRGRHWVFN GRMPTASRTL SNNSRASLRA FCAPACKISS ICEGLEVNAL
251 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq

```

1   ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCGATT TCCAGCACAT
51  AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCCTG CTGATAGGGT
101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
151 GGCATATTG CCCACCAAGT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
201 CTGCCCAACC TGCCGACTG TCCTTATCAT CGGTTTCCAT ACATTGCGCG
251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT
351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAAT CCAAACCGGC AATCGCCGTA
401 TTGTCGATAT ATATGACTTT GAAAACCGGT TCGGCGCGC TTTGTACCGC
451 GTTTTGGCGC TGTACCGCG TATTTWCGGA TTGCGCGCaC GGCaArGCAG
501 CAGGCAGCCG CCCAATACGG CAAAATAwGT wTTCAGCATT CCACAYTCCT
551 GATGTTTTCA AAATGCCGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC
601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
651 ATAATTCGCG TGCTTCTTTA CGCGCTTTCG CCGCGCCTGC CTGCAAAATC
701 TCTTCGATTT GCGAAGGGTC GCGGTCAGC TCGTTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep

```

1   MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
51  GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRALYR
151 VLRLYRRIXG FAATAQQAA AQYKXXXQH STXLMVSKCR LKRRRRRFRG
201 HRVHFNRMPT TASGTLNNS RASLRAFAAP ACKISSICEG SAVSSL*

```

Computer analysis of this amino acid sequence gave the following results:

m204/q204

[illegible]

a204.seq

1	ATGGCGGCGG	CGGAAATAAA	ACGCCCCCTC	GCTGTCGATT	TCCAGCACAT
51	AGCGTCCGTT	CTGCACGGCG	GCATAGCCGC	TTTTCGCTGC	CTGATAGGGT
101	TGCAGGGCGG	AATGCGAAAT	CAGGTAATCC	GTCAGTTTGC	CGCCGCTCTC
151	GGCGATATTG	CCCACAGTT	TGGCAAAACA	GGTATGGCAC	ACGCCGTTTG
201	CGGCCAGCC	CGAAGCGCG	CCCTTTCCGT	CGGTTTCCAT	ACATTTGCCG
251	ACGACGGCTT	CCAAGTCGTT	GGGATGCTTG	CCGTCAGCC	GGACGACGTT
301	TTGTTCCGGC	AAGCCTTT..
351
401
451
501
551AAGAG	GTTCGGACGG
601	CATTAGGTTT	ATTTCACCG	GCGGATACCG	ACCGCATCAC	GTACTTTGCC
651	CAATAAATTCG	CGTGCTCTTT	TACGCGCTTT	TTCGCGCCCT	CGCTGCAAAA
701	TCTCTTCGAT	TTGCGAAGGG	TCCGCGGTCA	GTCGTTGTA	G

a204.pap

```

1  MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVIRQFAAVF
51. GDIAHQFGKQ GMAHAVCRPA RRRALSVGEH TFADDGFQVV GMLAGQDDV
101 LFRQAF....
151 .....
201 HWVVFNGRIP TASRTLNNNS RASLRAFCAP ACKISSICEG SAVSSL*

```


m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVAVDFQHIASVLHGGIAAFACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLGGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSFGFHTFADDGFQVVGMLAGQDDVLFQAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQTGNRRIVDIYDFENRFRRLYRVLRLYRRIXGFAATAQQAAAQYKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKRLKRRRRFGRHRVHFNGRMPTASGTLNNRSLRAFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLPNRSLRAFCAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

g205.seq

```

1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcttgccgc
51  ctgcgccaaa tccgaaaata cggcggaaca gccgcaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctgggcgg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgccgtgcag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

g205.pep

```

1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNIA EDGGKLT DYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

m205.seq

```

1  ATGCTGAAWA CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGcYtTGCCG
51  tCGCGCAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CGGTACAAAG
101 CGCGCCGAAA CCGGTTTTC AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGGG AGCCGTCAGC GGCAAATGTA
301 TGGAAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTCGCATGC CGCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```


This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

m205.pep

```

1  MLXTXFAVLG GCLLXCRCGK SXNTAVQPQN AVQSAPKPVF KVIYIDNTAI
51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101 METDDKDSPA GWAENGVCHT LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFFYFRRRH Y*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

m205/g205

	10	20	30	40	50	60
m205.pep	MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE					
	:					
g205	MLKIPFAVLGGCLLLAACGKSENTAEQPQNAASAPKPVFKVKYIDNTAIAGLALGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m205.pep	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSGWAENGVCHT					
	:					
g205	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m205.pep	LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFYFRRRH					
	:					
g205	LFAKLVGNIAEDGGKLT DYLVSHALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFYFRRRH					
	130	140	150	160	170	180
m205.pep	YX					
g205	Y					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

a205.seq (partial)

```

1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
51  CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
101 ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC
151 TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACCTGAC
201 GGATTACCTG ATTTCGCATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251 GCGGCTATGC CGCCGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301 GAGGGGGCGT TTTATTTCCG CCGCCGCCAT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

a205.pep (partial)

```

1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
51  LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ AGKSGYAAVQ NGRYVLEIDS
101 EGAFFYFRRRH Y*

```

m205/a205 88.3% identity in 111 aa overlap

	50	60	70	80	90	100
m205.pep	KVIYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC					
	: :					
a205	SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC					
			10	20	30	
	110	120	130	140	150	160
m205.pep	METDDKDSGWAENGVCHTLFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQ					

480

```

||||| :|:|||||||||||||||||||||||||||:|:|:|||||
a205      METDGKGAPSGWAANGVCHTLFAKLVGNI AEDGKGLTDYLI SHSALQPYQAGKSGYAAVQ
              40          50          60          70          80          90

              170      180
m205.pep   NGRYVLEIDSEGAFYFRRRHYX
              |||||||
a205       NGRYVLEIDSEGAFYFRRRHYX
              100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 709>:

g205-1.seq (partial)

1	ATGCTGAAAA	TAcCTTTTGC	CGTGTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAATA	CGGCGGAACA	GCCGCAAAAT	GCGGCACAAA
101	GCGCGCGGAA	ACCGGTTTTC	AAAGTCAAT	ACATCGACAA	TACGGCGAAT
151	GCGGGTTTGG	CTTTGGGACA	AAGTAGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAAT	AGTTATCCGA	TTAAGGCTT	GCCGGAAACA	AACGCCGTCC
251	GGCTGACCG	AAAGCATCCC	AACGACTTGG	AAGCGCTCGT	CGGCAAAATG
301	ATGGAACCG	ACGGAAGAGA	CGCGCTTCG	GCTGTGGCGT	AAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTGAC	TGATTACCTG	ATTTCGCATT	CCGCCCTGCA	ACCCTATCAG
451	CGAGGCAAAA	GCGGCTATGC	CGCCGTGCAG	AACGGACGCT	ATGTGCTGGA
501	AATCGACAGC	GCGGGGCGGT	TTTA		

This corresponds to the amino acid sequence <SEQ ID 710; ORF 205-1.ng>:

g205-1.pep (partial).

1 MLKTPFAVLG GCLLLAACGK SENTAEQPN AAQSAPKPVF KVKYIDNTAI
51 AGLALGQSSE GKTNDGKKQI SYPIKGLPER NAVRLTGKHP NDLEAVVGKC
101 METDGDKAPS GWAENGVTCH LFAKLGNIA EDGGKLT DYL I SHSALQPYQ
151 AGKSGYAAVQ NGRVYLEIDS EGAF

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 711>:

m205-1.seq. .

1	ATGCTGAAAA	CATCTTTTGC	CGTATTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAATA	CGGCGGAAAC	GCCGCAAAAC	GCGGTACAAA
101	GCGCGCCGAA	ACCGGTTTTC	AAGTCAAAAT	ATATCGACAA	TACGGCGATT
151	GCCGGTTTGG	ATTTGGGACA	AAGCAGCGAA	GGCAAAACCA	ACGAGCGCAA
201	AAAACAAAT	AGTTATCCGA	TTAAAGGCTT	GCCGGAACAA	AATGTTATCC
251	GACTGATCGG	CAGCATCCCC	GCGGACTTTG	AAGCCGTCAG	CGGCAAAATG
301	ATGGAAACCG	ATGATAAGGA	CAGTCGCGCA	GGTTGGGCAG	AAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CATATATCGC	GAAGACGGCG
401	GCAAACTGAC	GGATTATCTA	GTPTTCGATC	CCGCGGTACG	ACCCCTATCAG
451	GACAGGCAAAA	GCGGCTACTG	GCGCGTCGAC	CAACCGACGCT	ATGTGCTGGA
501	AATCGACAGC	GAAGGGGCGT	TTTATTTCGG	CCGCGCCAT	TATTGA

This corresponds to the amino acid sequence <SEQ ID 712; ORF 205-1>:

m205-1.pep

1	MLKTSFAVLG	GCLLLAACGK	SENTAEQPQN	AVQSAPKPVF	KVKYIDNTAI
51	AGLDLGQSSE	GKTDNDGKKQI	SYPIKGLPEA	NVIRLIGKHP	GDLEAVSGKC
101	METDDKDSPA	GWAENGVCHE	LFAGLVGNIA	EDGGKLTDL	VSHAALQPYQ
151	AGSKGYAAVP	NGRYVLEIDS	EFAKYFRRRH	Y*	

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAAGCKSENTAEQPNAAQSAPKPVFKVKYIDNTAIAGLALGQSSE					
m205-1	MLKTSFAVLGGCLLLAAGCKSENTAEQPNNAVQSAPKPVFKVKYIDNTAIAGLDLGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEONAVRLTGKHPNDLEAVVGKCMETDGGKDAPSGWAENGVCHT					
m205-1	GKTNDGKKQISYPIKGLPEONVIRLIGKHPGDLEAVSGKCMETDDKDSPAWGWAENGVCHT					

481

```

              70      80      90      100     110     120
          130      140      150      160      170
g205-1.pep  LFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAF
|||||
m205-1      LFAKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          130      140      150      160      170      180
m205-1      YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
1  CCTCTTAAAG GCTTGCCGGA ACAAACGTC GTCGGGCTGA CCGGCAAGCA
51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101 AGGGCGCGCC TTCGGGCTGG GCGGCAAACG GCGTGTGCCA TACCTTGTTT
151 GCCAAACTGG TGGGCAATAT CGCCGAAGAC GCGGCGAAAC TGACGGATTA
201 CCTGATTTCG CATTCCGCCC TGCAACCCTA TCAGGCAGGC AAAAGCGGCT
251 ATGCCGCCGT GCAGAACGGA CGCTATGTGC TGGAAATCGA CAGCGAGGGG
301 GCGTTTATT TCCGCCGCCG CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
1  PLKGLPEQNV VRLTGKHPND LEAVVGKME TDGKGAPSGW AANGVCHTLF
51  AKLVGNI AEDGGKLT DYLI SHSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

          50      60      70      80      90      100
m205-1.pep KYIDNTA IAGLDL GQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKME
          ||:|||||:|: |||:|||| |||
a205-1      PLKGLPEQNVRLTGKHPNDLEAVVGKME
          10      20      30

          110     120     130     140     150     160
m205-1.pep TDDKDS PAGWAENG VCHTLFAKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNG
|| | :|:| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a205-1      TDGKGAPSGWAANGVCHTLFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNG
          40      50      60      70      80      90

          170     180
m205-1.pep RYVLEIDSEGAFYFRRRHYX
|||
a205-1      RYVLEIDSEGAFYFRRRHYX
          100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
1  atgttttccc ccgacaaaac ccttttcttc tgtctcggcg cactgctcct
51  cgccctatgc ggcacgacct ccggcaaaaca ccgccaaccg aaacccaaac
101 agacagtcgc gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctgggactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 ggcggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgcaat tcatccatgc ccccggcagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgcaaaaaa
501 ctaccttggg gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```


m206.veg

1	ATGTTTCCCC	CCGACAAAAC	CCTTTTCCTC	TGTCTCAGCG	CAC TGCTCCT
51	CGCCTCATGC	GGCACGACCT	CCGGCAAACA	CCGCCAACCG	AAACCCAAAC
101	AGACAGTCCG	GCAAAATCCAA	GCCGTCCGCA	TCAGCCACAT	CGACCGCACAC
151	CAAGGCTCTCG	AGGAATCTCA	GCTCCACAGC	CTCGGACTCA	TCGGCACGCC
201	CTACAAATGG	GGCGGCAGCA	GCACCGCACC	CGGCTTCGAT	TGCAGCGGCA
251	TGATTCAATT	CGTTTACAAT	AACGGCCTCA	ACGTCGAAGT	CGCGCGCACCC
301	GCCC GCGACA	TGGCGGCGGC	AAGCCGsAAA	ATCCCCGACa	GCCGcyTCAA
351	GGCCGCGCAC	CTCGTATTCT	TCAACACCGG	GGGCGCACAC	CGCTACTCAC
401	ACGTCGGAT	CTACATCGCG	AAACCGGAAT	TCACTCATGC	CCCCAGCAGC
451	GGCAAAACCA	TCAAAACCGA	AAAACCTCCT	ACACCGTTTT	ACGCCAAAAA
501	CTACCTCGCG	GCACATACTT	TTTTTACAGA	ATGA	

m206 . pep . .

1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GGTIKTEKLS TPFYAKNYLG AHTEFTE*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPDPKTLFLCL	SALLLASCGTTS	GKHROPKPKQT	VRQIQAVRISHI	DRTOGSQELML	HS
g206	MFSPDKTLFLCL	GALLLASCGTTS	GKHROPKPKQT	VRQIQAVRISHI	GRTOGSQELML	HS
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGS	STATGFDCSGMI	QFVYKNALNVKL	PRTARDMAAASRK	IPDSRXKAGD	
g206	LGLIGTPYKWGGS	STATGFDCSGMI	QLVYKNALNVKL	PRTARDMAAASRK	IPDSRLKAGD	
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSH	VGLYIGNGEFIH	APSSGKTIKTEKL	STPFYAKNYLGAH	TFFTE	
g206	IVFFNTGGAHRYSH	VGLYIGNGEFIH	APSSGKTIKTEKL	STPFYAKNYLGAH	TFFTE	
	130	140	150	160	170	

a206.seq

1	ATGTTTCCCC	CCGACAAAAC	CCTTTTCCTC	TGTCTCAGCG	CAGTGTCTCT
51	CGCCTCATGC	GGCAGGACCT	CCGGCAAACA	CCGCCAACCG	AAACCCAAAC
101	AGACAGTCCG	GCAATFCCAA	GCCGTCCGCA	TCAGCCACAT	CGACCCGACA
151	CAAGGCTCGC	AGGAAGTCAT	GCTCCACAGC	CTCGGACTCA	TCGGCACGCC
201	TACAAATGG	GGCGGCAGCA	GCACGCGAAC	CGGTTTCGAT	TGCAGCGGCA
251	TGATTCAATT	CGTTTACAAA	AACGCCCTCA	ACGTCAAGCT	GGCGCGCACC
301	GCCC CGGACA	TGGCGGCGGC	AAGCCGCAAA	ATCCCCGACA	GCCGCCTTAA
351	GGCCGCGCAC	CTCGTATTCT	TCAACACCGG	CGGCGCACAC	CGTACTACTAC
401	ACGTCGGACT	CTATATCGGC	AACGGCGAAT	TCATCCATGC	CCCCAGCAGC
451	GGCAAAACCA	TCAAAACCGA	AAAATCTCC	ACACCGTTT	ACGCCAAAAA
501	CTACCTCGGC	GCACATACTT	TCTTTACAGA	ATGA	

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
a206	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYKNALNVKLPR	TARDMAAASRKIPDSRXKAGD			
a206	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYKNALNVKLPR	TARDMAAASRKIPDSRLKAGD			
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGN	GEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
a206	LVFFNTGGAHRYSHVGLYIGN	GEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttgggcgcgt tgtttttcga
51  tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacgac atgattttca tcattttcgc ctgcatcggt tcggtcggcg
201 gcgggttcag ataggtttg gcaacatcg ttgccgcat aatgatgggc
251 aggatgtagt aggggtcgcc gcggtcgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgcccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 gtcgtcgccg tatttttctt tgatggtctg cagttcgggt gcggcggcac
501 gcattttcgc catcgaaagg taggaggcgt tggcfaatgg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagccccc agttgccgat
601 aatggttggt agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca gggtgctcgc gatgtttgcg
701 ataacggatg tggtttgccg accggcatac aggttgaccg ccattttcgg
751 ttttgcccc cgggttgga tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
1  MLRHLGNDEFA LGALFFDAV DVPLLGDGQE VVDHPVENQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDQDQVVG VGAAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQOHRQTAA QRVDLVFEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEP EERRCEPVYFT VFQCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDGSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAAGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGTT CGGTGCGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```



```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTGCGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCTG TCGGCGCTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTCGCTTTAG GTTGGAGAAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT CCCGAGCCAG CCGGTCGGGG TTTTGGCGAT GTATTGGGCC
951 TCGGATTGTC CGGATTTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

m209.pep

```

1 MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQT GREEEHHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDGQDVVGVA AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDGDLQQHRQAAA QRVDFLVCVK LHHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDDD* NDNRPAPVAD
201 DVVQLVQEP EERGGEVYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTLVLYSL LRRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

m209/g209

	10	20	30	40	50	60
m209.pep	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEHHDGENQRHDFHHFR					
g209	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVENQTGREEEHHDGENQRHDFHHFR					
	10	20	30	40	50	60
m209.pep	LHRVGRRRVQISLGEHRCRHNDGQDVVGVA AEVGNPTQPRCLAQFYGGEQCPIQSDG					
g209	LHRVGRRRVQIGLGEHRCRHNDGQDVVGVA AEVGNPAQPRCLAQFYGGEQCPVQADEG					
	70	80	90	100	110	120
m209.pep	LHRVGRRRVQISLGEHRCRHNDGQDVVGVA AEVGNPTQPRCLAQFYGGEQCPIQSDG					
g209	LHRVGRRRVQIGLGEHRCRHNDGQDVVGVA AEVGNPAQPRCLAQFYGGEQCPVQADEG					
	70	80	90	100	110	120
m209.pep	DLQQHRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW					
g209	DLQQHRQTAAQRVDFLVFEKLHHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGGVGQW					
	130	140	150	160	170	180
m209.pep	DLQQHRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW					
g209	DLQQHRQTAAQRVDFLVFEKLHHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGGVGQW					
	130	140	150	160	170	180
m209.pep	IQYGFDDDGXNDNRPAVADDVVQLVQEP EERGGEVYFAVVGQLQVVG DVCDDGCGLR					
g209	IQYGFDDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTVVFQQLQVVG DVCNCGCLR					
	190	200	210	220	230	240
m209.pep	IQYGFDDDGXNDNRPAVADDVVQLVQEP EERGGEVYFAVVGQLQVVG DVCDDGCGLR					
g209	IQYGFDDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTVVFQQLQVVG DVCNCGCLR					
	190	200	210	220	230	240
m209.pep	AGVEVDGGFGF-APFWMAAKGTLTLVLYSL LRRLMSMLHSPAAQTLCLPLGWRIQVDMK					
g209	: : : :					
	250	260	270	280	290	299
m209.pep	AGVEVDGGFGF-APFWMAAKGTLTLVLYSL LRRLMSMLHSPAAQTLCLPLGWRIQVDMK					
g209	TGIQVDRHFRFWPPGWDG					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

a209.seq

```

1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

```


485

```

51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGCTCAGGAG GTTGTGATC
101  ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151  AACCAAGGCG ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201  GCGGGTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251  AGGATGTAGT AGGGGTGCGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301  AGGTGCTTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351  TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401  ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451  GTCGTCGCCG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501  GCATTTTCGC CATCGAACGG TAAGAGCGT TGGTCAATGG ATACAGTACG
551  GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601  GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCAGT
651  GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTGCGGC GATGTTTGGC
701  ATAACGGATG TGGTCTGTGG GCGGCGTAG AGGTTGATGG AGGCTTCGGT
751  TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGCTGTA
801  CAGCTTGTCG TTGCGGCGTT TGATGTGCGT ACGGCAGTCG CCAGCGGCGC
851  AAACGCTTTG TCCGCCTTTG GGTGAGGA TCCAGGTGGA CATGAAGTGG
901  TGTTCATCA TGCCGAGCCA GCCGTCGGG GTTTGCGGA TGTATTCGGC
951  CTCGGATTG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1  MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDQDVGVG AAEVGNPTQP
101  RCLAQFYGGE QCPIQSDG DLQQRQAAA QRVDFLVCVK LHHGLLLRHT
151  VVAVFLFDGL QFGRGTHFR HRTVRGVQW IQYGFDDG* NDNRPAPVAD
201  DVVQLVQPK EGGGEPVYFA VVFGQLQVVG DVCDNGCGLW AGVEVDGGFG
251  FAPFWIAAKG TLTLVLYSL LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301  CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSP V*

```

m209/a209 95.6% identity in 341 aa overlap

	10	20	30	40	50	60
m209.pep	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR					
a209	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m209.pep	LHRVGRRRVQISLGEHRCRHNDGQDVVGVAEAVGNPTQPRCLAQFYGGEQCPIQSDG					
a209	LHRVGRRRVQIGLGEHRCRHNDGQDVVGVAEAVGNPTQPRCLAQFYGGEQCPIQSDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m209.pep	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
a209	DLQQRQAAAQRVDFLVCVKLHHGLLLRHTVVAVFLFDGLQFGRGTHFRHRTVRGVQW					
	130	140	150	160	170	180
	190	200	210	220	230	240
m209.pep	IQYGFDDGXNDNRPAVADDVVQLVQEPEERGGEVYFAVFGQLQVVGDVCDGCGLR					
a209	IQYGFDDGXNDNRPAVADDVVQLVQPKKEGGGEVYFAVFGQLQVVGDVCDGCGLR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m209.pep	AGVEVDGGGFGFAPFWMAAKGTLTLVLYSLSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW					
a209	AGVEVDGGGFGFAPFWIAAKGTLTLVLYSLSLRRLMSIRQSPAQTLCPPLGWRIQVDMKW					
	250	260	270	280	290	300
	310	320	330	340		
m209.pep	CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSPGVX					


```
g211.seq
1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atgggtcggc
51  ggtgggaaac ggggtcgata agtttgggcg tgggtctgat aatcaggttg
101 agtttttggg aggaacactg attgtagtcg gcgcgtccgg gcgtgccctg
151 gtaacggtag ccgtggcgca attcagagct gcgtttcttg tcttccagcg
201 agaagttacc ttctttggcg aagatgatgt tgtcgccgcc gtttttgtcc
251 tgttcgcgca ggaacaggtt ttcatgatg ccgattcgg tgtcaaaggt
301 ttcgacgaaa taaacctgct cgttgcgctt gcccaagtta ttgaactcgc
351 cggttccac caaagacaat tctctgttct gcttcaaaat ttcggcatat
401 tcggcgctgc gca gctctgc ccacggatc acccaaagct gcatgacggc
451 aatcaggatg gcaaacggca cggcaaacgt catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatag
```

g211.pep

1	MLRIAAANQL	GGRNGAAVGN	GVDFKGRGAD	NQVEFLEGNL	IVVGASGRAA
51	<u>VTVAVAQFER</u>	<u>AFVVLQREVT</u>	<u>FFGEDDVVAA</u>	<u>VFVLFAQEQV</u>	<u>FHDAGFGVKG</u>
101	FDEINPAVAL	<u>AQVIELAGFH</u>	<u>QRQFLLLLQN</u>	FGIFAAAQLC	PRYHPKLHDG
151	NQDGKRHGKL	HDGAYPLFQR	QSQF*		

```
m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTGGA AGGAAACCTG ATTGTAGTCG GCGGTCCGG CCGTCCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTGTTG TCGTTCCAGC
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTCGCCGCC GTTTTGTGCC
251 TGTTGCGGCA GGAACAGGTT TTTTCATGAT CCGGATTCGG TATCGAAGGT
301 TTCGACAAA TAAACCCTGC CGTTGCGCTT GCCCAAAGT TTGAACTCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGGCTG GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAACG GCAAAACGCC CGGCAAAGT CATCACCGGG CGTATCCATT
501 GTTCAATGC CAATCCGCAg GATAG
```

m211.pep

1	MLRVAAANQL	GGRNGTAVGN	GVDEFGRGAD	NQVEFLEGNL	<u>IVVGASGRAA</u>
51	<u>VTVAVAQFER</u>	AFVVVQREVT	<u>FFGEDDVVAA</u>	VFVLFAQE ^{QV}	FHDAGFGIEG
101	FDKINPAVAL	AQT ^{VE} LACLH	<u>QRQFLILLQD</u>	FSVFAAAXLC	PRYPHKLHDG
151	NQNGKRHGKL	HHRAYPLFCQ	QSAG*		

m211/g211

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLI	VVGASGRAAVTVAVAQFER				
	:					
g211	MLRIAAANQLGGRNGAAVGNGVDKFRGADNQVEFLEGNLI	VVGASGRAAVTVAVAQFER				
	10	20	30	40	50	60

	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACL					


```
a211.seq
  1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGCATG AATCAGTTG
101 AGTTTTTGGA AGGAAACCTG ATTGTAGTCG GCGGTTCCG GCGTGCCGCT
151 GTAACGGTAG CCGTGCGCA ATTCCAGCGT GCGTTGTTG TCGTTACGGC
201 AGAAGTTACT TTCPTTGGCG AAGATGATGT TGTGCGCGCC GTTTTTTCC
251 TGTCGCGCA GGAACAGGTT TTTCATGATG CCGGATTCG TATCGAAGGT
301 TTCACAAAA TAAACCTGCG CGTTGCGCTT GCCCAAAGT TGAACCCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAAACGCC CCGCAAAGT CATCACCGG CGTATCCATT
501 GTTCAATGC CAATCCGCAG GATAG
```

```
a211.pep
  1  MLRVAAANQL  GGRNGTAVGN  GVDEFGRGAD  NQVEFLEGNL  IVVGASGRAA
51  VTVAVAQFER  AFVVVQREVT  FFGEDDVVAA  VFVLFAQEQV  FHDAGFGIEG
101 FDKINPAVAL  AQTVPEACFL  QRQFLLLQLD  FSVFAAA*LC  PRYHPKLHDG
151 NQNGKRHGKL  HHRAYPLFQC  QSAG*
```

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
a211	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVAAVFVLFAGEQVFDAGFGIEGFDKINPAVALAQTVELACLH					
a211	AFVVVQREVTFFGEDDVVAAVFVLFAGEQVFDAGFGIEGFDKINPAVALAQTVEPACLH					
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLNHRRAYPLFQCQSAGX					
a211	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLNHRRAYPLFQCQSAGX					
	130	140	150	160	170	

```
g212.seq (partial)
      1 atggacaatc tcgtatggga cggcattccc gacatccgca cactcgacca
     51 aaccatccgc aaacacgcac acccgctcaa cctgattgtc tgccctccccg
    101 ataatcagat tcccgatttt caaacgcgac aagatgcttc ggactcggaa
    151 tgccgtctga agcaccgttt ggatcaggca acccagtgcc tccagttcga
    201 cagcatcaac ctcatcgaac acatcctgcc cgatgtccgc ttctggetgg
    251 ttcccccttc acgcaccgc cgctgcacg aacatttcca ccacattctc
    301 tggcagaccg aagccatccc gcaaacggaa agcaagtcca acaaaccttc
    351 gtttgcactt ccacaaacat ccgaacggaa aaaaccggaa cacgtcctcg
```



```

401 tcatcgggtgc aggcattgcc ggcgcatcga ccgcccacgc cttagcatca
451 cacggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctccgacaca tcctgcccga ctccgacact tggggcgga acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcaccctcct cagccatccg ctgatcgaa tatatgaaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacattttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacccggc tcacaccgtc caccctgtt tccgaacaac tgcgttgccg
1101 cgtttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgcga agcattggca caccttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL POTSERKKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCTCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCCTTT GGATCAGGCA ATGCAGTGCC TCCAGTTGCA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCTCTTC ACGCACCAC CACCTGCACG AACATTCCA CCACATTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACCT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GCGCGCGCAA CCGCCACGC CTTAGCATCA
451 CACGGCATT TCCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCAAGCCGC
501 CAGCGGCAAC CGCAAGGGC TGCTCTACGC CAAATCTCG CCGCAGACA
551 CCGAACAGAC CGAACTTTTG CTTGCCGGCT ACGGCTACAC CAAACGCTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGBA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTCTGTC
851 GCACCTCTCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCTTGT
901 ACCGACATTT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCCTTGCCT
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCAGGCA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCACG
1301 CCGCCATACG CTGGCAGAGC CCGGACCACC TTCCCTAGT CCGCGCACTC
1351 GCGGACATTG CCGCATGCG GCAGACCTAC ACCAACTCG CGCTGGACAA
1401 AAATACCGC ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGACTCGCCA CCGCCCCAT CTGCGCGCC

```


1501 GmCAwTGCAG CCCAAATCst AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLI CLPDNQIPDF QTAQDASDAE
 51 CRLKHLRDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHPHHIS
 101 WQTEAIPQTE SKPDKPWFAL POTSERQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTPT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGFIP NSSHTGWNEA
 401 EEASNRQALA HLNPALESSE FAANPNPKH QGHAAIRCDS PDHPLVVGAL
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

m212.pep	10	20	30	40	50	60
	MDNLVWDGIPDIRTLDQAIRKHAPPLNLIICLPDNQIPDFQTAQDASDAECRLKHLRDQA					
g212	MDNLVWDGIPDIRTLDQIRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRKHLRDQA					
	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHPHHISWQTEAIPQTESKPDKPWFAL					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRLHEHPHHISWQTEAIPQTESKSDKPWFAL					
	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
	POTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
g212	PQTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
	SEQLRCAVSGESYISPSWHGLHCYGFIPNSSHTGWNEAEASNRQALAHLPALSESSE					

	:
g212	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSNTGWNEAEEASNQALAHLPALAESL
	370 380 390 400 410 420
	430 440 450 460 470 480
m212.pep	FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN
g212	F

```

a212.seq
1 ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AACCATCCGC AAACACGCGA ACCCGCTCAA CCGATTGTCT TGCCTCCCCG
101 ATATACAGAT TCCCAATTTT CAAACCGCAG ATGAGTGCTT GGCACGGGAA
151 TGCCGTCTGA AGCACCCTTT GGATCAGGCA ACCCAGTGCC TCCAGTTCTGA
201 CAGCATCAAC CTGATTGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCGC CGCCTGCACG AACACTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACGGAA AGTAAGCCCG ACAAACTCTG
351 GTTTGCACTT CCACAAACAT CCGAAGCGCA AAAACCGGAA CACATCCTCG
401 TTATCGGAGC GGGCATATCC GGCSCGGCAA CCGCCCACGC CTTAGCATCA
451 TACGGCATT T CCGTACCCTT ATTGGAAGCG CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCCAA CGCAAGGGC TGCTCTACGC CAAATCTCG CCGCACGACA
551 CCGAACAAAC GCGAATCTGT CTTGCCGGCT ACGGCTACAC AACAGCCCTG
601 CTCGGACATA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAAAC ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCA CTCTACCGCA GCATCACGCA GGCAGAAGCC
751 GAAAAAATCG CGCGCATCCC TCTGAACACG CCCTACGCCG AACCAATTATG
801 CGGACTGTTT TGGCAGTACG GCGTATGGCT CAATCCTCCC ACATTCTGTC
851 GCGCCCTCTC CAGCCATCCG CTCATTGGAC TACACGAAGA CACACCCTTA
901 ACCGACATTT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GGCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTG
1001 ACCTACCCGA AACCAACCTC GCCACCCTGC CCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCCTTGCGC
1101 CGTTTCAGCG GAAAGCTACA TCAGCCCGTC GTGGCAGGCA CTGCACTGCT
1151 ACGGCGCGAG TTTATTCCC AACACGAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CGGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CAAAAACAC CAAGGGCAGC
1301 CGGCATACG CTGCGACAGC CCGGACCACC TTCCCTAGT CGGCGCACTC
1351 GCGCACTTG CCGCTATGCA ACAACTTTAC GCCAACTCG CGCTGGACAA
1401 AAACATACGC ATGATGCCCC CTCTGCCGTA CCGTCCCAAT GCCTACGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCCAT CTGCGCCGCC
1501 GCGTTTGAG CCGAAATCCT AGGCTTGCCC CATCCCTCT CAAAACGCCT
1551 CGCCACGCGC ATACACCCCA ACCCGCCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT ACACCCCTTAA

```

```
a212.pep
  1 MDNLAWNGIP DIRTLDQ TIR KHAHPLNLIV CLPDNQIPNF QTAQDASDAE
51 CRLKHRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKPKDPWFAL PQTSEQRKPE HILVIGAGIS GAATAHALAS
151 YGISVTVLEA RKAAQAASGN RQGLLYAKIS PHDTEQTLEL LAGYGYTKRL
201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYSITQAEA
251 EKIAGIPLNT PYAEPLCGLF WQYGVWLNPP TFVRALLSHP LIGLHEDTPL
301 TDISHDGEKW IASTPNGTFT ATHLIYCTGA NSPYLPETNL ATLPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
401 EEASNRQALA HLNLPALSEL FAANPNPQKH QGHAAIRCDS PDHLPLVGAL
451 GDIAAMQQTY AKLALDKNYR IDAPCPYLPN AYANTAHGTR GLATAPICAA
501 AVAAEILGLP HPLSKRLRHA LHPNRAIIRA IVRRKDLTP*
```

m212.pep MDNLVWDGIPDIRTLDAQIRKHAPPLNLIICLPDNQIPDFQTAAQDASDAECRLKHLRDLQA
|::||:|||||:
a212 MDNLAWNGIPDIRTLDQIRKHAHPLNLIVCLPDNQIPINFQTAAQDASDAECRLKHLRDLQA

491

	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1   atgatacaaa agatatgtaa gctatttggt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcttc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaaggcggcg aatccgtgag ggcggaagg
251 tcgcccgctc gcttcagcca aacgttggac gggggcaaag ggacggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcggcg gcgacgttgc cgaagggtcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep


```

1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQRTTFS
51  GNVIIIRQGT L NISASCVNVT RGRQRRRIRE GGRFARPLQ P NVGRGQRDGA
101 RSGKQRYLF L RRKHCRSDRQ CQSAARRRRC RRCGHYLQHQ NRSLYHQHQH
151 EIGCEIRFQ N RQQRHHPAF KHTKNRITPM PSETETQFR R HLPTEMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTACAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTACGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGTAAT GCCAAAGTAC AGCGGCGCG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNVT RGRQRRRIRE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRC LFI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQHQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

```

m214/g214

      10      20      30      40      50      60
m214.pep  MIQKICKLFVLIAFFSASPAFALQSDSRQPIQIEADQGS LDQANQSTTFSGNVVIRQGT L
          |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
g214       MIQKICKLFVLIVIFATSPA FALQSDSRRP IQIEADQGS LDQANQRTTFSGNV IIRQGT L
          10      20      30      40      50      60

      70      80      90      100     110     120
m214.pep  NISAARVNVT RGRQRRRIRE GGRFASPLQ PDIGRRQRHGARTGKQRC LFI CRQHRSLNRX
          |||: |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
g214       NISASCVNVT RGRQRRRIRE GGRFARPLQ PNVGRGQRD GARSQRYL FLRRKHCRSDRQ
          70      80      90      100     110     120

      130     140     150
m214.pep  CQSTARRRCRRRCGDYIQHQ NRSLYHQHQH KI
          |||: ||| ||| |::|::|::|::|::|::|
g214       CQSAARRRCRRRCGHYLQHQ NRSLYHQHQHEIGCEIRFQNRQQRHHPAFKHTKNRITPM
          130     140     150     160     170     180

g214       PSETETQFRRLPTEMPRDY
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTACAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGC.GGC AAAGCGGCG AATCCGTGAG GCGGAAGGTT
251 TCGCCAGTCC GCTTACGCCA GACATTGGAC GCGGCAAAG GCACGGTGCG
301 CGGACAGGCA AACAACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```


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```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
  1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGSL DQANQSTTFS
 51 GNVVIRQGTI NISAARVNV T RGXQRRRIRE GGRFASPLQP DIGRRQRHGA
101 RTGKQRCLFI CRQHRSLNR* CQSTARRRRCR RRCGDIYQHQ NRSLYHQHQH
151 KIRRKIRFOI RQGRRYPAF EYAKIRIIPM PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

```

              10      20      30      40      50      60
m214.pep    MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGSL DQANQSTTFS GNVVIRQGTI
              |||||
a214         MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGSL DQANQSTTFS GNVVIRQGTI
              10      20      30      40      50      60

              70      80      90      100     110     120
m214.pep    NISAARVNV TRGRRRRIRE GGRFASPLQ PDIGRRQRH GARTGKQRCL FICRQHRSLNRX
              |||||
a214         NISAARVNV TRGXQRRRIRE GGRFASPLQ PDIGRRQRH GARTGKQRCL FICRQHRSLNRX
              70      80      90      100     110     120

              130     140     150
m214.pep    CQSTARRRRCRRRCGDIYQHQNRSLYHQHQHKI
              |||||
a214         CQSTARRRRCRRRCGDIYQHQNRSLYHQHQHKIRRKIRFOIRQGRRYPAF EYAKIRIIPM
              130     140     150     160     170     180

a214         PSETXTWFG RHLPTEILKRYLX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTTCGAAC
 51 TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGTAC CACATTAGC
151 GGCAATGTCA TCATCAGACA GGGTACGCTC AACATTCCG CCTCGCGCGT
201 CAACGTACAC CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTACGCCAA ACGTTGGACG GGGGCAAAGG GACGGTGCGC
301 GGTACGGCAA ACAACGTTAC CTATTCTCTC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CGGCAGCACG
451 AAATCGGGTG CGAAATCCGC TTCCAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
  1 MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGSL DQANQSTTFS
 51 GNVIIHQGTI NISASRVNV T RGGKGGESVR AEGSPVRFQ TLDGGKGTVR
101 GQANNVTYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
 51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTACG
151 GGAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCGCGT

```



```

201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGCG TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51 GNVVIRQGT L NISAAARNVT RGGKGGESVR AEGSPVRF S Q TLDGGKGTVR
101 GQANNVAY S AGSTVVLTGN AKVORGGDVA EGAVITYN T K TEVYTISGST
151 KSGAKSASKS GRVSVVIQPS STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

```

          10      20      30      40      50      60
m214-1.pep MIQKICKLFVLIAFFSASPAFALQSDSRQPIQIEADQGS L DQANQSTTFSGNVVIRQGT L
          |||
g214-1      MIQKICKLFVLIVIFATSPAFALQSDSRRP IQIEADQGS L DQANQSTTFSGNVIRQGT L
          10      20      30      40      50      60

          70      80      90      100     110     120
m214-1.pep NISAAARNVT RGGKGGESVRAEGSPVRF S Q TLDGGKGTVR G QANNVAY S SAGSTV VLTGN
          |||
g214-1      NISASRVNVT RGGKGGESVRAEGSPVRF S Q TLDGGKGTVR G QANNVY S SAGSTV VLTGN
          70      80      90      100     110     120

          130     140     150     160     170
m214-1.pep AKVORGGDVAEGAVITYN T K TEVYTISGST KSGAKSASKS GRVSVVIQPS STQKSE X
          |||
g214-1      AKVORGGDVAEGAVITYN T K TEVYTINGST KSGAKSASKT GRVSVVIQPS STQKTE X
          130     140     150     160     170

```

g214-1/p38685

sp|P38685|YHBN_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_0185 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQPIQIEADQGS L DQANQSTTFSGNVVIRQGT L NISAAARNVT R --GGKGG 76

Sbjct: 24 PAFAVTGD TDQPIHIESDQQLDMQGNVVTFTGNVIVTQT IKINADKVVVTRPGGEQK 83

Query: 77 ESVRAEGSPVRF S Q TLDGGKGTVR G QANNVAY S SAGSTV VLTGN AKVORGGDVAEGAVIT 136

Sbjct: 84 EVIDGYGKPATFYQMDNGK -PVEGHASQMHYELARDFVLTGNAYLQQVDSNIKDKIT 142

Query: 137 YNTKTE 142

Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

```

1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51 GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGCG TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

```


495

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSSQ TLDGGKGTVR
 101 GQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLI	AFSASP	FALQSDSRQPIQIEADQGS	LDQANQSTTFSG	GNVVIRQGTI	
m214-1	MIQKICKLFVLI	AFSASP	FALQSDSRQPIQIEADQGS	LDQANQSTTFSG	GNVVIRQGTI	
	10	20	30	40	50	60
a214-1.pep		70	80	90	100	110
m214-1		70	80	90	100	110
		70	80	90	100	110
a214-1.pep		130	140	150	160	170
m214-1		130	140	150	160	170

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq

1 atgaaagtaa gatggcggta cgggaattgcg ttcccattga tattggcggg
 51 tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
 101 tgcaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
 151 ttggacggaa ggcggtttga cgaacaggga tacttgaaag aacatttgag
 201 cgcgaaaggt gcgaaacagt ttcccgaata cagcgacatc cattttgatt
 251 cgccgcatct cgtgttcttc caagaaggca ggctgtgtga cgaagtcggc
 301 agcgatgaag ccgtttacca taccgaaaac aaacagggtc tttttaaaaa
 351 caacgtttgtg ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaag
 401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc
 451 gatacgcttg tcagtttcca atatggcggc tcgcacgggc aggcgggcgg
 501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
 551 aagcccgcat ttatgataca aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep

1 MKVRWRYGIA PPLILAVALG SLSAWLGRIS EVEIEEVRIN PDEPOYTMDG
 51 LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPLHVFF QEGRLLYEVG
 101 SDEAVYHTEN KQVLFKNVNV LTKTADGRRQ AGKVETELKH VDTESQYQAT
 151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAALYDT KDM*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)

1 ..AGCCTGTCGG CATGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
 51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGACAGC TTGGACGGCA
 101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTTGAG CGCGAAGGGC
 151 GCGAAACAGT TTCCGAAAG CAGCGACATC CATTTTGATT CGCCGCATCT
 201 CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG
 251 CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA CAACGTTGTG
 301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
 351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG
 401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC
 451 GACCACAAwA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
 501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)

1 ..SLSAWLGRIS EVEIEEVRIN PDEPOYTMDG LDGRRFDEQG YLKEHLSAKG
 51 AKQFPENSDI HFDSPLHVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNVNV
 101 LTKTADGRRQ AGKVEAEKLH VDTESQYQAT DTPVSFQYGA SHGQAGGMTY

496

151 DHXTGMLNFS SKVKATIYDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40	
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
		:				
g215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
	10	20	30	40	50	
	50	60	70	80	90	
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEG	RLLYE	VGSD	
	:					
g215	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEG	RLLYE	VGSD	
	70	80	90	100	110	
	110	120	130	140	150	
m215.pep	LTKTADGKRQAGK	VEAEKLHVD	TESQYAQ	TDTPV	SFQYG	
	:					
g215	LTKTADGKRQAGK	VEAEKLHVD	TESQYAQ	TDTPV	SFQYG	
	130	140	150	160	170	
	170					
m215.pep	SKVKATIYDTKDMX					
	:					
g215	SKVKAAYDTKDM					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq	
1	ATGAAAGTAA GATGGCGGTA CGGAATTGCG TTCCCATGTA TATTGGCGGT
51	TGCCTTGGGC AGCCTGTCGG CATGGTTGGG ACGCATCAGC GAAGTCGAGA
101	TTGAAGAAGT CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACGGA
151	TTGGATGGCA GCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTTGAG
201	TTCGAAGGGC GCGAAACAGT TTCCCGAAAG CAGCGACATT CATTTCGACT
251	CACCGCATCT CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC
301	AGCGATGAAG CCGTTTACCA TACCGAAAAC AAACAGGTTT TTTTAAAAA
351	CAACGTTGTG CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG
401	TTGAAGCCGA AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC
451	GATACGCCTG TCAGTTTCCA ATATGGTGCA TCGCACGGTC AGCGGGGCGG
501	CATGACTTAC GACCACAAA CAGGCATGTT GAACTTCTCA TCTAAAGTGA
551	AAGCCACGAT TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep	
1	MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
51	LDGRRFDEQG YLKEHLSSKG AKQFPSSDI HFDSPHLVFF QEGRLLYEVG
101	SDEAVYHTEN KQVLFKNNVV LTKTADGKRQ AGKVEAEKLH VDTESQYAQT
151	DTPVSFQYGA SHGQAGGMTY DHKTGMLNFS SKVKATIYDT KDM*

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40	
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
		:				
a215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
	10	20	30	40	50	
	50	60	70	80	90	
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEG	RLLYE	VGSD	
	:					


```

|||||:|||||
a215      YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
           70      80      90      100     110     120

           110     120     130     140     150     160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
           |||||||
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHKTGMLNFS
           130     140     150     160     170     180

           170
m215.pep  SKVKATIYDTKDMX
           |||||||
a215      SKVKATIYDTKDMX
           190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcagagtc ggtacccagc gacgaaatca ccgccatcat
51  ccccgactc aaacgcaaag acattaccct cgtctgcata accgcccgc
101 ccgattcaac catggcgcgc catgccgata tccacatcac cgcacggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggtt ttgggcgacg cgttgggcgt cgtcctgctg cgcgcccgcg
251 cggtcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcgge
301 aaacgcctgc ttttgccgct tgccgacatt atgcacaaag gcggcggcct
351 gcccgccgtc cgactcgga cgccttgaa aggagccatc gtcagcatga
401 gcgagaaagg tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt ttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDI TLVCI TARP DSTMAR HADI HITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHRGGGLPAV RLGTPLKGAI VSMSEKGLGM WAGTDQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGC GCGAAAT TGCAGCGGAA TTGACAAAA
101 ACTTCGTCCT TCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGCGA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCG TCCTGCTGCG CgcACGCGG TTCACGCCCG
551 ACGATTTCGC CTTGAGCCAT CCTGCCGGA GCCTCGGCAA ACGCCTACTT
601 TTGCGGTTG CCGACATTAT GCACAAAGG GCGGCGCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCGC CTGTTCATA GAATGCGACA ATTTTACCGG
801 TCTTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LKKNFVLAAD ALLHCKGRVV

```


Homology with a predicted ORF from *N. gonorrhoeae*

m216/q216

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

a216.seq

1	ATGGCGATGG	CAGGAAACGA	AAAATATCTT	GATTGGGCAC	GCGAAGTGT
51	GCACACCGAA	CGCGAAGGCT	TGCGCGAAAT	TGCGGCGGAT	TTGGACGAAA
101	ACTTCGCCCT	TGCGGCGGAG	CGCTTGTGTG	ACTGCAAAAG	CAGGGTCGTT
151	ATCACGGGCA	TGGGCAAGTC	GGGACATATC	GGGCGCAAAA	TGGCGGCAAC
201	CATGGCTCTG	ACGGCGACGC	CGCGCTTTTT	CGTCCACCTT	CGGGAAGCGG
251	CACACGGCGA	TTTGGGCATG	ATTGTGGACA	ACGACGTGGT	CGTGCAGATT
301	TCCAAATCCG	GTGAAAGCGA	CGAAATCGCC	GCCATCATCC	CCGCGCTCAA
351	ACGCAAAAGT	ATCACGCTTG	TCTGCATCAT	CGCCCGCCCC	GATTCAACCA
401	TGGCGCGCCA	TGCCGACATC	CACATCACGG	CGTCGGTTTT	CAGAAGAAGC
451	TGCCCGCTGG	GGCTTGCCCC	GACCACACAG	ACCACCGCCG	TTATGGCTTT
501	GGGCGATGCG	TTGGCGGTTG	TCCTGCTGCG	CGCCCGCGCG	TTACGCCCCG
551	ACGACTTCGC	CTTAGCCAC	CCTGCCGGCA	GCCTCGGCAA	ACGCCTACTT
601	TTGCGCGTTG	CCGACATTAT	GCACAAAGCG	GGCGGCCTGC	CTGCGGCTCG
651	ACTCGGCACG	CCCTTGAAAG	AAGCCATCGT	CAGCATAGTG	GA AAAAGGGC
701	TGGGCATGTT	GGCGGTAAAG	GACGGGCAAG	CCGCTGTGAA	AGCGGTATTC
751	ACCGACGGCG	ATTTGCGCCG	CCTGTTTCAA	GAATGCGACA	ATTTTACCGG
801	TCTTTTGATA	GACGAAGTCA	TGCATACGCA	TCCTAAACC	ATCTCCGCCG
851	AACGCTCTCG	CACCGAAGCC	CTGAAAGCTA	TGCAGGCANA	CCATGTGAAC
901	GGGCTTCTGG	TTACCGATGC	AGTAGGCGTG	CTGATCGGCG	CGCTGAATAT
951	GACAGACCTT	TTGGCGGCGC	GGATTGTATA	G	

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

a216.pep

1	MAMAGNEKYL	DWAREVLHTE	AEGLREIAAD	LDEFNLAAD	ALLHCKGRVV
51	ITGMGKSGHI	GRKMAATMAS	TGTPAFFVHP	AEAAHGDLGM	IVDNDVVVAI
101	SNSGESDEIA	AIIPALKRKD	ITLVCITARP	DSTMARHADI	HITASVSKEA
151	CLPLGAPPTS	TTAVMALGDA	LAVVLLRARA	ETPDDFALSH	PAGSLGRKLL
201	LRLVDIMHKG	GGLPVAVRLGT	PLKEAISVMS	EKGLGM LAVT	DQGMRLKGVF
251	TDGDLRRLRFQ	ECDNFTGLSI	DEVMHTHPKT	ISAERLATEA	LKGQMOANHVN

301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENKYLQWAREVLHAEAEGLREIAAEIXKNFVLAADALLHCKGRVVITGMVKSCHI					
a216	MAMAGNEKYLQWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVVITGMKSGHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLGMIVDXDVVVAISNSGESDEIAAIIIPALKRKD					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLGMIVDNDVVVAISNSGESDEIAAIIIPALKRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITARPDMSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
a216	ITLVCITARPDMSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLEAIVSMSEKGLGMLAVT					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRKLGKVFDTGDLRRLFQECNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN					
a216	DGQGRKLGKVFDTGDLRRLFQECNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGV LIGALNMHDL LAARIVX					
a216	GLLVTDADGV LIGALNMHDL LAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg\acgggtttgtt gcggaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttccgaggtt ttggactgcc
101  ttttggatcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151  acgcgccacc cattcgccga ccgtcgcaagg ttgccgccat atccgggcaa
201  tatccgacag ggtttcgagg aaggcggcaa aacgtccgaa catggcgggtt
251  tgattcacgt cggcatacca cgcgtgaca tcctgccaca tcgggttgcc
301  gccttcgggc agcatccagc ccaatatcat acgggtctgc gcctgcttcc
351  aggtaaacag ctgatccgtg ccgcgcgcga tttctccgtc caatccccaa
401  tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451  ggtcagtcgg aaacggcgca acacggggcg gggtttccaa agcgcgagca
501  ctattgccag ttcaaaacgg ctttccagca agtcggacac gactccaac
551  gcataaaaaa acggttgccg gcggctgatt ttcacgtccg aaacggaata
601  cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttcataa
651  aaggcgataa gggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101  AFGQHPAQYH TVCRLLPGKQ LIRAAHFSV QSPMDVQIGN HIVQKRQIVP
151  GQSETAQHGR GFQKREHFAD FKTAFOQVGH ALQRIKKRLP AADPHVRNGI

```


500

201 RQCLRAGLRL SEHGFKRRI GFDIRG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGGCGGATG ACGGTGTGCG GCGGCAACTG TCCGAAAAT TGCGCCAATT
51  CGGTTTCCGC CTrCCATTG ACCCATTCGT TTTCAAGGTT TTGGACTGAC
101 TTTTGGTCAT CCGCTTCAGC TTGGAACAAT GTTTCAGCA AATCCCGGCA
151 ACGCGCCACC CATTGCGCGA CCGTTGCGGG CTGCCGCCAT ATCCGTACAA
201 TATCCGTGAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CATGGCGGTT
251 TGATTACAGT CCGCATACCA CGCGCTGACA TCCTGCCACA TCGGATTGCC
301 GCCTTTGGGC AGCATCCAGC CCAATATCAT GCGTCTTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 TGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGTA AATCGTCCTC
451 AGTCAGTCCG AAACGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGGCG GCGGCTGATT TTCACGTCTG ACACGGAATA
601 CCGCAATGCC TGCGCACCgG GctGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVERRQL SGKLRQFGFR LPFDPFVFKV LDXLLVIGFS LEQCFKQIPA
51  TRHPPADRCG LPPYPYNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPVDVQIGN HVVQKRXLIVL
151 SQSETAQHGR GFKKHKHFID FKSAPQOVEQ AXQSMKQRLA AADFHVXHGI
201 RQCLRTGLRL SEHGFDKRRRI GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVERRQLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHPPADRCG					
	: : : : : :					
g217	MADDGLLRQLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHPPADRRR					
	10	20	30	40	50	60
m217.pep	70	80	90	100	110	120
	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
m217.pep	130	140	150	160	170	180
	LIRAAAHFSVQTPVDVQIGNHVQKRXLIVLSQSETAQHGRGFKKHKHFIDFKSAFQQVEQ					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFQKREHFADFKTAFQQVGH					
	130	140	150	160	170	180
m217.pep	190	200	210	220		
	AXQSMKQRLAAADFHVXHGI RQCLRTGLRLSEHGFDKRRIGFDIRGX					
	: : : :					
g217	ALQRIKKRLPAADFHVRNGIRQCLRAGLRLSEHGFKRRIGFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG ACGGTGTGCA GCGGCAACTG TCCGAAAAT TGCGCCAATT
51  CGGTTTCCGC CTGCCATTG ACCCATTCGT TTTGAGGCT TTGGACTGCC
101 TTTTGGTCAT CGCCTTCGAC TTGGAACAAT GTTTCAGCA AATCCCGGCA
151 ACGGCCACC CATTGCTCAA CCGTCGAGG TTGCCGCCAT ATCCGTACAA

```


501

```

201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTCG GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TGC GCGCCGG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

a217.pap

```

1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEEA LDCLLVIAFD LEQCFKQIPA
51 TRHPFVNRRR LPPYPYNIHQ GFEEGGKTSE QGGLVHVIGIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KHKHFID FKSFAQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRRRI GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

	10	20	30	40	50	60
m217.pap	MADDGVRRQLSGKLRQFGFRLPFD	PFVFKVLDXLLVIGFSLEQCFKQIP	ATRH	PFADRCG		
a217	VADDGVQRQLSGKLRQFGFRLPFD	PFVFEALDCLLVIAFDLEQCFKQIP	ATRH	PFVNRRR		
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pap	LPPYPYNIHQGFEEGGKTSEHGGLI	HVIGIPRADILPHRIA	AFGQHPAQYHAFYRLLPGEQ			
a217	LPPYPYNIHQGFEEGGKTSEHGGLV	HVIGIPRADILPHRIA	AFGQHPAQYHAFYRLLPGEQ			
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pap	LIRAAAHFSVQTPVDVQIGNHV	VQKRQIVLSQSE	TAQHGRGFKHKHFIDFKSAFQQVEQ			
a217	LIRAAAHFSVQTPADVQIGNHV	VQKRQIVLSQSEMAQHGRGFKHKHFIDFKSAFQQVEQ				
	130	140	150	160	170	180
	190	200	210	220		
m217.pap	AXQSMKQRLAAADFHVXHGIRQCL	RTGLRLSEHGFDKRRIGFDIRGX				
a217	AXQSMKQRLSAADFHIRNGIRQCL	RAGLRLSEHGFDKRRIGFDIRGX				
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

g218.seq

```

1 atggttgccg tggatcctta tacggcaaaa gtggtcaaca ccatgccgcg
51 caatcagggg tggatcaca ctatggatga aatccacggc gatgatgagc
101 tcggtgcccg aggcgattat cttttggaaa cggcagcttc actgaccatt
151 attatgggtg tcagcgggctt gtacctttgg tgggcgaaac agcgcggcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tgggtggcga
251 atctgcacgg cgcgtttgga acttgggtgt cgttgatttt actgtgtgtc
301 tgcctgtcgg gtattgcttg ggcaggtatt tggggcgcca aattcgtgca
351 ggcttggaat cagttcccgg ccggcaaatg ggggtgtcga ccgaaccccg
401 tttcaatcgt gccgaccac ggcgaggtat tgaatgacgg caaggttaag
451 gaagtgcggt ggattttgga gcttatgcct atgcctgtct cagggacgac
501 tgtgggtgaa aacggcatta accccaccga gcccaataac attggaaacc
551 gtcgaccggt tcgcgcggga aatcggtttc aaagggcggt atcagttgaa
601 tttgcccaaa ggcgaggacg ggggtatggac tttgtcgagc gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

g218.pap

```

1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```


502

51 IMVVSGLYLW WAKQGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAF NRQORALSVE
 201 FAQRRGRGMD FVAGFYEL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq

1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC
 101 TCGGTGCGGC AGGCGATTAT CTTTGGGAAA CGGCAGCTTC ACTGACCATT
 151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAT GGCGCGTTCT TGGTGGCGGA
 251 ATCTGCACGG CACGTTTGGG ACTTGGGTGT CGTTGATTTT GCTGTTGTTT
 301 TGCCTGTCCG GTATTGCTTG GCGGGTATT TGGGGCGGCA AGTTCGTACA
 351 GGCTTGGAGT CAGTTCCTTG CCGGTAATG GGGTGTGCGA CCGAACCCCG
 401 TTTCACTCGT GCCGACCCAC GCGGAGGTAT TGAATGACGG CAAGGTTAAG
 451 GAAGTGCCGT GGGTTTGGG GCTTACGCTT ATGCCTGTTT CAGGGACGAC
 501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAAACCG
 551 TCGACCGCTT TCGCGCGnGA AATCGGTTTC AAAGGGCGTT ATCAGTTGAA
 601 TTTGCCCAA GCGGAGGACG GCGTATGGAC TTTGTCGAG GATTCTATGA
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep

1 MVAVDPYTAK VVSTMPRNQG WYYTMDIHS DMMLGAAGDY LLETAASLTI
 51 IMVVSGLYLW WVKRRGIKAM LLPSKXARS WWRNLHGTFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWILELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRQORALSVE
 201 FAQRRGRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMDIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
g218	MVAVDPYTAKVVNTMPRNQGWYHTMDIHDMMMLGAAGDY LLETAASLTI IMVVSGLYLW					
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
g218	WAKQGIKAMLLPPKSRARSWWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
g218	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVEVPWILELMPMPVSGTTVGENGINPTEPNN					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRQORALSVEFAQRRGRMD FVAGFYEL					
g218	IGNRRPFRAFNRQORALSVEFAQRRGRGMD FVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1  ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
201 CAAGCGGATG CTGCTGCCGC CAAAAGGCAG GGCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGGG ACTTGGGTGT CGTTGATTTT ACTGTTGTTT
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCAA CCGAACCCTG
401 TTTCAGTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCTG GGGTTTGGG GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAACCG
551 TCGACCGTTT TGCGCGG.GA AATCGGTTTC AAAGGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GGCGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1  MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLE
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQG	WYYTMD	EHSDMMLGAAGDY	LLETAASLTI	IMVVSGLYLW	
a218	MVAVDPYTAKVVSTMPRNQG	WYYTMD	EHSDMMLGAAGDY	LLETAASLTI	IMIISGLYLW	
	10	20	30	40	50	60
	70	80	90	100	110	120
m218.pep	WVKRRGIKAMLLPSKXARS	WWRNLHGT	FGTWVSLILL	LFCLSGIAWAGI	WGGKFVQAWS	
a218	WVKRRGIKAMLLPPKGRARS	WWRNLHGT	FGTWVSLILL	LFCLSGIAWAGI	WGGKFVQAWS	
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSVVPTH	GEVLNDGKVK	EPWPVLELTP	MPVSGTTVGK	DGINPDEPMT	
a218	QFPAGKWGVEPNPVSVVPTH	GEVLNDGKVK	EPWPVLELTP	MPVSGTTVGK	DGINPDEPMT	
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFQRLS	VEFAQRRGRMD	FVAGFYEL			
a218	LETVDRFARXNRFQRLS	AEFAQRRGRMD	FVAGFYEL			
	190	200	210			

1	atgacggcaa	ggttaaggaa	gtgccgtgga	ttttggagct	tatgcctatg
51	cctgtctcag	ggacgactgt	gggtgaaaac	ggcattaacc	ccaccgagcc
101	caataacatt	ggaaaccctg	gaccctttcg	cgcgggaaat	cggtttccaa
151	ggcgcttatc	agttgaattt	gcccaaaagg	gaggacgggg	tatggacttt
201	gtcgcaggat	tctatgagtt	atgacatgac	cagcccgttt	gccgacgcga
251	cgggtacatat	cgaccagtac	agcggcgaga	ttcttgccga	catccgtttt
301	gacgattaca	accctgtcgg	caaattttatg	cgggcaagca	ttgcgtctga
351	<u>tatggggagt</u>	ttgggctggg	ggagcgtggt	ggcgcaagctc	gtgttctgcc
401	ttgcgctgat	ttttatcgcc	atcagcggct	cgctgatgtg	gtggaaacgc
451	cgtccgctcg	gcgtggcggg	cattgttctc	ccggcgcaaa	aaatcaaact
501	gcccgcctgg	tgggcgtatg	cattgccgct	gctgttgatt	gcactgcgtt
551	tcccgcagcg	gctgcttgcc	attgccgtga	tttggctggt	ggataccttg
601	ctgctgtcgc	ggattcctgt	gttgaggaat	tqgtttaaat	qa

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

1	MTARLRKCRG	FWSLCLCLSQ	GRLWVKLTALT	PPSPITLETV	DRFAREIGFK
51	GRYQLNLPKG	EDGVWTLSDQ	SMSYDMISPF	ADRTVHIDQY	SGEILADIRF
101	DDYNPFPGKFM	PAASIALHMG	LGWWSVLANY	VFCLAVIFIG	ISGCVMMWKR
151	RRSPGAGIVP	AQKIKLPVW	WAMALPLLLI	ALLFPTALLA	IAVIWLLDTL
201	LLSRGIVLVR	WFK*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

1	ATGACGGCAA	GGTTAAGGAA	GTGCCGTGGG	TTTTGGAGCT	TACGCCTATG
51	CCTGTTTCAG	GGACGgCyGt	gGGCAAAGAC	GGCATTAAAC	CTGACGAGCC
101	GATGACATTG	GAACACCGTC	ACCCTTTTGC	GCcGnGAAAT	CGGTTTCAAA
151	GGGCGTTATC	AGTTGAATCG	GCCAAAGGC	GAGGACCGCG	TATGACTTTT
201	GTCGCAGGAT	TCTATGAGTT	ACGACATGAT	CAGCCCGTTT	GCCGACCGCA
251	CGGTACATAT	CGACCAGTAC	AGCGGCAAAA	TCCTTGCCGA	CATCCGTTTT
301	GACGATTACA	ACCCTGTCGG	CAAAATTATG	GCCGCAAGCA	TTGCGCTGCC
351	TAGTGGGACT	CTGGGCTGGT	GGAGCGTGTT	GGCGAACGTC	TTGTTCTGCA
401	TTGCCGTCAT	TTTTATCGGT	ATACGCGGCT	CGGTGATGTG	GTGAAACGCG
451	CGTCCGACCG	GAGCGGTGGG	CATCGTCCG	CCGGCGCAGA	AAGTCAAGCT
501	GCCCGTTTGG	TGGATGTATG	CATTGCCCGCT	ATTGGCAATT	GCATCGTCTT
551	TCCCGACCTC	ACTGCTTGCC	ATTGCCCGTA	TTTGGCTGTT	GGATACGCTG
601	CTGTTGTGCG	GGATTCTCTG	TTTGAGGAGA	TGTTTAAAT	GA

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```

1  MTARLRKCRG FWSLRRLCLFQ GRXWAKTALT LTSRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPPGKFM AASKIALHMG T LGWWSVLANY LFCLAVIFIG ISGCVMMWKR
151 RPTGAVGIVP PAQVKVLVW WMMALPLLAI ALLFPTSLA IAVIWLIDTL
201 ILSRIPTVIR WPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m219.pep	MTARLRKRCRGFWSRLCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
g219	MTARLRKRCRGFWSLCLCLSQGRLLVVKLTALPPSPITLETVDRFAREIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSQLSDMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFQKGFMAASIALHMG					
g219	EDGVWTLSQLSDMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFQKGFMAASIALHMG					

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVKL PVWMMALPLLAI					
	: : : : :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMWKRRPSGVAGIVPPAQKIKLPVWMMALPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : : :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFK					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1   ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTCG GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCAGTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTT
301 GACGATTACA ACCCGTTCGG CAAATTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GGCGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGTCGG GCGCGGTGGG CATGGTTCGG CCGGCGCAAA AAATCAAGCT
501 GCCCCTCTGG TGGGCAATGG CGGTGCCTG GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
  
```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1   MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG LGWWSVLANV LFCLAVIFIG ISGCVMWKRR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*
  
```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLTSRXHWKPS TALRGEIGFKGRYQLNLPKG					
	: : : :					
a219	MTARLRKCRGFWSLRCLFQGRWAKTVLTLTSRXHWKPS TVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	: : : :					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVKL PVWMMALPLLAI					
	: : : :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPSGAVGMVPPAQKIKLPVWAMAVPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatgcggcga gccgtaaadc adatcgacgc tgacggattt gaaccctgcc
101 tcacgggcgg catcgatgac ttctttgggt tcttcgtagc tttggatgcy
151 gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgtcga
201 tgcggttgaa gccgagtctg ccgagcatga ggacggtgtc gcggtgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggtg tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcggcgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcggcg cggtttttgt ctttggatg gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcgg
551 ttgttttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MFADHAEDTF DLFVAQKRR AAAEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151 GIGAAFVFGD DFVAAAVVAD GVAERNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAA
51  CGACGCTGAC GGATTTGAAC CCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTGCGCG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCCG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGAAGAC
301 ACGTTCGATC TGTTCTGCGC TCAAAAAGGt GCGTGCCCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCCATT
401 TCTTTTTCAT GATATTCGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451 GATGATTTTG TTGAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTGTGTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAHEHED GVAADFARVD FDGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAFVFG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

m221/g221

	10	20	30	40	50
m221.pep	MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE				
g221	MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE				
	10	20	30	40	50
	60	70	80	90	100
m221.pep	ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-				
g221	ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKRR				
	70	80	90	100	110
	120	130	140	150	160
	170				


```
a221.seq
1  ATGGTGGTTT  TGATGCTCCG  AAGTCTGGTG  CGGCAGGCCG  TAAATCAAAT
51  CGACGCTGAC  GGATTGAAC  CCCGCTTCGC  GCGCCGCATC  GATGACTTCT
101 TTGGTTTCTT  CGTAACTTTG  GATCGGGTTG  ACCGCCGCCT  GCACTTTGGG
151 TTCGAAATCC  TGAATGCCGA  TGCTAATCGC  GTTGAAGCCG  AGTCTGCCGA
201 GCATGAGGAC  GGTGTCGCGG  CTGACTTTGC  GCGGGTCGAT  TTCGATGGAG
251 TATTCGCCGG  TGGGGATTAA  CTCGAAATGT  TTGCGTATCA  TCGCGAAGAC
301 ACGTTCGATT  TGGTCGTCGC  TCAAAAAGGT  CGGCGTGCCG  CCGCCGAAGT
351 GCAGTTGGGC  AAGCTGGTGC  CGTCCGTTCA  GATGTGGAGC  GAGCAGTTCC
401 ATTTCTTTT  CAGAAGAAAT  GATGTAGGCA  TCGCGCGCGC  TTTTGTCTTT
451 GGTGATGATT  TTGTTGCAGC  CGCAGTAGTA  CGAGGTGGTG  TTGCAGAACG
501 GAATGTGAAT  GTAAAGGGAA  AGCGGTTTGT  TTAAT
```

```

a221.pep      1  MVVLMRLSLV  RQAVNQIDAD  GFEPFRFARRI  DDFGFFVFTL  DAVDRRLHFG
      51  VEILNADAH  AVEAESAEHD  GVAADFQARMD  FDGVFAGGD*  LEMFAYHAED
     101  TFDLVVAQK  GRRAAAEVQL  KLVPSPQMWSS  EQFHFFFKKF  DVGIGAAAFVF
     151  GDDFVAAAV  ADGVAERNVN  VKGKRFV*

```

		10	20	30	40	50	60
m221.pep		MXVLMXRSLSVRQAVNQIDADGFEPRFARRIDDFGFFVTLD	DAVDRRLHFGVEILNADAH				
a221		MVVLMLRSLSVRQAVNQIDADGFEPRFARRIDDFGFFVTLD	DAVDRRLHFGVEILNADAH				
		10	20	30	40	50	60
m221.pep		70	80	90	100	110	119
		VEAESAEHEDGVAADFARVDFDGVFAGGD	XLEMFAYHAEDT	FDLFVAQKGA-CPAEV	QLG		
a221		VEAESAEHEDGVAADFARVDFDGVFAGGD	XLEMFAYHAEDT	FDLVVAQKGRRAAAE	VLG		
		70	80	90	100	110	120
m221.pep	120	130	140	150	160	170	
		KLVP	SVQM	WSEQ	FHFF	FKIF	FDVGIGAA
a221		KLVP	SVQM	WSEQ	FHFF	FKIF	FDVGIGAA
		130	140	150	160	170	

```
g223.seq
  1  atggaattca  ggcaccaggt  agtggtagtt  ggtgtcgaac  catttggtca
51  tttcgatggc  gaattgggtct  ttgttgccgc  gcgccagttg  gaagaattgt
101 tccaaaggca  ggttttggct  atcgaagccg  aaacggggcg  gaatcgcgcc
151 cgtggatact  ttcaaggtcga  ggatgtgatg  tagaaaagtg  aatcacgta
201 cagcaacgta  atcagcggtta  ggagcagctt  ggtgtttcca  gttttttcgc
251 ccaggtcttt  tggcaacgtc  gagcagctct  tgttcactga  tctctttgcg
301 ccagtatctt  tcttgggcga  atttcaattc  acggaagcgc  ccgacacgcg
351 qaaagcctta
```

g223.pcp..

1 MEFRHQVVVV GVEFFGHFDG ELVFVAARQL EELFQRQVLA IEAETGGNRA
 51 RGYLQVEDVM VESEITYSNV ISVRSSLVFP VFLAQVFGNV EQLLFTDLFA
 101 PVFFLGEFQF TEGADTREAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 789>:

m223.seq
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGGTCA
 51 TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
 101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCCTAC
 201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTCCAG TTTTCTCGC
 251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTGGCG
 301 CAGTATTTT CTGTGCGAA TTCAATTCTG CGGAAGGCGC CGACACGCG
 351 GAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

m223.pep
 1 VEFRHQVVVV GVEFFGHFDS ELVFVTARQL EELFQRQVLA VEAEGGNRA
 51 GGDQVEDVV VESEIXYNE IGVGSDLVFP VFLAQVFSNS QQFLADFFA
 101 PVFFLGEFQF AEGADTREAA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

m223/g223

	10	20	30	40	50	60
m223.pep	VEFRHQVVVGV	VEFFGHFDS	ELVFVTARQL	EELFQRQVLA	VEAEGGNRAG	GGDLQVEDVV
g223	MEFRHQVVVGV	VEFFGHFDS	ELVFVAARQL	EELFQRQVLA	IEAETGGNRA	RGYLQVEDVM
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYNEI	GVGSDLVFP	VFLAQVFSNS	QQFLADFFA	PVFFLGEFQF	AEGADTREAX
g223	VESEITYSNV	ISVRSSLVFP	VFLAQVFGNV	EQLLFTDLFA	PVFFLGEFQF	TEGADTREAX
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

a223.seq
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGGTCA
 51 TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
 101 TCCAAAGATA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCGCCTA
 201 CGGCAACGTA ATCGGCGTTG GCAGCGGCTT GGTGTTTCCA GTTTTCTCG
 251 CGCAAGTCTT TAGCAACAGC CAGCAATCTT TGCTCGCTGA TTTCTTGGC
 301 CCAGTATTTT TCTGTGCGA ATTCAATTC GCGGAAGGCA CCGACACGCG
 351 GGAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

a223.pep
 1 VEFRHQVVVV GVEFFGHFDS ELVFVTARQL EELFQR*VLA VEAEGGNRA
 51 GGDQVEDVV VESEIAYGNV IGVGSLVFP VFLAQVFSNS QQFLADFFA
 101 PVFFLGEFQF AEGDTREAA*

m223/a223 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
m223.pep	VEFRHQVVVGV	VEFFGHFDS	ELVFVTARQL	EELFQRQVLA	VEAEGGNRAG	GGDLQVEDVV
a223	VEFRHQVVVGV	VEFFGHFDS	ELVFVTARQL	EELFQRXVLA	VEAEGGNRAG	GGDLQVEDVV
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYNEI	GVGSDLVFP	VFLAQVFSNS	QQFLADFFA	PVFFLGEFQF	AEGADTREAX
a223	VESEIAYGNV	IGVGSLVFP	VFLAQVFSNS	QQFLADFFA	PVFFLGEFQF	AEGDTREAX

q225.seq

g225.pep

m225.seq (partial)

m225.pep (partial)

m225/q225

10 20 30 40 50
 m225.pep FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPIINRAPARRAG
 | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| |||||
 g225 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDROPVLPIINRAPARRAG

510

	10	20	30	40	50	60
m225 . pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
g225	NADELIG-----GAMGLNEQPVVRVNRAXARRAGNA					
		70	80	90		
m225 . pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
g225	DKLIGSAMRLLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225 . pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225 . pep	240	249				
	VKKN DPSRFLNX					
g225	VKKN DPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225 . seq
  1  ATGGATTCTT  TTTTCAAACC  GGCAGTTTGG  GCGGTTTTGT  GGCTGATGTT
 51  TGCCGTCCGC  CCCGCCCTTG  CCGACGAGTT  GACCAACCTG  CTCAGCAGCC
101  GCGAGCAGAT  TCTCAGACAG  TTGCGCGAAG  ACGAACAGCC  CGTTTTACCC
151  ATCAACCGAN  CCCCCGCCCG  GCGGGCGGGC  AATGCCGACG  AACTCATCGG
201  CAGCGCGATG  GGGCTTAACG  AACAGCCCGT  TTTACCCGTC  AACCGANTCC
251  CCGCCCCGGC  GCGGGGCAAT  GCCGACNAAC  TCATCGGCAA  CGCGATGGGG
301  CTTAACGAAC  AGCCCGTTTT  ACCCGTCAAC  CGAGTCCCGC  CCCGGCGGGC
351  GGGCAATGCC  GACGAACTCA  TCGGCAACGC  GATGGGGCTT  AACGAACAGC
401  CCGTTTTACC  CGTCAACCGA  GCCCCGCCCC  GGCGGGCGGG  CAATGCCGAC
451  GAACTCATCG  GCAACGCGAT  GGGACTTTTG  GGTATTGCCT  ACCGCTACGG
501  CGGCACATCG  ATTTCTACCG  GTTTTGACTG  CAGCGGCTTC  ATGCAGCACA
551  TCTTCAAACG  CGCCATGGGC  ATCAACCTGC  CGCGCACGTC  GGCAGAACAG
601  GCGCGGATGG  GTACGCCGGT  TGCCCGAAGC  GAATTGCAGC  CCGGGGATAT
651  GGTGTNTTTC  CGCACGCTCG  GCGGCAGCCG  CATTTCCTTC  GTCGGACTTT
701  ATATCGGCAA  CAACCGCTTC  ATCCACGCGC  CGCGCACGGG  GAAAAATATC
751  GAAATCACCA  GCCTGAGCCA  CAAATATTGG  AGCGGCAAAT  ACGCGTTCGC
801  CCGCCGGGTC  AAGAAAAACG  ACCCGTCCCG  CTTTCTGAAC  TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225 . pep
  1  MDSFFKPAVW  AVLWLMFAVR  PALADELTNL  LSSREQILRQ  FAEDEQVLPV
 51  INRXPARRAG  NADELIGSAM  GLNEQPVLPV  NRXPARRAGN  ADXLIGNAMG
101  LNEQPVLPVN  RVPARRAGNA  DELIGNAMGL  NEQPVLPVNR  APARRAGNAD
151  ELIGNAMGLL  GIAYRYGGTS  ISTGFDCSGF  MQHIFKRAMG  INLPRTSAEQ
201  ARMGTPVARS  ELQPGDMVXF  RTLGGSRISH  VGLYIGNNRF  IHAPRTGKNI
251  EITSLSHKYW  SGKYAFARRV  KKN DPSRFLN  *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225 . pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRXPARRAG				
	10	20	30	40	50
m225 . pep	60	70	79	80	
	NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA				

511

```

|||||
a225      NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
              70      80      90      100      110      120

m225.pep  90      100      110      120      130      140
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
|||||
a225      DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
              130      140      150      160      170      180

m225.pep  150      160      170      180      190      200
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
|||||
a225      MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
              190      200      210      220      230      240

m225.pep  210      220      230      240      249
IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX
|||||
a225      IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX
              250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1   atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcgcgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag ttgcccgaag acgaacagcc cgttttacct
151 gtcaaccgag ccccccggcg gcggggcggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251 ccgcccggcg ggcgggcaat gccgacaaac tcatcggcag cgcgatcgcg
301 cttttgggta ttgctacccg ctacggcggc acatcggtgt ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgcgcgc cagctcggcg gaacaggcgc ggatggcgcg acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggaacaac cgcttcatcc
551 acgcgcgcgc cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgccgcg cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1   MDSFFKPAVAV AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDQPVLP
51  VNRRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFFRTLGGSR SHVGLYIGNN RFIHAPRTGK NIETTSLSHK
201 YNSGKYAFAR RVKKNDSRFL LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1   ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTGTG GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTGCCCgaag ACgaACAGCC CGTttTACCC
151 ATCAACCGAG CCCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCGGTC AACCGAGTCC
251 CCGCCCGGCG GCGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGCCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAATCA TCGGCAACGC GATGGGACTT TTGGGTATTG
401 CTTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTGA CTGCAGCGGC
451 TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCGCGCAC
501 GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCCGA AGCGAATTGC
551 AGCCCCGAGA TATGGTGTtT TTCCGCACGC TCGGCGGCAG CCGCATTTCC
601 CATGTCCGAC TTTATATCGG CAACAACCGC TTCATCCACG CGCGCGCAC
651 GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701 AATACCGGTT CGCCCGCGG GTCAAGAAAA ACgACCGGTC CCGCTTTCTG
751 AACTGA

```


This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQPVLPV NRVPARRAGN ADELIGNAMG
101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAB QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

              10      20      30      40      50      60
m225-1.pep  MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
              |||||
g225-1      MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPVNRAPARRAG
              10'     20      30      40      50      60

              70      80      90      100     110     120
m225-1.pep  NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
              |||
g225-1      NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
                      70      80      90

              130     140     150     160     170     180
m225-1.pep  DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSABEQARMGTPVAR
              |||||
g225-1      DKLIGSAMRLIGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSABEQARMGAPVAR
              100     110     120     130     140     150

              190     200     210     220     230     240
m225-1.pep  SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPARTGKNIEITSLSHKYWSGKYAFARR
              |||||
g225-1      SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPARTGKNIEITSLSHKYWSGKYAFARR
              160     170     180     190     200     210

              250
m225-1.pep  VKKNDPSRFLNX
              |||||
g225-1      VKKNDPSRFLNX
              220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCTGTCGC CCGGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCCTCCCG GCGGCGGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCGC CCCGCGGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTTACC CGTCAACCGA GCGCCCGCCC GCGGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGA CTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAA ACCTGTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR S ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNNDPSRFLN *

```


a225-1/m225-1 88.6% identity in 280 aa overlap

```

      10      20      30      40      50      60
a225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDBQPVLPINRXPARRAG
|||||
m225-1      MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDBQPVLPINRAPARRAG
      10      20      30      40      50      60

      70      80      90     100     110     120
a225-1.pep NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
|||||
m225-1      NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA
      70      80      90

      130     140     150     160     170     180
a225-1.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
|||||
m225-1      DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
      100     110     120     130     140     150

      190     200     210     220     230     240
a225-1.pep MQHIFKRAMGINLPRTSABQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
|||||
m225-1      MQHIFKRAMGINLPRTSABQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
      160     170     180     190     200     210

      250     260     270     280
a225-1.pep IHAPRTGKNIETISLSHKYWSGKYAFARRVKNDPSRFLNX
|||||
m225-1      IHAPRTGKNIETISLSHKYWSGKYAFARRVKNDPSRFLNX
      220     230     240     250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGTACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tcccgcctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcca
451 tttctgttgc ctccgcctct cctgcgcgcg ctcggcccgc atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag ccctcctcc
551 cagttgtggt cttttctcct Cggggcctcg cccctcccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1  MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRRIKFNQ WLPVIVSOLA
101 GSVTGIVTGM YFAAWLGPDT QFSFPPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLLPR LGPHTLRRFT ILPKKLRFK PLLPVVLSL PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGTACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```


514

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGTATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep
 1 MNEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
 101 GSVTGIVTGM YFAKWGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226.pep	MNEILRQPSVLLFLTLAVYALAIIVRTRTG NIFCNPVLVS TIVLIAYLKI LGIDYAVYHN					
	:					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTG NIFCNPVLVS TIVLIAYLKI LGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226.pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVS QLAGSVTGIVTGM YFAKWGAER					
	:					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVS QLAGSVTGIVTGM YFAAWLGPD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226.pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLV GQIAGYKMLK NTVVMPSSVG					
	:					
g226	QFSFPPRLQYLLFTPSGIPHTLYARVLPPFLPPPLPRLGPHTLRRFTILPKKLRPFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC
 51 CGTGTACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCCTA CCTGAAAATC
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATT
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAACC
 251 GCCGTAAAAT CTTCAACCAA TGGCTGCCCG TCATCGTTTC GCAGCTTGC
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGCATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep
 1 MNEILRQPSI LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
 101 GSVTGIVTGM YFAKWGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

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```

m226.pep  MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPLVSTIVLIAYLKILGIDYAVYHN
          |||||||:|||||||||||||||||||||||||||||||||||||||||
a226      MNEILRQPSILLFLTLAVYALAIIVRTRTGNIFCNPLVSTIVLIAYLKILGIDYAVYHN
          10      20      30      40      50      60

          70      80      90      100     110     120
m226.pep  AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
          |||||||:|||||||||||||||||||||||||||||||||||||||||
a226      AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
          70      80      90      100     110     120

          130     140     150     160     170     180
m226.pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
          |||||||:|||||||||||||||||||||||||||||||||||||||||
a226      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
          130     140     150     160     170     180

          190     200     210     220     230
m226.pep  MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPLVGLFX
          |||||||:|||||||||||||||||||||||||||||||||||||||||
a226      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPLVGLFX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgccgccgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccggc agcatcgtcg
101 gcatggcggt gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttcct
201 cgtgccgccc tgcgtggcgg tcatcagcta tttggatttg attgccgacg
251 attggtttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaagggtca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1  MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLEA LLQAGWLKTS
51  WLQQLTDALM ANLTFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1  ..ACGCTTTkGC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTtG GATTtGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1  ..TSXLQQLTDA LMSNLTLFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227

          10      20      30
m227.pep  TSXLQQLTDALMSNLTLFLVPPCVAVISYL
          || |||||:|||||||||||||||||
g227      TAVFLAGIKLPGSIVGMGVLEFALLQAGWLKTSWLQQLTDALMANLTFLVPPCVAVISYL
          20      30      40      50      60      70

          40      50      60

```


516

```

m227.pep    DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
             |||||
g227        DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
             80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1   ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51  CGAAACCGCC GTTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTGGC CTTTGCAGG CGGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TCGGTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGGTTTTC GATACTGGT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1   MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LLOAGWVKTS
51  WLQQLTDALM ANLTFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep                                10      20      30
                                         TSXLQQLTDALMSNLTFLVPPCVAVISYL
                                         || |||||
a227      TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTFLVPPCVAVISYL
           20      30      40      50      60      70

           40      50      60
m227.pep    DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
             |||||
a227        DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
             80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1   ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51  TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1   MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51  VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1   ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51  TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

a228.pep
 1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
 101 KMKDAAK*

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

g229.seq
 1 atggctgccg tatcgggcgg cgggtgcggtc ttctgataa tgcttcaca
 51 tattgcccgc gttagcgcgc agccgccagc gttagcccaa gcgtcgggag
 101 aaatcgccat tgaagccgcc ggcgaattg tatcggtgc cgcaccaagag
 151 gttttgccc acaaacggca cgggtccgaa cgagcgcgtt accgaacggt
 201 tttgatggcc gaacgacagg cgcaggttct gttagctgaa atctttgtta
 251 tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgccc
 301 gccgcattg atttcgcgcg acacgcccaa gccgtagcgc aaaccgtgtg
 351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gccgcgaaat
 401 tcaatcgttt tttcggacga agcgttgatt atagcggatt aacaaaaatc
 451 aggacaaggc ggcgggccgc aggcagtacg gatggtacgg aaccggttcg
 501 cccggtgctt ggacgcctta gggaaccgtt ccctttgagc cggggcgggg
 551 caaccgtac cggttttgtg tcatccgccg tattgtgttg a

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

g229.pep
 1 MAAVSGGGAV FLIMLPHIAR VQROPFAFAQ ASGEIGIEAA GEIVSAAAOE
 51 VLPDKRHGAE RARYRTVIMA ERQAQVLPFAE IFVIPIMHAA ADAVEEMMP
 101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTKI
 151 RTRRRAAGST DGTEPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

m229.seq (partial)
 1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
 101 CGCGTTACCG AACGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTT
 151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
 201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCCGCGCA CACGCCTAAG
 251 CCTAGCGCA AACCCTGTGC CTTTTCGCGC AGGCTGTCGG CGGTTTTCGT
 301 CCAGCTTCTG CCCGCAAAAT CAATCGTTTT TTCGACGAA GCGTTGTTTA
 351 TAGCGGATTA AAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
 401 AATAGTACGG AACCGATTCA CTTGGTGCTT CAGCACCTTA GAGAATCGTT
 451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

m229.pep (partial)
 1 ..AQALGEIGIE AADEIVSAAA XEVLIDKRHD AERARYRTVF IAERQAQALF
 51 AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTV LLRQAVGGFR
 101 PASARKFNRF FGRSVVYSGL TKIRTRQSA DSTNSTEPIH LVLQHLRESR
 151 SLFCSSAILC *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

			10	20	30
m229.pep			A Q A L G E I G I E A A D E I V S A A A X E V L L D K R H D A E		
g229	M A A V S G G G A V F L I M L P H I A R V Q R Q P P A F A Q A S G E I G I E A A G E I V S A A A Q E V L P D K R H G A E	10	20	30	40
	40	50	60	70	80
m229.pep	R A R Y R T V F I A E R Q A Q A L F A E I F V I P I M H A A A A D A A V E E M M P A R I D F A R H A X A L A Q T V C L L				
	: : : :				
g229	R A R Y R T V L M A E R Q A Q V L F A E I F V I P I M H A A A - D A A V E E M M P A R I D F A R H A Q A V A Q T V C L L	70	80	90	100
	100	110	120	130	140
m229.pep	R Q A V G G F R P A S A R K F N R F F G R S V V Y S G L T K I R T R Q R S A D S T N S T E P I H L V L Q H L R E - - - -				
	: : : : : : :				
g229	R Q A V G G F R P A S A R K F N R F F G R S V V Y S G L T K I R T R R R A G S T D G T E P V R P V L G R L R E P F P L	120	130	140	150
	150	160			
m229.pep	- - - - S R S L F C S S A I L C X				
	: :				
g229	S R G G A T R T G F C S S A I L C				
	180	190			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

a229.seq (partial)

```

1  ATGGCTGTCG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51  TATTGCCAC  GTTCAGCGTC AGCCGCCA.. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTTGCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCCGCTGATG TCTCCGTAGA GGAAATGATG
301 CCCGCCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCTGCA
401 AATTCAATCG TTTTTCGGA  CGAAGCGTTG TTTATAGCGG ATTAACAAAA
451 ATCAGGACAA GGCGACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTCAGCACC TTAGAGAATC GTCTCTTGA  GCTAAGGCGA
551 GGCAACGCCG TACTGGTTTT TGTTTCATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

a229.pep (partial)

```

1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51  VLLDKRHDAE *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADVSEEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRFEG RSVVYSGLTK
151 ITRRRRSADS TDSTEPIHLV LQHLRESSL* AKARQRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

			10	20	30
m229.pep			A Q A L G E I G I E A A D E I V S A A A X E V L L D K R H D A E		
a229	M A V V S G G G A V F L I T L P H I A H V Q R Q P P X F A Q A S G E I G I E A A D E I V S A A A X E V L L D K R H D A E	10	20	30	40
	40	50	60	70	80
m229.pep	R A R Y R T V F I A E R Q A Q A L F A E I F V I P I M H A A A A D A A V E E M M P A R I D F A R H A X A L A Q T V C L L				
	: : :				
a229	X A R Y X T V F I A E R Q A Q A L F A E I F V I L I V H A A A A D V S E E M M P A R I D F A R H A Q A V A Q T V C L L	70	80	90	100
	110	120			

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	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
	: :					
a229	AKARQRRTGFCSSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

g230.seq

1	atgttccatt	ccatcgaaaa	atacagaaca	cccgcccaag	tcttattagg
51	cctgattgca	ttacttttg	tcggcttcgg	cgtcagcacg	gtttcccatc
101	cgggcgcgga	ctacatcgtc	caagtgggcg	acgaaaaaat	cagcgagcac
151	tcaatcaaca	acgccatgca	gaacgagcag	gcggacggcg	gcagcccttg
201	gcgcgacgcg	gtgttccaat	ccctgctgca	acgcgcctac	ctgaaacagg
251	gcgcgaagct	gatgggcatt	tcggtttctt	ccgaacaaat	caagcagatg
301	attgtggacg	atcccaattt	ccacgacgca	aacggcaaat	tcagtacgcg
351	gcttttgagt	caatacctgt	cgcaacgcca	tatgtctgaa	gaccagtgtg
401	tcgaagaaat	ccgcgatcag	tttgccttgc	agaatttggt	aagcctcgtc
451	caaaacggcg	tattggtcgg	cgacgcgcag	gcggaacagc	tgatcaggct
501	gacgcaggtc	aaccgcacca	tccgttcgca	cactttcaac	cccgcagagt
551	tcacgcccc	agtcaaagcg	tctgaagccg	atttgcagaa	attttataat
601	gcgaacaaaa	aagactatct	gctgcgcgag	gcggtcaaat	tggaaatagt
651	cgccttgaat	ctgaaggatt	ttgcagacaa	gcagaccgtc	agtgaacagg
701	aagtgaaaaa	tgcgtttgaa	gagcgctggg	cgcgtttgcc	ggcacatgaa
751	gccaaacctt	ctttcgagca	ggaaaaagcc	gccgtcgaaa	acgaattgaa
801	aatgaaaaag	gcggttgccg	acttcaacaa	ggcaaaagaa	aagctgggcg
851	acgatgcggt	caatcatccc	tcctcgcttg	ccgaagccgc	caaaaacagc
901	ggtttgaaag	tggaaaccca	agaaacttgg	ctgagcaggc	aggacgcaca
951	aatgtccggc	atgcccgaaa	acctaataca	tgccgtattc	agcgacgacg
1001	tattgaagaa	aaaacacaat	tccgaagtgc	tgaccatcaa	cagcgaaaacc
1051	gcgtgggtcg	tcgcgcgcaa	agaagtccgc	gaagaaaaaa	acctactgtt
1101	tgaagaagcc	aaagatgcgg	tgcgtcaggc	ctatatccgt	accgaagccg
1151	ccaaactttt	gaaaacaatg	taa		

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

g230.pep

1	MFHSIEKYRT	PAQVLLGLIA	LTFVGFVST	VSHPGADYIV	QVGDEKISEH
51	SINNAMQNEQ	ADGGSPWRDA	VFQSLQRAY	LKQGAKLMI	SVSSEQIKQM
101	IVDDPNFHDA	NGKFSHALLS	QYLSQRHMSE	DQFVEEIRDQ	FALQNLVSLV
151	QNGVLVGDAQ	AEQLIRLTQV	NRTIRSHTFN	PDEFIAQVKA	SEADLQKPYN
201	ANKKDYLLPQ	AVKLEYVALN	LKDFADKQTV	SETEVKNAFE	ERVARLPAHE
251	AKPSFEQEKA	AVENELKMKK	AVADFNKAKE	KLGDADFNNHP	SSLAEAAKNS
301	GLKVETQETW	LSRQDAQMSG	MPENLINAVF	SDDVLKKKHN	SEVLTINSET
351	AWVVRKEVR	EEKNLLFEEA	KDAVRQAYIR	TEAAKLLKTM	*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

m230.seq (partial)

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACCCTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTGCCGA	CTACATCGTC	CAAGTGGGCG	ACGAAAAAaT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	GCGGACGGCG	GCGGCCCTTC
201	GCC.GACGCG	GTGTTCCAAT	CCCTGCTGCA	ACGCGCCTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAACAAAT	CAAGCAAATT
301	ATCGTGGACG	ATCCCAATTT	CCACGACGCA	AACGGCAAAT	TCGACCACGC
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGCCA	TATGTCTGAA	GACCAGTTTG
401	TCGAAGAAAT	CCGCATCAG	TTTGCCTTGC	AGAATTTGGT	AAACCTCGTC

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451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCCGCAG GCGGTCAAAT TGGAAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCATTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTGCGG ACTTCAACAA GGCAAAGAA AAATTGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
  1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
 51 SINNAIQNEQ ADGGGSPSDA VFQSLQRAY LKQGAALMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSD QFVVEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKK AVADFNKAKE KLGDDAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKHKN SEVLITINSET
351 AWWVRAKEVR EEKTLPPAEA KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230.pep	ADGGGSPSDAVFQSLQRAYLKQGAALMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAALMGISVSSEQIKQIMIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230.pep	RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN					
g230	QYLSQRHMSDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN					
	130	140	150	160	170	180
m230.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230.pep	ERVARLPANEAKPSFEQEKA AVENELMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQEKA AVENELMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300

521

	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPFABAKDAVRQAYIRTEAAKL					
	:					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACCTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTGCCGA	CTACATCGTC	CAAGTGGGCG	ACGAAAAAAT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	GCGGACGGCG	GCGGCCCTTC
201	GCGCGACGCG	GTGTTCCAAT	CCCTGCTACA	ACGCGCCTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAACAAAT	CAAGCAGATT
301	ATCGTGGACG	ATCCCAATTT	CCACGACGCA	AACGCGAAAT	TCGACCACGC
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGTCA	TATGTCTGAA	GACCAAGTTG
401	TCGAAGAAAT	CCGCGATCAG	TTTGCCCTGC	AGAATTTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTGGTCGG	CGACGCGCAG	GCGGAACAGC	TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA	TCCGTTTCGA	CACTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCTGAAGCCG	ATTTGCAGAA	GTTTTATAAC
601	GCAAAACAAA	AAGACTACCT	GCTTCCCAAA	GCGGTCAAAT	TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT	TTGCAGACAA	ACAGACCGTC	AGCGAAACAG
701	AAGTGAAAAA	TGCGTTTGAA	GAGCGCGTGG	CGCGTTTGCC	GGCAATGAA
751	GCCAAACCTT	CTTTCGAGCA	GGAAAAAGCC	GCCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	GCGGTTGCCG	ACTTCAATAA	GGCAAAAGAA	AAGCTGGGCG
851	ATGACGCGTT	CAACCATCCT	TCCTCGCTTG	CCGAAGCCGC	CAAAAACAGC
901	GGTTTGAAAG	TCGAAACCCA	AGAACTTGG	CTGAGCAGGC	AGGATGCGCA
951	AATGTCCGGT	ATCCCCGAAA	ACCTGATCAA	TGCCGTATTC	AGCGACGACG
1001	TATTGAAGAA	AAAACACAAT	TCCGAAGTGC	TGACCATCAA	CAGCGAAACC
1051	GCGTGGGTCG	TCCGCGCCAA	AGAAGTCCGC	GAAGAGAAAA	CCCTGCCGTT
1101	TGCCGAAGCC	AAAGACGCGG	TACGTCAGGC	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTT				

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

1	MFHSIEKYRT	PAQVLLGLIA	LTFVGFVST	VSHPGADYIV	QVGDEKISDH
51	SINNAIQNEQ	ADGGGPSRDA	VFQSLQRAY	LKQGAKLMGI	SVSSEQIKQI
101	IVDDPNFHDA	NGKFDHALLN	RYLSQRHMSE	DQFVEEIRDQ	FALQNLVNLV
151	QNGVLVGDAQ	AEQLIRLTQV	NRTIRSHFTN	PDEFIAQVKV	SEADLQKFYN
201	ANKKDYLLEK	AVKLEYVALN	LKDFADKQTV	SETEVKNAFE	ERVARLPANE
251	AKPSFEQEKA	AVENELMKKK	AVADFNKAKE	KLGDDAFNHP	SSLAEAAKNS
301	GLKVETQETW	LSRQDAQMSG	MPENLINAVF	SDDVLKKKHN	SEVLTINSET
351	AWVVRKEVR	EEKTLPFAEA	KDAVRQAYIR	TEAAKL	

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
a230	ADGGGPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

522

m230.pep	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGDA	QAEQLIRLT	QVNRTIR	SHTFN
a230	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGDA	QAEQLIRLT	QVNRTIR	SHTFN
	130	140	150	160	170	180		
m230.pep	PDEFIAQ	VKVSEAD	LQKFYN	ANKKDYLL	PQAVKLE	YVALNLK	DFADKQ	TVSETV
a230	PDEFIAQ	VKVSEAD	LQKFYN	ANKKDYLL	PKAVKLE	YVALNLK	DFADKQ	TVSETV
	190	200	210	220	230	240		
m230.pep	ERVARLP	PANEAKP	SFEQEKA	AVENELK	MKKAVAD	FNKAKEK	LGD	DAVNH
a230	ERVARLP	PANEAKP	SFEQEKA	AVENELK	MKKAVAD	FNKAKEK	LGD	DAVNH
	250	260	270	280	290	300		
m230.pep	GLKVETQ	ETWLSRQ	DAQMSG	MPENLIN	AVFSDD	VLKKKH	NSEVL	TINSET
a230	GLKVETQ	ETWLSRQ	DAQMSG	MPENLIN	AVFSDD	VLKKKH	NSEVL	TINSET
	310	320	330	340	350	360		
m230.pep	EETKLP	FAEAKD	AVRQAY	IRTEAA	KL			
a230	EETKLP	FAEAKD	AVRQAY	IRTEAA	KL			
	370	380						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACCTTTG TCGGCTTCGG CGTCAGCACG GTTTCCTATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCTTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCCGACCA TCCGTTTCGA CACTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCGCTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TGGAAACCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCGGCG ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTGC TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TCGCTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAACAAG GCAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCCTATG TCAGACTGAC CGTCTGCCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCCTGCGA AACAGGCTTT GCGCAACAGC CAGTCTGCCA
1451 ATACTTTCGA CCTGCTGATC CGCTATTTC ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMONEQ ADGGSPWRDA VFQSLQRAY LKQAKLMGI SVSSEQIKQM
101 IVDDPNFHDH NGKFSHALLS QYLSQRHMS DQFVEEIRDQ FALQNLVSLV

```



```

151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKRDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKHHN SEVLINSET
351 AWVVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TFPEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGCGG CCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGAGC ATCCCAATT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGCTGTA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTGCTTTCG AGAATTTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCCGACCA TCCGTTGCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTGTCAGAA ATTTTATAAT
601 GCGAACAATA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCATTGTA GAGCGCGTGG CCGGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTTGGCG
851 ACGATGCGGT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCGGGT ATGCCGAAA ACCTGATCAA TGCCGTATTG AGCGACGAGC
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAACAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCGAGGCG TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCTACG TCAGGCTGAT CGGTCTGCCG
1351 CGACCCGCTG TTGTCGAAAT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGGCAACAG CAGTCTGCCA
1451 ATACTTTCCA CTTGTTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTGCA CAACGCGGAC GGTCAAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDERISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAALMGI SVSSEQIKQI
101 IVDDEFHDA NGKFDHALLN RYLSQRHMSD QDFVEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKRDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKHHN SEVLINSET
351 AWVVRAKEVR EEKTLPFEEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TFPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

```

          10      20      30      40      50      60
m230-1.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDERISDHSINNAIQNEQ
          |||||
g230-1      MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDERISEHSINNAIQNEQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m230-1.pep ADGGGPSRDAVFQSLQRAYLKQGAALMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN
          |||||
g230-1      ADGGGPSRDAVFQSLQRAYLKQGAALMGISVSSEQIKQIIVDDPNFHDANGKFSHALLS
          70      80      90      100     110     120

          130     140     150     160     170     180
m230-1.pep RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN

```


a230-1.seq

1	ATGTTCCATT	CCATCGAAAA	ATACAGAAGC	CCCGCCCAAG	TCCTTTTGGG
51	CCCTGATGCA	TTAACTTCTG	TCCGCTTCGG	GGTCAGCAGC	GTATCCCATC
101	CGGGTGCCGA	TCACATCGTC	CAAGTGGCGG	ACGAAAAAAT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	CCGGACGGCG	CGCGCCCTTC
201	CGCGCAGCGG	GTGTTCCAAT	CCCTGCTACA	ACGCGCCTAC	CTGAAACAGG
251	GCGCCAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAAACAAAT	CAACGAGAT
301	ATCGTGGAGC	ATCCCAATTT	CAGCGACGCA	AACGGCAAAAT	TAAGCAGCGC
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGTCA	TATGCTGAA	GACCACTTTG
401	TCGAAGAAAT	CCGCGATCAG	TTGCGCTTGC	AGAAATTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTGGTTCG	CGACGCGCAG	CGCGAACACG	TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA	TCCGTTCCGA	CACTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCGAAAGCCG	ATTTCGAGAA	GTTTTATAATC
601	GCAAAACAAA	AAGACTACCT	GCTTCCCAAA	CCGGTCAAAAT	TGGAATATGT
651	CGCCTTGAAAT	CTGAAAGACT	TTCGACAGAA	ACAGACCTTC	AGCGAAACAG
701	AAGTAAAAAT	TGGCTTTGAA	GAGCGCGTGG	CGCGTTTGGC	GGCAAAATGAA
751	GCCAAACCTT	TTCTCGAGCA	GGNAAGAACG	CCCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	GCGGTTGCCG	ACTTCAATAA	GGCAAAAGAA	AAGCTGGCGC
851	ATGACGCGTT	CAACCACTCT	TCTTCGCTTG	CCGAAGCGCG	CAAAAAACAGC
901	GGTTTGAAGT	TACGAACCCCA	AGAAACTTTG	CTGAGCAGCG	AGGATGCGCA
951	AATGTCCGGT	ATGCCCGAAA	ACCTGATCAA	TGCCGTATTG	AGCGACGACG
1001	TATTGAAGAA	AAAAACAAT	TCCGAAGTGC	TGACCATTAA	CAGCGAATCC
1051	CGGTGGGTGC	TCCCGGCCAA	AGAACTCCGC	GAAGAGAAAA	CCCTGCCGTT
1101	TGCCGAAGCC	AAAGACGCGG	TACGTCAGGC	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTTGC	CGAAAACAAG	GCAAAAGACG	TGCTTATCCA	ACTGAACGCG
1201	GGCAAGGCTG	TTGACGTGAA	GTGTCGGTAA	GTGTCGGTTT	TGGCGCGCAC
1251	GCAGGCAAGG	CAGTCCATGC	CGCCCCAGGC	TTATGCGGAA	CTGCTGAAAG
1301	CAAAACCGCG	AAACCGGCAA	CCGCGCTTGC	TACAGGCTAG	CGGTTCTGCC
1351	GCACCGCTGA	TTGTCGAAT	ACAGGCTTGA	ACCCCGCGCG	ATGATATCGC
1401	CGCACAGCTT	CCGCTTGCAA	AACAGGCTTT	GGCGCAACAG	CAGTCTGCCA
1451	ATACTTTCGA	CTTGTGTGTA	CGTTATTATCA	ACGGCAAAAT	CAACAGACCC
1501	AAAGGAGCGC	AATCGGTCGA	CAACGGCGAC	GGTCAGTAA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFGVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGA KLMI SVSSEIQKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRakeVR EEKTLPF AEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIRQT
501 KGAQSVNDGD GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

```

g231.seq
1   atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
51  gccgccgttg caaaataatc cgccatttta cgtaaaaaac cgccgcctga
101 acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151 gcgcgcggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtctt
201 accaaatgcc caaccattcg ccacggaat ccatccaatc cttattgccc
251 ccgcccgtcc tgccgtcccg gcggtacgcc cacggcgctt gcggattttt
301 agctttccac aatcctttgc gttcccttcc cgctgaatt tgagcgctcg
351 catagtcggc aaaatccgcc ttatcctgct gttcttttagc ataactttta
401 taatgccacg ccgcccgcgc ctgcacctgc atcagggttca aatcggtttt
451 gccggcggtt acctgcgcca cttcgcgctg atagcggtcg gtttcaaaca
501 cactgtacact gactttccta ccctccgccc cgcgcgcgag gttgtcgcgc
551 gaacgtgtac cgtaagcctg tttcatctcc ggtgcgtcga tatacgccat
601 ccgaatttta tgtttcgcgc cgtcgcgctc gatgacgtga aggtatcgc
651 cgtcatagac tttggacacc gtgcctgtgt agctgtggcc ggatttcgcc
701 gatgcccgtc ggcgaaacgg gcgctcgaaa cccacgtccc ctgcagtgcc
751 gactacgtcg agtacggcaa ccgcccgtcc caccgcctca ctgtcatatc
801 ccgtataacc caacgcgccc aaaagcgaca ggcgcgacgg aagccatttc
851 atgatttttt taatctgcat atttttcaca tgccgatgcc gtctgaacat
901 ctctga

```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

```

g231.pep
1   MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFVAV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAPFP RLNLVGIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYT DFPTLRRAQ VVARTCTVSL FHLRCVDIRH
201 PNFMFRAVAV DDVKGIAVID FGHRAVAVA GFRRCPSANG RVETHVPCSA
251 EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMMPSEH
301 L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```

m231.seq (partial)
1   ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGCGGGAAC
51  GCCGCCGTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG GC....

```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```

m231.pep (partial)
1   MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFVAV QGRAVSLPNA QPFG.....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

```

m231/g231
      10      20      30      40      50      60
m231.pep  MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          |||||||||||||||||||||||||||||||||||||||||||||||
g231      MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          10      20      30      40      50      60

      70
m231.pep  QGRAVSLPNAQPFG
          |:|||||||||:
g231      QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFQSFAPFPRLNLVGIVG
          70      80      90     100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

a231.seq (partial)

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCCG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTGGAACA
501 CGCGGACGCT GACTTTCTTG CTTCCGCGC CCGCGCGCAG GTTGTGCGGC
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GGCGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPOKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPPG					
a231	QSRVSLPNAQPPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAGGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCCG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCCG ccgcgcgCAG GTTgtcgcGC
551 GAACgTGTAC CGTAagcgtg TTtcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTTta tGtttcgcgc cgtgcgcGtc gatGACGTGA AGGgtatcGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGATttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```


101 SFPQSFAFPF RLNLVGIIVG KIRLILLEFS ITFIMPRRPV LHLHQVQIGF
 151 AGGYLRHFAL IAVGFKHTYN EFTRLRRRAQ VVARTCTVSV FHLRCVDIRH
 201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
 151 GCGCGCGGTT TTCAGACGGC ATTGCGGTT CAAAGCCGTG CGGTGTCTTT
 201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCG
 251 CCGCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
 301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCTGAATT TGAGCGTCGG
 351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTA
 401 TAATGCCAGC CGCCCCGTC CTGCACCTGC ATCAGGTTC AATCGGTTT
 451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTATCGAACA
 501 CGCGCACGCT GACTTTCCTG CCTTCCGCGG CCGCGCGCAG GTTGTCCGCG
 551 GAACCGCTGC CGTAAGCCTG TTTCATCTCC GCGCGCTCGA TATACGCCAT
 601 CCGGATTTTG TGTTCGCGC CGTCCGCGTC GATAACGTGA AGGGTGTCCG
 651 CGTCATAGAC TTTGGACACC GTGCCGTGTG AGCGGTGGCC GGATTTGCGC
 701 GATGCTCGGC GCGGGCGGG CGCGTCGGA CCGCGCTCC CTGCCGCGCC
 751 GAGTACGTC AGTACGGCAA CCGCGTCCG CACCGCTCG CTGCCGTACC
 801 CCGTATAACC CAACGCACC AAAAGCGACA GCGCGACGGG AAGCCATTTC
 851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
 901 ATCGGAATCG GATTTCAGAC GGCATCTTA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

1 MSKRKSINRP YQKPAELPPL QNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51 ARGFTAFQAV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
 101 SFPQSFAFPF RLNLVGIIVG KIRLILLEFS ITFIMPRRPV LHLHQVQIGF
 151 ADRLNRHFAL VAVGIEHAHA DPAFRRRRAQ VVARTRAVSL FHLRRVDIRH
 201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRQDGG KPFHDFNLH IFQMPMPSEH
 301 IGIGFTAS*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
g231-1.pep	QGRAVSLPNAQPFAGHGHPIILIAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVGIIVG					
m231-1	QSRVSLPNAQPFAGHGHPIILIAAPACSAVRPRRLRIFSFPQSFAFPFRLNLVGIIVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g231-1.pep	KIRLILLEFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFTRLRRRAQ					
m231-1	KIRLILLEFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGIEHAHADPAFRRRRAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
	250	260				
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQDGGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG

529

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CGCGCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTC CGCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTGTCGAACA
501 CGCGGACGCT GACTTTCCTG CCTTCGCGCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTATCTCC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTGCGC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGCTCCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTCAGAC GGCATCTTA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPOSFAFFP RLNLVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLRHFFAL VAVGVEHADA DFPFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVD FGHRAVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRGDGG KPFHDFNLH IFQMPMPSEH
301 IGIGQTASX

```

a231-1/m231-1 99.0% identity in 309 aa overlap

a231-1.pep	10	20	30	40	50	60
m231-1	10	20	30	40	50	60
a231-1.pep	70	80	90	100	110	120
m231-1	70	80	90	100	110	120
a231-1.pep	130	140	150	160	170	180
m231-1	130	140	150	160	170	180
a231-1.pep	190	200	210	220	230	240
m231-1	190	200	210	220	230	240
a231-1.pep	250	260	270	280	290	300
m231-1	250	260	270	280	290	300
a231-1.pep	310					
m231-1	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatacctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctgttt

```


530

```

151 atgccgtccg tacccgcaa ggctgccgat acccaaatcg agtgggaatat
201 tgtccgtggt acaaaatccc tgctgcgtga aacgggtgcgg cacaatccccg
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggt attgccgcg
401 gtccgtact gtgtgccaaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacggttg gtgcgttggg ttcgacggtt tgcggcctgg ttttggtgtg
501 gctgacgcac ggacaccgtt ttgaagggtt gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cggatgatgac gctgatcggc
601 ttttccggcg gattttttctc cgttccgctc tatacctggc tgcaaacccg
651 cagcagcgag actttccgcg cccgcgccgt tgcggccaac aatatcgta
701 acggcatctt tatggtttcc gccgcggtt tgagcgcggt attgctgtt
751 ttgtttgaca gcattttccct gctgtatctg attgtcgctt tgggcaatat
801 tccgttggcg gtatttttga ttaagcgcga aaggcggtt ttaggcgcg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGNLGI FWFLSQWAY PMAVMTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1 ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCTG CCATCCTGTT
51 CCGTCAGATT TTGGGAACGG CCGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCCGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCGGTGGC AAAAAATCCC TGCTGCGTGA AACGGTGCGG CACAAGCCCG
251 TTTTACC CGC CATTATCGGT ATTCGTGGT TTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTT AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TGCGGCTTGG TTTTGGTGTG
501 GGTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CGGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTCTC CGTTCCGCTC TATACCT (g) TG CAAACGCCA
651 TAGCGAGATT TCCGCGCCCg GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATG TTTCCGCTGC CGTTTGTAGC GCGGTGTTGC TGTTTTGTGTT
751 TGACAGCATT TCCTTGTGTT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCCGTATT TTTGATTAG CGCGAAAGGC GGTTTTTAGG CGCGCGGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGNLGI FXFLSQWAY PMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

          10      20      30      40      50      60
m232.pep  MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
          |||
g232      MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```


531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232.pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWVGAVYTTQLPTFTQIHLGGNDNVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m232.pep	NLMLALPSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGNLGI					
g232	NLMLALPSIGIAAGSVLCAKFSXERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGNLGI					
	130	140	150	160	170	180
	190	200	210	220	230	
m232.pep	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMVS					
	190	200	210	220	230	240
	240	250	260	270	280	289
m232.pep	AAVLSAVLLFLFDSISLLYLIALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIALGNIPLAFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

a232.seq	1	ATGTACGCTA	AAAAAGGCGG	TTTGGGACTG	GTTAAAGACC	GCCGTTTCGC
	51	ACCTCTTTTC	GCTACGCAGT	TTCTCGGCGC	GTTCAACGAC	AATGTGTTCA
	101	AAACCGCGCT	GTTTGTGATG	ATTGGGTTTT	ACGGTTTGGG	GCAAAACGGC
	151	TTCTGCGCTG	CCGCACAGAT	GTTGAACTTG	GGCGCGTTGC	TGTTTATTTT
	201	CCCGTATTTC	CTGTTTTCCT	CGCTGTCGGG	GCAGTTGGGT	AACAAATTCG
	251	ACAAGGCCGT	TTTGGCGCGT	TGGGCCAAGG	TGCTGGAAT	GATCATTATG
	301	GCGGTGGCGG	CATACGGGTT	TTATATCCGG	TCTGCCCCGC	TGCTTTTGGC
	351	GTGTCTGTTT	TGCATGGGCG	CGCAATCGAC	GCTGTTCGGG	CCGCTGAAAT
	401	ACGCCATCCT	GCCCGATTAT	CTCGACGACA	AAGAGTTGAT	GATGGGCAAC
	451	AGCCTGATTG	AATCGGGTAC	GTTTGTTCGC	ATCCTGTTTC	GTCAGATACT
	501	GGGACTGCG	GTGGCAGGTG	TACCGCCTTA	TATTGTTCGG	ATACTGTTT
	551	TGCTGGTTCG	CGTAGGAGGC	ACGGTCGGCA	GCCTGTTTAT	GCCGTCGGTA
	601	CCCGCCAAGG	CTGCCGATAC	ACAAATTGAG	TGGAATATTG	TCCGGGGTAC
	651	AAATCCCTG	CTGCGTGAAA	CGGTGCGGCA	CAAGCCCGTT	TTTACCGCCA
	701	TTATCGGTAT	TTGCTGGTTT	TGGTTGTGTC	GCGCGGTTTA	TACCAACGCA
	751	CTGCCGACCT	TTACCCAAAT	CCATCTAGGC	GGCAACGACA	ATGTTTTCAT
	801	CCTGATGCTT	GCCCTGTTT	CCATCGGTAT	TGCCGCCGGT	TCGGTACTGT
	851	GTGCCAAGTT	CAGCAGGGAA	CGGCTGAGGT	TGGCTTGGGT	AACGGTTGGT
	901	GCGTTGGGTT	TGACGGTTTG	CGGCTTGGTT	TTGGTGTGGC	TGACGCACGG
	951	ACACCGTTTT	GAAGGGCTGA	ACGCGATTTT	TTGGTTTTTA	TCGCAAGGAT
	1001	GGGCATATCC	CGTGATGGCG	GTGATGACGC	TGATCGGCTT	TTTCGGCGGA
	1051	TTTTTCTCCG	TTCGCTCTA	TACCTGGCTG	CAAACCGCCA	GTAGCGAGAC
	1101	TTTCCGCGCC	CGCGCGTTG	CCGCCAACAA	TATCGTTAAC	GGTATTTTAA
	1151	TGGTTTCCGC	TGCCGTTTTC	AGCGCGGTGT	TGCTGTTTTT	GTTTGACAGC
	1201	ATTTCTTGT	TGTATCTGAT	TGTCGCTTTC	GGCAATATTC	CGTTGTCGGT
	1251	ATTTTGTATT	AAGCGCGAAA	GGCGGTTTTT	AGGCGCGGCG	GCAATCAGGA
	1301	AAAAACCTTG	A			

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

a232.pep	1	MYAKKGLGL	VKSRRFAPLF	ATQFLGAFND	NVFKTALFVM	IGFYGLGQNG
	51	FLPAGQMLNL	GALLFILPYF	LFSSLSGQLG	NKFDKAVLAR	WAKVLEMIIM
	101	AVAAAGFYIR	SAPLLLACLF	CMGAQSTLFG	PLKYAILPDY	LDDKELMMGN
	151	SLIESGTFVA	ILFGQILGTA	VAGVPPYIVG	ILVLLVAVGG	TVGSLFMPSV
	201	PAKAADTQIE	WNIVRGTKSL	LRETVRHKPV	FTAIIGISWF	WVGAVYTTQ
	251	LPTFTQIHLG	GNDNVFNLM	ALFSIGIAAG	SVLCAKFSRE	RLRLAWVTVG


```

m232.pep                                10      20      30
                                         MMGNSLIESGTFVAILFGQILGTAVAGVPP
                                         |||||
a232    ACLFCMGAQSTLFGPLKYAILPDYLDDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP
      120      130      140      150      160      170

      40      50      60      70      80      90
m232.pep    YIVGILVLLVAVGGTVGSLFMPSPVAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG
      |||||
a232    YIVGILVLLVAVGGTVGSLFMPSPVAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG
      180      190      200      210      220      230

      100      110      120      130      140      150
m232.pep    ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMMLALFSIGIAAGSVLCAKFSXERLMLAW
      |||||
a232    ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMMLALFSIGIAAGSVLCAKFSRERLRLAW
      240      250      260      270      280      290

      160      170      180      190      200      210
m232.pep    VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMVAVMTLIGFFGGFFSVPL
      |||||
a232    VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMVAVMTLIGFFGGFFSVPL
      300      310      320      330      340      350

      220      230      240      250      260
m232.pep    YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS
      || :|| :|
a232    YTWLQTASSETFRARAVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS
      360      370      380      390      400      410

      270      280      289
m232.pep    VFLIKRRERFLGAAAIRKKPX
      |||||
a232    VFLIKRRERFLGAAAIRKKPX
      420      430

```

g233.seq					
1	atgaaacgca	aaaatatcgc	gctgattccc	gccgcggcca	tcggggtgcg
51	tttcggtgcg	gaca aaacca	agcaatatgt	cgaaatcgga	agcaaaaaccg
101	ttttagaac	tgtactttggg	at ttttgaac	ggcatgaggc	cgctcgatttg
151	accgtcgttg	tgtcttcgcg	cgaagacacg	tttgcgcgata	aggttccagac
201	ggcatttcca	caggttcggg	tgtggaaaaa	cggtggacag	accgcgcgcg
251	aaactgtccg	caacgggtgtg	gcaa aactgt	tggaaaccgg	tttg gcgcgcg
301	gaaaccgaca	atattcttgtt	acacgatgcc	gccccgtctgt	gcctgcgcgtc
351	tgaagctctg	gcgcggttga	tagaaacaggc	gggcaacgcc	gcggaaggcg
401	ggatttttgcg	agtccccgtt	gcgcatacgc	tcaagcgcgc	agaaa gcgga
451	caaatcagtg	caactgtcga	ccgttcgggg	ctttggcagg	cgcaaacgcc
501	gcagcttttt	caagcgggtt	tgctgcaccg	cgcattggct	gcggaaaact
551	tgggcggcat	taccgatgaa	gcgtccgcgc	tggaaaaaact	gggtgttcgt
601	cgctactga	tacaggggca	gcgcgcgaat	tggaaactga	cgcagccgca
651	ggacgcatac	atcgtcagcg	tgctgctcaa	tgccgtctga	

g233.pep

1	<u>MKRKNIALIP</u>	<u>AAGIGVRFGA</u>	DKPKQYVEIG	SKTVLEHVLG	IFERHEAVDL
51	TVVVVSPEDT	FADKVQTAFP	QVRVWKNGGQ	TRAETVRNGV	AKLLETGLAA
101	ETDNILVHDA	ARCCLPSEAL	ARLIEQAGNA	AEGGILAVPV	ADTLKRAESG

533

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGV
 201 PLLIQGDARN LKLTQPDAY IVRLLLNAV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTCAGAC
 201 GGCATTTCCTA CAGGTTCCGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG
 401 GGATTTTGGC AATCCCATG GCGGATACGC TCAAGTGC GCACGGTGGG
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
 101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
m233.pep	70	80	90	100	110	120
	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	130	140	150			
	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
	:					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTCAGAC
 201 GGCATTTCCTA CAGGTTCCGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACGTCCTG CAACGGTGTG GCAAACTGT TGGAAACCGG TTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG
 401 GGATTTTGGC AATCCCGTT GCGGATACGC TCAAGTGC GCACGGTGGG
 451 AACATTAGTG CAACCGTCGA GCGGACGAGC CTTTGGCAGG CGCAAACGCC
 501 GAAAGCTTTT CGCGCCGGGC TGCTGCACCG CGCATTTGCT GCGGAAACT
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC
 601 CCTTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNIVLHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDV*
```

m233/a233 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m233.pep	MKRKNIALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
a233	MKRKNIALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233.pep	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
a233	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
a233	TRLIEQAGNA AEGGILAI PVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA					
	130	140	150	160	170	180
a233	AENLDGITDEASAVEKLGIRPLLVQGDARNLKLTQPQDAYIVRLLLDVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgcgcg catcgctttt gccgcgcgtg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat caccgtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggttaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaaatcg gcatttcgag caaagcgag aacctgaaag gcgcagatta
351 tgctggtacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcggcggaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaaccg
651 cgcattggcaa tccaaccggt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRFNV LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGTSGY DATLNGKVLD
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACCG CAAAGTTTTA GACTTGGCAA
101 TCCGCGAAGC .gTCAACAGC CTGTTTCAAG CTGTTGACAA CGGCGCATGG
151 CAACCAACCC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

535

m234.pep (partial)
 1 ..GAGEYALSNR EIIGFGGTSG YDATINGKVL DLAIKAVNS LVQAVDNGAW
 51 QPNR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng)
 from *N. gonorrhoeae*:

m234/g234

				10	20	30
m234.pep				GAGEYALSNREI	IGFGGTSGYD	ATINGKVL
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQ	GAGEYALSNREI	IGFGGTSGYD	ATINGKVL		
	140	150	160	170	180	190

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
g234	DLAIREAVDNLVQAVDNGAWQSNRX		
	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)
 1 AACCGCACCT ATTTGAACGC ATTAAAACAG GAATCCGGCA TTTCGGCAA
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTGTTGGGT
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCAC TTCGCTACGAT
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)
 1 NRTYLNALKQ ESGISGKAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD
 101 ATLNKVLDDL AIREAVNSLV QAVDNGAWQP NR*

m234/a234 100.0% identity in 54 aa overlap

				10	20
30					
m234.pep				GAGEYALSNREI	IGFGGTSGYD
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQ	GAGEYALSNREI	IGFGGTSGYD	ATINGKVL	
	50	60	70	80	90

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
a234	DLAIREAVNSLVQAVDNGAWQPNRX		
	110	120	130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

536

```

1  atgaaacctt tgatttttagg gcttgccgcc gtggttggtc tgtctgcctg
51  ccaagttcga aaagctcccg acctcgacta cacgtcattc aaagaaagca
101 aaccggcttc aattttggtg gttccgcgcg tgaacgagtc gcttgatgtc
151 aacggcactt gggggatgct ggcttcgacc gccgcgccga ttccggaagc
201 cggctattac gtctttcccg ccgcagtcgt ggaggaaacc ttcaaagaaa
251 acggcttgac caatgccgcc gatattcacg ccgtccggcc ggaaaaactg
301 catcaaattt tcggcaatga tgcggttttg tacattacgg ttaccgaata
351 cggcacttca tatcaaattt tagacagcgt gacgaccgta tccgccaaag
401 caggctgggt cgattcccgc aacgggaaag agttgtggtc ggggtccggcc
451 agcatccgcg aaggcagcaa caacagcaac agcggcctgt tgggggcttt
501 hqifgndavl yitvteygts yqildsvttv sakarlvdslr ngkelwsgsa
551 atcaggtttc caaaaccgcc gcatacaacc tactgtcgcc ctattccgcg
601 aacggtatct tgaagggtcc gagattcgtc gaagagcagc ccaaataa

```

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

```

1  MKPLILGLAA VLALSACQVR KAPDLDTYTSF KESKPASILV VPPLNESPDV
51  NGTWGMLAST AAPISEAGYY VFPAAVVEET FKENGLTNAI DIHAVRPEKL
101 HQIFGNDABL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVGA VVNQIANSLT DRGYQVSKTA AYNLLSPYSR
201 NGILKGPRFV EEQPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

```

1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTACAG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGTTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAG
401 NACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTGAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC CAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAGGTCC GAGATTCGTT GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235.pep

```

1  MKPLILGLAA VLALSACQV KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAI DIHAVRPEKL
101 HQIFGNDABL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST					
g235	MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
g235	AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

m235.pep	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
g235	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
	130 140 150 160 170 180
	190 200 210
m235.pep	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
g235	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
	190 200 210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTCTGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGCCG GAAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGGTTTTC TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAAGCGA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

	10 20 30 40 50 60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
a235	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
	10 20 30 40 50 60
	70 80 90 100 110 120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIAVHVRPEKLHQIFGNDAVLYITVTEYGTS
a235	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIAVHVRPEKLHQIFGNDAVLYITVTEYGTS
	70 80 90 100 110 120
	130 140 150 160 170 180
m235.pep	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
a235	YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
	130 140 150 160 170 180
	190 200 210
m235.pep	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
a235	DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
	190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq


```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTA ATGCCAGCAG
101 CGTTTCGATT TTTCCGCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTCCGCGCGC GGTAATTTTCG
251 GCTTCCGCCT GCAAggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAgTTC GGCTTCGGCT TTTTCGTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCGC CCGCCGATGA TGTCCCACGC
451 TTCTTCGCGG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 TCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGGGCGGGC GCGGCTGTCTG
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGAAGG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTTCGAG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCACAC ATATCCGCTT GTTGCACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAACagG AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGTTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcccgt gTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCGCGC CCGAATTCGT TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACATTTTG CGGCCGTTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAAFAFFAV AGFGGNGKFI
51 TDFHPCFRHQ QGKAQFFAQS IQIAGHFRRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRN NQENQAARDV VQGLLRAAAG AAVGFGGVEA VFQDVEVERA
201 QVFRARNNV FHGEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAO
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTGCGC GCGCAAAGGC TCGATGGCGG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATT TTTCAACAGT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCTCTTTCGC CGCCGCCGwT GaYGTCCAC GCTTCTTCGC
201 CCGTGAAGCA CAAATCGGT GCAATCAAGA GAACCAAACT GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTTCA GGATGTGCGG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACA-TG TCTTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCTGCCAG ACACCTCTTG AGCTGACGTG CCAATACCAC
451 GCGGTAGCGG TCGATTTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTTCTT TGGAAATCGC
601 CAATTGCGCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTGCGCTTC GCCGTCGACA ACGAAACCAT GGTTCAGCAG
751 CTGTTTATAC GGCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRIDGFGV AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPMSME
51 EDAVXFAAAX DVPRFFAGEA QNRNQNENQT ACDVIQSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFRAE RNXFYQKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDPHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236


```

a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGCAGA
51  CGGTTTTCATG GCCTGCAACC GCGCCCATAT CGCGGGTGTA GTGCCAGCAG
101 CGTTCGCATT TTTCAACATT ACTGGCTTTA GCGGCAACGG CAAGTTCGCT
151 GCGTACTTTC ACTTCTGCTT TAGACACAG CAAAGCAAAG CGCAATCTTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCCGGCGC GGTAAATTCG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTGCGCGC GCAAAGGCTC
301 GATGGCGCGG GTTACCGCTT CGCGGGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAAGTC GGCTTCGGCT TTTTCGTTGA TGGTCGGGAA CTCTGCCAA
401 TTATGGA AAA GCACGCTGTC TTCTCGCGCG CGGCCGATGA TGTCCACGCG
451 TTCTTCGCGG GTGAAGCACA AAATCGGGTG AATCAAGAGA ACAGGCTGCG
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGGCGGGGC GCGGCTGTCG
551 GCTTTGGTGG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTC TTTCACTGCA AAGTGGAAAG
651 CATAACGCGG ATAAAAATCA CGGGCAACGC GTTCTTGCAG CCGCCTTGCC
701 AACACCAAGG CATAGCGGTC GATTTCACC ATATCGCGCT GTTGCAACGG
751 ATCTTCAATA GGATTGAAGT CGCTCAAGTT GGCAAACAAA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTTGAG GATTTCTTTG
851 GAAATCGCCA ATTCGCGCGT GTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCCGGC CCGAACTCGT TATACACTTC TTGCGCGCGC ACGACGTTGC
951 CGATGGATTT CGACATTTTT GCGCCGTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTTGTACGG CGCGCAGACC ATTGA

```

a236.pep

1	MARFAFSADI	LCTAFADGFM	ACNRAHIAGV	VPAAFAFFTI	TGFSGNGKFA
51	AYFHFCEFRHQ	QSKAQFFAQS	IQIAGHFRRR	GNFGFGLQGR	TDFGVGAQRL
101	DGGGYRFAGF	ADCRPFPHQF	QGFGFVDGRE	LVPSEKHAHV	FCAAADVPR
151	FFAGEAQNRC	NQENQAARDV	VQGGRLAAAG	AAVGFGGIEA	VFQDIEVERA
201	QVFRAERNHF	FHGKVEGITR	IKITGNAFLO	PPCQHQGIAY	DFHHIRLLHG
251	IFNRIEVAQV	GKQKAQGIAD	TAVAFGYALE	DFFGNRFQAA	VIGGCRPQAO
301	DVRAELVIHF	LRRDDVADGF	RHFAFVLIHH	ETMGQOLFVR	RATH*

[illegible]

q237.seq

1	atgcggggaca	aggttgccgg	taatatcgca	ctccccgcc	cacgaatat
51	cgattctaac	atcggcaagc	tgcggaaaaa	ctttaagcat	atcttgccgg
101	acaagctcgg	tcatacgcg	aggattgtcg	ataaattcgt	tatccttacc
151	gccgaaaagc	agcctgcctg	ccgcgctgag	gcggtaataa	tccaaaatat
201	ggcggttgtc	gcatactgcc	atattgtgtc	ggataagccc	ttttgtgcgc
251	gcgcccgaag	gttcggtggc	aataataaag	gtgctgacgg	caatcgccct
301	gcgttcctaa	ggccggaata	tcgggttcaa	accgacataa	gtattgacgg
351	catagaccac	atttttacac	tcgacgctgc	cttcgggcgt	gtaaacccgc
401	caaccgtttt	gatacggttc	gatgcgcgtc	atcggggatt	gctcgaataa
451	ctgcgcgcgc	gcttcggcag	cggcgctggc	aacaccaaac	gtgtaattga
501	gcggatgaag	atgccggag	aagggatcga	actgtgcgcc	ttgtgtacata
551	tcgctgtcaa	gctgtctgtt	caactcggct	ttatcccaaa	gttgataatg
601	actcgcaccg	taatgccgtt	gggcgtgttc	atgccactgc	tgcaactctt
651	cccaatgctg	cggacggacg	gcaaccgtgg	cataaccgcg	ctgccaatcg
701	caatcgatgg	catgttttgc	gacgcgttcg	tccaccagtt	cgaccgcctg
751	caaagactgt	tgcaaaaacc	atgtgcctct	ctccaagccg	acctgttttt
801	caatttcccc	cataccgcag	cgcgtagtgc	tgataaacctg	cccgccaact
851	ctgccggacg	cgccgaagcc	gatacgtgcg	gcttccaaaa	cgacggcttc
901	atgtccgtgt	tccgccacgg	gcaatgcggt	acacaaaccg	ctcaaaccgc
951	cgccgataat	gcaggtttcg	gctttcagac	ggcatctggg	tttcggataa
1001	acagtatcgg	gattaaccga	actaaaataa	taaggaaggca	gatattcttg
1051	aaaatacggg	cgaatcattg	tgtttgcctt	atacgggtata	ttcttggcag
1101	gaatgataca	gactgtccgg	ccatatcgtc	caaacagaaa	atcggttgaa

g237.pep

1 MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51 AEKQPAVRAE AVIIQNMAVV AYCHIVADKP FCARAOGFGG NNGGADGNRL


```

101 AFORPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLLLEN
151 LRAFGSGAG NTQVIERMK MPQGIELCA LVHIAVKLLF QLGFIPLKIM
201 TRTVMLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF
301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRQIFL
351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

```

m237.seq
1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TCGGAAAAA CTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATACGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGGCGGC
251 GCCCCAAGG GTTCGGTCGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG
351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTCGGGCGT GTAAACCAAGC
401 CAACCGTTTT GATGCGGTTT GATGACGTC ATCGGGGATT GCTCGAAAAT
451 CTGCGCACCG GCTTCGGCAG CCGCACGAGC GATGCCCAA GTGTAAGTGA
501 GCGGATGCAG GTGTCCGGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA
551 TCGCTGTCAA GCTGTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG
601 ACTCGCACCG TAATCCCGTT GGGCGTGTT ATGCCACTGC TGCAACTCTT
651 CCCAATGCTG CCGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
701 CAATCGACCG CATGTTTTCG GACGCGTTCG TCCACCAATT CGACCGCCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
801 CAATTTCCCC CATAACCGAG nCGTAATCGC TGATAACCTG CCGCCACTC
851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCCAATCCGC
951 GCGCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCAGGTGTA TTTTCGGACG
1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAWACAGAAA ATCGGTGTA

```

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

```

m237.pep
1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT
51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGKADSNRL
101 AFORPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLLLEN
151 LRTGFGSGTS DAQSVSERMQ VSGXGVLCPL LVHIAVKLLF QLGFIPLKIM
201 TRTVMLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRRAET DTRGFQHNRF
301 MSLLRQGQCS AQTTQSAADD TGIGFQTALK FRINSMRINR TEIIRRQIFL
351 KIRANHCVCF IRCIFGRNDT GCRAISSKQK IG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

```

m237/g237
10 20 30 40 50 60
m237.pep MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH TL RIVDKLVILTAEKQSAVRAE
|||||:|||||:|||||:|||||:|||||:|||||
g237 MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH TR RIVDKFVILTAEKQPAVRAE
10 20 30 40 50 60

70 80 90 100 110 120
m237.pep AVIIQNMAVVAYCHIVTDKPFCARPQGFGRNNGKADSNRLAFORPEYRVQTCISIDSIDH
|||||:|||||:|||||:|||||:|||||:|||||
g237 AVIIQNMAVVAYCHIVADKPFCAQAQFGGNNKGADGNRLAFORPEYRVQTDISIDGIDH
70 80 90 100 110 120

130 140 150 160 170 180
m237.pep IFALDAAFGRVNQPTVLMRFDARHRGLLLENLRTGFGSGTSDAQSVSERMQVSGXGVLCPL

```


[illegible]

```
a237.seq
1 ATGCGGGGACA AGGTTGGCGG TAATGTCGCA CTCCCGCCCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAAGCAT ATCTTGGCGG
101 ACAGGCTCGG TCATACGCGC GGGATTGTGC ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAA
201 GACGGTTGTC GCATACTGCC ATATTTGTTGC GGATAAGCCC TTTTGCACGC
251 GCGCCAAGG GTTCTGTGCC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 CGCCTCCAAA GCGTTGAATA TCGGATTCAA ACCGGCATAA GTATTGACGG
351 CGTACACCAG ATTTTTGCAAT TCGACGCTGC CTTCGGGGGT GTAAACCAGC
401 CAACCGTTTT GATAAGGTTT AATGCGTATC ATGGGAGAAT GCTCAAAAAA
451 CTTCTGACCA GCTCGGCAGC CGCGCGGGCG ACTGCCCAAC GTGTAATTGA
501 GCGGATGGAG ATGCCCGGAC AAGGGATCGA CATGTGCGCC TTTGGTACATA
551 TCGCTGTCAA GCTGCTGCTT CAGTTCAGTG TTATCCCAGA GTTGATAATG
601 AGTTGCACCG TAATATTTTT GGGCGTGCTC ATGCAATTGT TGCAATTCCT
651 CCAATAGCTG CGAACGGATG GCAACCGTGG CATAACCGCG CTGCCAATCG
701 CAATCAATGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGGCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCCAAACCG ACCTGTTTTT
801 CAATTTCTCT CATACCGCAG GCGTAACTCG TGATAACCTG CCCCGCACTC
851 CGTCCCGACG CCGGAAAACC CATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCAAAGG GCAATGCAGT GCACAACAAC CTCAAATCCG
951 CGCGATGATG ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAAGGA GATATCTCTT
1051 AAAATCAGGG GAAATCATTG TGTTTGCTTT ATCGGGTATA TTTTCGGACG
1101 GAATGATACA GCGTGTGCGG CCNATATCGT CAAACAGAAA ATCGGTTGA
```

```
a237.pep
  1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGHTR GIVDKLVILT
51 AEKQSAVRAE AVIIQNMTVQ AYCHIVADKP FCTRAQGGFC NNGKAGDSNRL
101 ALQRLEYRIQ TGISIDGVHV IFADFDAFGG VNQPTVLFRG NAYHGRMLKN
151 LRTSFGSGAG DAQRVIERME MPQGQIELCA LVHIAVKLLL QFSVIPELIM
201 SCTVIFLGLV MPLLQFFPML RTDGNRGITA LPIAINGMFA DAFVHQFDRL
251 QRLPKPLRL LQTDLFFNFL HTAGVIADNL PATFSRRAET DTRGFQHNRF
301 MSLLRQGQCS AQTTQSAADD TIGGFQTALK FRINSMRINR TEIIRQIFL
351 KIRANHCVCVF IGYIFGRNDT GCRAISSKOK IG*
```


543

m237/a237 85.6% identity in 382 aa overlap

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
a237	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE					
	10	20	30	40	50	60
m237.pep	70	80	90	100	110	120
	AVIIQNMAVVAYCHIVTDKPFPCARQGGFGRNNKGADSNRLAFQRPYRVQTCISIDSIDH					
a237	AVIIQNMTVVAYCHIVADKPFCTRAQGGFCGNNKGADSNRLALQRLYRIQTGISIDGVHQ					
	70	80	90	100	110	120
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMRFDAHRGGLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	IFAFDAAFGGVNQPTVLIREFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
	130	140	150	160	170	180
m237.pep	190	200	210	220	230	240
	LVHIAVKLLFQLGFIPKLMTRTVMPLGVEMPLLQLFPMLRTDGNRGITALPITIDGMFA					
a237	LVHIAVKLLQFSVIPELIMSCTVIFLGVLMPLLQFFPMLRTDGNRGITALPIAINGMFA					
	190	200	210	220	230	240
m237.pep	250	260	270	280	290	300
	DAFVHQFDRLQRLLPKPLRLLQADLFFNFPHATXVIADNLPATPSRRAETDRGFQHNRF					
a237	DAFVHQFDRLQRLLPKPLRLLQDLFFNFLHTAGVIADNLPATPSRRAETDRGFQHNRF					
	250	260	270	280	290	300
m237.pep	310	320	330	340	350	360
	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
a237	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
	310	320	330	340	350	360
m237.pep	370	380				
	IRCFGRNDTGCRAISSXQKIGX					
a237	IGYIFGRNDTGCRAISSXQKIGX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatatc
51 gatgctgcat atccccatta gtcacgcgaa cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctgcggcag tgtaaaaaat cgggtttgcg ccgtccaaac
201 atttgatgca actgcggtcg gcccatact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtccgtt cgataatcat gattcaaaaa gcactttctga
351 tttcagcggc gccgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggcc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttcgcgaa gccctttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttcggt ttttctcagc
601 cgtgcggatg aagcaggaaa actgatatgg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgatggt atgatattcg cggcatcgtc caagggtcgg
701 ttaatccttt ttaacgggt tttcaagggg tagggattgg ggcaattaca
751 gacagtgcgg taagcccggc cacagatata gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcaciaa cttgccgcgg

```


544

```

851 cgagcctatt acaggacagt gcctttgctg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgccttggcc gtacgagagg ccgagggtac ggtttggcgc ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg ttaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttgggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFM LLA AISMLH IPISHANGLD ARLRDDMQAK HYEPPGKYHL
51 FGNARGSVKN RVC AVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGT TKT KINTVQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWR NRMDDIRGIV QGAVNPFLTG FQGVGIGAIT
251 DSAVSPVTD T AAQTLQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGIN
301 ARQWADAHPN ITATAQTALA VAEAAGTVWR GKKEVLPNTK WDWVKNITGYK
351 KPAARHMQTV DGE MAGGNRP PKSITSEGKA NAATYPKLVN QLNQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGE GA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYT IDSNEKRNKI KNHNLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTGCT CTATTCAAAA ATTCATGATG CTGTTTGCG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTGGTAAATG CTCGCGGCAG TGTAAAAAG CGGGTTTACG CCGTCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCACCTCTGA
351 TTTCAGCGGC GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTTCATCGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCGGC CCCCCGAGG AGCAAGGAT ATATACAGCT ATTATGTCAA
501 AGGAACTTCA AAAAAACAA AGACTAATAT TGTCCTCAA GCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTTG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAGTCC GGAAGCACAA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCGG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TTAATAATAC CGGTATATAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAACT CGATACACTA GTTAGATGG AAAAATTACA ATTATAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTCAG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAATTTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFM LFAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGKYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```


545

151 DYPPPGGARD IYSYYVKGTS TKTKTNIIVPQ APFSDRWLKE NAGAASGFPS
 201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
 251 DSAVSPVTD TAAQQTLOGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS
 301 AKQWADAHNP ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK
 351 KPAARHMOTL DGEMAGGNKP IKSLPNSAAE KRQNFEEKFN SNWSSASFDS
 401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
 451 LDSNGNAVKT GNLOGKQAKD YLQQQTHIRN LDK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng)
 from *N. gonorrhoeae*:

m238/g238

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAAISMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEVIGYETHFSGHGHEVHSPFDHDSKSTSDFSG					
g238	RVCAVQTFDATAVGPILPITHERTGFEVIGYETHFSGHGHEVHSPFDNDSKSTSDFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGSYPPPGGARDIYSYYVKGSTTKTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGYPEPQGARDIYSYHIKGTSTTKTKINTVPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m238.pep	APFSDRWLKENAGAASGFPSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFPSRADEAGKLIWENDPDKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m238.pep	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQLAAASLLQDSAFAVKDGINS					
g238	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGNLSPEAQLAAASLLQDSAFAVKDGINS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m238.pep	AKQWADAHNPITATAQTALSAAEAAGTVWRGKKVELNPTKWDVVKNTGYKKPAARHMOTL					
g238	ARQWADAHNPITATAQTALAVAEAAAGTVWRGKKVELNPTKWDVVKNTGYKKPAARHMOTV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m238.pep	DGEMAGGNKPIKSLPNSAAEKRQNFEEKFNSNWSSASFDSVHKTLPNAPGILSPDKVKT					
g238	DGEMAGGNRPPKSI-TSEGKANAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
	430	440	450	460	470	480
m238.pep	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLDNSNGNAVKTGNLOGKQAKDYLQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTSGGGWLSRDGTRQYRPPEKKSQFATTGIQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```
a238.seq (partial)
  1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
 51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTAAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTTGA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACTTCTGA
351 TTTAGCGGCG GCGTAGACG GTGGTTTAC CGTTTACCAA CTTTCATCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACTTCA ACAAAAACAA AGAGTAATAT GTTCCCGCA GCCCATTTT
551 CAGACCGCTG GCTAAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGTGTATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGCAG TAAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTCGGGGC GGTAAGAAAG
1001 TAGAACTTAA CCCGACCAAA TGGGATTGGG TTAAGAAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA
```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```
a238.pep (partial)
  1 MNLPIQKFM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGKYHL
 51 FGNARGSVKN RVYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQTLQGIN HLGNSPEAQ LAAATALQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAAATVWG GKVELNPTK WDWVKNTRYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ
```

m238/a238 91.9% identity in 385 aa overlap

m238.pep	10	20	30	40	50	60
	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
a238	10	20	30	40	50	60
	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
m238.pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHHDHDSKSTDFSG					
a238	70	80	90	100	110	120
	RVYAVQTFDATAVGPILPITHERTGFEGIIIGYETHFSGHGHEVHSPFDNHDHDSKSTDFSG					
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYVKGTS TKTKTNIVPQ					
a238	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYVKGTS TKTKSNIVPR					
m238.pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDVIRGIVQGAVNPFLMG					
a238	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDIRGIVQGAVNPFLMG					
m238.pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTD TAAQTLQGINDLGKLSPEAQLAAASLLQDS AFAVKDGINS					

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|||||
a238      FQGVGIGAITDSAVSPVTDTAQQTLQGINHLGNLSPEAQLAAATALQDSFAVVDGINS
          250      260      270      280      290      300

          310      320      330      340      350      360
m238.pep  AKQWADAHNPITATAQTALSAEEAAGTVWRGKKVELNPTKWDVWKNTGYKKPAARHMQTL
          |||||
a238      ARQWADAHNPITATAQTALAVAEAAATTVWGGKKVELNPTKWDVWKNTGYKTPAVRTMHTL
          310      320      330      340      350      360

          370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRKQNFEEKFNSNWSSASFDSVHKTLTPNAPGILSPDKVK
          |||||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttccacc ataaaggat tgcccgaaac cggcggatgg aggttttgg
51  tttctgccgc cgccctgacg gcttcgtgat tcgccaaacg cgccctgttc
101 agcctcattt gcgcataatc ctgctccaag gcgatttctt gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaagc ggaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacggt tttctctgtt attattccgg tatcggaccg
301 gcagtcgct cgcgcacacg caaaactgcg ctctcgccc tcgggttggc
351 ggcaatttcc gcttcaccgc gctttaatgc cctgcccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg cgcggcagct cggcaggggc
451 tcgtgttgcg aatatttttt gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaagcccc gccctcttcc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttaataaag
601 atgcggttg cctggaaggt gcgctcgca ggatcctgcc cccgctcgcg
651 agtacggacg tttgtgcca cgatctgcgc cagcttgagg gttgtatcga
701 ttggacttcc cgcgggttgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLRRI LLQGDFLFFR
51  LVQSCEVEPV LVLHHNGKS GNAHRKQOKE IRFVHCRSDV FLCYSGIGP
101 AVRSATRKA LALGLAAIS ASPGFNALPT IFRGGSGKSA SLTAAQLGRG
151 SCCBYFLTNC FIMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAOKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWR
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKGATGG AGGTTTGTG
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTCG TGATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCAG GCTTTAATGC CCTGCCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCACAGC CGGCAGGGGC
451 GCGTGTGCG AATATTTTTT GACAACTGC TTCACAATGC GATCTTCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCG GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGATCGA
701 TTGGACTTTC CGCCGTTGC GCAACAATGG CGCGCGCAAT CCGCGGCTa
751 AACCGCTCTT cACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

m239.pep

```

1 MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
51 LIQSCEIEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTAL LALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRTANKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIRRL
251 NRSSP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRIILQGDFLFFRLIQSCEIEPV					
	:					
g239	MFHHKGIARNRRMEVLFFCRRPDRFVIRQTRLLQPHLRRIILQGDFLFFRLVQSCEVEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQOKEIRFVHCRSDVFLCYYSIGIGPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLRGSGCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTCGNTAPTSSSSRLIKMRTANKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239	RRHMTCGNTAPTSSSSRLIKMRTANKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIRRLNRSSPX					
g239	ATMARTIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq

```

1 ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTGTGT
51 TTTCTGCCGC CGCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCATTTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGC AATTTCC GCCTCACC CGCTTAATGC CCTGCCCCG ATTTTCAGGG
401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGCAGGGC
451 GCGTGTTCG AATATTTTT GACAACTGC TTCACAATGC GGTCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTAATTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGATTG CCTGGAAGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTGCGG GTTGATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA
751 AACCGCTCTT CACCATAA

```


This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
  51 LIQSCEVEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
 101 AVRSATRKTAL LALGLAAIS ASPGFNALPA IFRGGSGKSA SLTAAQGRG
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
 201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
 251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

```

      10      20      30      40      50      60
m239.pep MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRIILQGDFLFFRLIQSCEIEPV
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLRRIILQGDFLFFRLIQSCEVEPV
      10      20      30      40      50      60

      70      80      90     100     110     120
m239.pep LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS
      70      80      90     100     110     120

      130     140     150     160     170     180
m239.pep ASPGFNALPTIFRGSSGKSASLTAAQGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      ASPGFNALPAIFRGSGKSASLTAAQGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF
      130     140     150     160     170     180

      190     200     210     220     230     240
m239.pep RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC
      190     200     210     220     230     240

      250
m239.pep ATMARAI RRLNRSSPX
      ||||| |||||
a239      ATMARAIWRLNRSSPX
      250
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacatatt ctteggcgcc gaaacgcgca gacagtttgc
  51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
 101 gggtaaacad gggatatcat gcgcacggga gacggtccga ttttataagg
 151 ctgcgtattc agccgttcgt tcaaatcggg tttgcccgca tccaatgcct
 201 tcgcaatcac gaacggtttg attgccgaac cagggttcgat catatcggtt
 251 acggcacggg tgccgcgctg ttcgctgtct gcccgccggg gtctgttggg
 301 atcgtaggcg ggcgtatttg ccaaggcgag gatttcccc gtgcgggcat
 351 ccaaaaccac caccgttcg gcttttgct gatggtattc gaccgccttg
 401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
 451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
 501 ccacaatatt gccctgccgg tcccgcacaa caacttcgcg gccgtcttcg
 551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttcct gacctttgcc
 601 gtcaatatcg gtaaatccga tgacgtgtgc aaacagggtg cccatcggtt
 651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
a240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
  51 LRIQPFVQIG FARIQCLRNH ERFDCTRFD HIGYGTVAPL FAVCPAGSVG
 101 IVGGRIGQGE DFPRAGIQNH HRSFGCLMVF DRLVQLFIGQ GLNPLIEGKD
 151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTLTFFA
```


550

201 VNIGKSDDVC QVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

```

m240.seq
1   ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGGATC
301 GTAGCGGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AaACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTC
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGCTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTGCCCC ATCGGGTAAT
651 GGCCTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

```

m240.pep
1   MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IORGVMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVAHVHNL LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

```

m240/g240

      10      20      30      40      50      59
m240.pep MIEVIHFFGTETRRQFACADVGRFLHDAAHIORGVNMGIAHGRRSDFIRLRIQPFVQIG
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      MIEVIHFFGAETRRQFACADVGRFLHNAAHIORGVNMGIIAHGRRSDFIRLRIQPFVQIG
      10      20      30      40      50      60

      60      70      80      90      100     110     119
m240.pep FARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIQGEDFPRAGIQXH
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      FARIQCLRNHERFDCRTRFDHIGYGTVAPLFAVCPAGSVGIVGGRIQGEDFPRAGIQNH
      70      80      90      100     110     120

      120     130     140     150     160     170     179
m240.pep HRSFGCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      HRSFGCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRCFIARGVQAVHNIALPVPQNNFR
      130     140     150     160     170     180

      180     190     200     210     220
m240.pep AVFAMQAVFKRKQTFLTFAVNIGKSDDVCKQVAHRVMAFX
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      AVFAIQAVFKRKQTFLTFAVNIGKSDDVCKQVAHRVMAF
      190     200     210     220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

```

a240.seq
1   ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG

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251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AAACCAACCAC CGTTCGGCT TTTGCCGAT GGTATTCGAC CGCCTTGTTC
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTATGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
  1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
  51 RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
 101 VGGRIGQGED FPRAGIQNH H RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
 151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFILFAV
 201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH					
a240	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFIARGVQAVHNIALPVPQNDFRA					
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVFKRKFQTFILFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFQTFILFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
  1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
  51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
 101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
 151 CGTATTCAGC CGTTCGTTC AATCGGTTTT GCCCGCATCC AATGCCTTCG
 201 CAATCACAAA CGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
 251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
 301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
 351 AACCACACAC CGTTCGGCT TTTGCCGAT GGTATTCGAC CGCCTTGTTC
 401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
 451 GTCTTTGCCG TTTTCGGGG CTTTATGCG CGGGGAGTCC AAGCTGTCCA
 501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
 551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTCCGTC
 601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
 651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
  1 MPTRPTAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```


51 ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
 101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVHRLA VGNIGYTIDD
 151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
 201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
 251 NSHICPFRNS RLITGAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)
 1 ..CGGCAATCAG TGGTGGTGAT GACCGTCCGG GCCGTGGACA TGACCGTGTG
 51 CGATTTCTC ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
 101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
 151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
 201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
 251 GCATCTTCGA TACGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
 301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
 351 CCTCTTCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
 401 ATCGGTTCTT CGGTTTTGTC CAAAGCTGA TTGTTGGCAT CATACTCTC
 451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCCTT
 501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)
 1 ..RQSVVMTVR AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVHRLA
 51 VGNIGYTIDD NIAGFRIVGF KHHADDFDNR EHARIFDQDQ LRILLAERIV
 101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
 151 IMQRNHGIFH DSHICPFRNS RLITGAF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVMTVR	AVDMTVCDL	IGCIAHAFNC
g241						
	70	80	90	100	110	120
m241.pep	40	50	60	70	80	90
	SLKADFHACQ	RMVAVHRLA	VGNIGYTIDD	NIAGFRIVGF	KHHADDFDNR	EHARIFDQDQ
g241						
	130	140	150	160	170	180
m241.pep	100	110	120	130	140	150
	LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV	QKLIVGIIHL
g241						
	190	200	210	220	230	240
m241.pep	160	170				
	IMQRNHGIFH	DSHICPFRNS	RLITGAFX			
g241						
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq
 1 ATGCAACAC GTCCAACCTG CGCCGCAAAG CATCCAACCC CGCCAACCTG
 51 GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
 101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
 151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
 201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAAACCTT TTCAGACGGC

553

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251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCTCTC ATCGGATGCA TCGCGCACAC
351 TTTC AACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCG GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
1  MPTRPTRA AK HPTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRREN FHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSC RQSVVVMTVR
101 TVDMTVCD FL IGCI AHFN R SLKADFHACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIV GF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRL FH QRENAVVTAV QIRNRFFGFV QKLIVGLIHL IMQRNHGILH
251 DSHICPFR NS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

m241.pep                                10      20      30
                                      RQSVVVMTVRAVDMTVCD FLIGCIAHAFNC
a241      QPTYLLHPSN KMPSEMEQTL FRRHQIPPSC RQSVVVMTVR TVDMTVCD FLIGCIAHFN R
              70      80      90      100     110     120

m241.pep              40      50      60      70      80      90
SLKADFHACQ RMVAVHRLAVGNIGYTIDD NIAGFRIVGF KHHADFDENR EHARIFD TDQ
a241      SLKADFHACQ RMVAVHRLTVGNIGYTIDD NIAGFRIVGF KHHADFDENR EHARIFNTDQ
              130     140     150     160     170     180

m241.pep              100     110     120     130     140     150
LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGLIHL
a241      LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGLIHL
              190     200     210     220     230     240

m241.pep              160     170
IMQRNHGIFHDSHICPFRNSRLITGAFX
a241      IMQRNHGILHDSHICPFRNSRLITGAFX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
1  ATGATAGAAG TCATACATTT CTTCCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGACGAT TTCTGCATGA TGCCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGGATC
301 GTAGCGGGGC GTATTGGCCA AGCGGAGGAT TTCCCCCGTG CGGGCATCCA
351 AaACCACCAC CGTTCGGGCT TTGCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCITTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCTGAC CTTGCGGTC
601 AATATCGGTA AATCCGATGA CGTGTCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

554

g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTHPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDFL IGCIAHAFNR SFKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCCGTGGACA TGACCGGTGT CGATTTCTCT ATCGGATGCA TCGCGCACGC
351 TTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCG GCATCTTCGA TACGGACCAA CTCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CCGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAAATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
101 AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVGF KHADDFDNR EHARIFDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPYPYRPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPYPYRPSVQTHPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSNKMPSETEQLFRRHQIPPSCRQSVVMTVRVAVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSETEQLFRRHQIPPSCRQSVVMTVRTVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m241-1.pep	SLKADFHACQRMVAVHHRLAVGNIGYTIDNIAAGFRIVGFKHHADDFNREHARIFDQ					
g241	SFKADFHACQRMVAVHHRLAVGNIGYTIDNIAAGFRIVRFKHHTDLDFNRERARIFDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
	190	200	210	220	230	240
	250	260				
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

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555

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101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAAC AAAATGCCGT CTGAAATGGA ACAAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGGCG
301 ACCGTGGACA TGACCGTGTG CGATTTCTCT ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRA AK HPTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPFSC RQSVVMTVR
101 TVDMTCDFL IGCIAHTFNR SLKADFACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFNTDQ LRILLAEIRV GRKRHDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFEGFV OKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRA	ANPPTPPT	WLQTAYC	PRPPYRPS	VQTRTPRE	PASSTCAAKS
a241	MPTRPTRA	AKHPTPPT	WLQTAYC	PRPPYRPS	VQTHTPHE	PASSTCAAKS
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSN	KMPSETEQTL	FRRHQIPPS	CRQSVVMT	VRVDMTVCD	FLIGCIAHAFNC
a241	QPTYLLHPSN	KMPSEMEQTL	FRRHQIPPS	CRQSVVMT	VRTVDMTVCD	FLIGCIAHTFNR
	70	80	90	100	110	120
m241-1.pep	SLKADFACQ	RMVAVHRL	AVGNIGYT	IDDNIAGF	RIVGFKH	ADFDNRHARIF
a241	SLKADFACQ	RMVAVHRL	TVGNIGYT	IDDNIAGF	RIVGFKH	ADFDNRHARIF
	130	140	150	160	170	180
m241-1.pep	LRILLAEIRV	GRKRHDRIA	AGILTVQRL	FHQRENAV	VTAVQIRN	RFFGVQKLIVGIIHL
a241	LRILLAEIRV	GRKRHDRIA	AGILTVQRL	FHQRENAV	VTAVQIRN	RFFGVQKLIVGIIHL
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIF	HD	DSHICPFRNS	RLITGAF	X	
a241	IMQRNHGIL	HD	DSHICPFRNS	RLITGAF	X	
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aacttggtgt tttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaatttgtc gatttcgctg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtagc gcggtgcccg cggatttcgc
201 tttcgctcgcg cacgccgccc aaggccatac ggacatattt ccgccccgtt
251 gctttggcga tggattcgcc caaagagggt ttgccacgc ccgaggggcc
301 gaccaaacac agaatcggac ctttgagcgt gtccatacgt tttggacgg
351 cgaggatttc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcggcg tttggcgatg tctttgctga cgcgggattt
451 tttcttcac ggcagtcgga gcagggtgct gatgtagttg cgtacgacgg

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556

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501  tggattcggc agacatcggc ggcattcattt tgagtttttt cagttcggac
551  aggcattttt cttccgcttc tttggtcata cccgcctttt tgatgcctgc
601  ctccaaggca tccagttcgc cgttttcgtc ttcttcgccc aattcctttgt
651  gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701  atttggcggt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgct
751  gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801  cgggaatctc caaatctgtg tggcggtgcg ccagtttcaa ctgcaaatgc
851  gctgcgaccg tatcggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

```

g242.pep
1  MIGELVVLFFV IEHFKQRAGG IAPKVAAQFV DFVEQEQRVS YACFCHILQN
51  LAGHRADIGT AVPADFAFVA HAAQGHDTDF PPRCFDGF A QRGFAHARRA
101 DQTQNRTEFEL VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRRHHFEFF QFGQAFFFRF FGHTRLFDAC
201 LQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNL QNLLALRQFQ LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

```

m242.seq
1  ATGATCGGCA AACTTGTGTG TTTGTTCCGG ATCGAGCACT TCGAGCAACG
51  CGCTGGCGGG ATCGCCTCGG AAGTCGTAC CCAATTTGTC GATTTCGTGC
101 AGCAGGAACA AGGGGTTTTT CACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGTGCG GCGGTGTCCC CTGATTTCGC
201 TTTCGTGCGC CACGCCGCCC AAAGCCATGC GGACATATT CCGCCCCGTT
251 GCTTTGGCGA TGGATTCCGC CAAAGAGGTT TTGCCACGC CCGGAGGGCC
301 GACCAGGCAC AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAAATCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCG
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCTTTGCTGA CGCGGGATT
451 TTTCTTCAC GGCAGCTCGA GCAAAGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCCGT GGCATCATTT TGAGCTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCTGC TTCTTCGCCC AGTTCTTTGT
651 GTATCGCTTT AATCTGTTCG TTCAGATAAT ATTCCGCGTG GGATTTTTTC
701 ATTTGGCGTT TGACGCTCC CCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATT
801 CGGGAATTC CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

```

m242.pep
1  MIGKLVVLFV IEHFEQRAGG IASEVVTQFV DFVEQEQRVS HAGFCHILQN
51  LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFDGF A QRGFAHARRA
101 DQAQNRFAFEF VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRRHHFEFF QFGQAFFFRF FGHTRLFDIC
201 FQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNF QNLLALRQFQ LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

```

m242/g24290.3% identity in 289 aa overlap
          10      20      30      40      50      60
m242.pep  MIGKLVVLFVIEHFEQRAGGIASEVVTQFVDFVEQEQRVSFVHAGFCHILQNLGTGHRADIGA
          |||:||||| |||:||||| :||:||||| |||:| |||||:|||||:
g242       MIGELVVLFFVIEHFKQRAGGIAPKVAAQFVDFVEQEQRVSFVHAGFCHILQNLGTGHRADIGT
          10      20      30      40      50      60

          70      80      90     100     110     120
m242.pep  AVSPDFAFVAHAAQSHADIFPPRCFGDGF A QRGFAHARRADQAQNRFAFEFVHTFLDGEVF
          || |||||:|||||:|||||:|||||:|||||:|||||:|||||:
g242       AVPADFAFVAHAAQGHDTDFPPRCFGDGF A QRGFAHARRADQTQNRTEFELVHTFLDGEVF
          70      80      90     100     110     120

```


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	130	140	150	160	170	180
m242 . pep	QNPFFDFQAVVVG	IQHQS	SGFGDV	FADAGFFL	PRQLEQ	SVDVVAYDGGFRRHRWHHFELF
g242	QNPFFDFQAVVVG	IQHQS	SGFGDV	FADAGFFL	PRQSEQ	QGVDDVVAYDGGFGRHRHHFFEFF
	130	140	150	160	170	180
	190	200	210	220	230	240
m242 . pep	QFGQAFFFRFGH	TRLE	DICFQGIQ	FAVFVFFA	QFFVYR	NLFVQIIFALGFFHLAFDAS
g242	QFGQAFFFRFGH	TRLE	DACLOGI	QFAVFVFFA	QFFVYR	NLFVQIIFALGFFHLAFDAS
	190	200	210	220	230	240
	250	260	270	280	290	
m242 . pep	AYAFFGLHNVEF	GFQLCQ	QEFH	PFADFG	NFNLLAL	RQFQLQMRCDRIGX
g242	AYAFFGLHNVEF	GFQLCQ	QEFH	PFADFG	NFNLLAL	RQFQLQMRCDRIGX
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 921>:

a242 . seq	1	ATGATCGGCG	AACTTGTGT	TTGCTCGGG	ATCAAGCACT	TCGAGCAACG
	51	CGCTGGCGGG	ATCGCCCCG	AAGTCGCTAN	CCAATTTGTC	GATTTCTGTCG
	101	AGCAGGAACA	ATGGGTTTT	TACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
	151	CTTACCGGGC	ATGGAGCCGA	TATAGGTGCG	GCGGTGTCCC	CGGATTTCCG
	201	TTTCGTGCG	CACGCCGCC	AAAGCCATGC	GGACATATTT	CCGCCCCGTT
	251	GCTTTGGCGA	TGGATTCGCC	CAAAGAGGTT	TTGCCACACG	CTGGAGGGCC
	301	GACCAGGCAC	AGAATCGGGC	CTTTGAGTTT	GTCCATACGT	TTTGGACGG
	351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTCCAGGCC	GTAGTGGTCG
	401	GTATCCAGCA	CCAATCCGGC	TTGGCGATG	TCTTTGCTGA	CGCGGGATTT
	451	TTTCTTCCAC	GGCAGTTCGA	GCAGGGTGTC	GATGTAGTTG	CGTACGACGG
	501	TGGATTCGGC	AGACATCGGC	GGCATCATTT	TGAGCTTTTT	CAGTTCGGAC
	551	AGGCATTTTT	CTTCCGCTTC	TTTGGTCATA	CCCGCCTTTT	TGATATCTGC
	601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTCGTC	TTCTTCGCC	AGTTCTTTGT
	651	GTATCGCTTT	AATCTGTTCG	TTCAGATAAT	ATTCGCGCTG	GGATTTTTCC
	701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
	751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATT
	801	CGGGAATTTC	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAAATGC
	851	GCTGCGACCG	TATCGGTTAG			

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242 . pep	1	MIGELVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
	51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHAWRA
	101	DQAQNAFEF	VHTFLDGEVF	QNPFFDFQAV	VVVGIQHQS	FGDVADAGF
	151	FLPRQFEQGV	DVVAYDGGFG	RHRHHHFELF	QFGQAFFFRF	FGHTRLEF
	201	QGIQFAFV	FFAQFFVYR	NLFVQIIFAL	GFFHLAFDAS	AYAFFGLHNV
	251	EFQFQLCQE	FHPFADFGNF	QNLLALRQFQ	LQMRCDRIG*	

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242 . pep	MIGKLVLVLF	GIEHFEQR	AGGIASEV	VTQFVDF	VEQEQGVF	HAGFCHILQ
a242	MIGELVLLG	IKHFEQR	AGGIAPEV	AXQFVDF	VEQEQWVF	YAGFCHILQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m242 . pep	AVSPDFAFVA	HAAQSHAD	IFPPRCFG	DGFAQRGF	FAHARRAD	QAQNAFEF
a242	AVSPDFAFVA	HAAQSHAD	IFPPRCFG	DGFAQRGF	FAHAWRAD	QAQNAFEF
	70	80	90	100	110	120
	130	140	150	160	170	180
m242 . pep	QNPFFDFQAV	VVG	IQHQS	SGFGDV	FADAGFFL	PRQLEQSV
	130	140	150	160	170	180

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```

a242      QNPFFDFFQAVVVGIQHQSFGDVFADAGFFLPRQFEQGVDDVAYDGGFGRHRRHHFELF
           130      140      150      160      170      180
m242.pep  QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRFNLFVQIIFALGFFHLAFDAS
           190      200      210      220      230      240
a242      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRFNLFVQIIFALGFFHLAFDAS
           190      200      210      220      230      240
m242.pep  AYAFFGLHNVEFGFQLCQOEFHFPADFNGFNQNLALRQFQLQMRCDRIGX
           250      260      270      280      290
a242      AYAFFGLHNVEFGFQLCQOEFHFPADFNGFNQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcc cgAGTTaccg CCGATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGCGAACA GGTCTTCCTC
201 TTCCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTTGTTC
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRTSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCCACACG GGGCGAaYA GGTCTTCCTC
201 TTCCTGCAAA CCGGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTC
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSISASD SSRTSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

m243/g243

```

m243.pep      10      20      30      40      50      60
MVIVWLPELPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243          10      20      30      40      50      60
MVIVWLPELPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT

m243.pep      70      80      90      100     110
GANRSSSSCKPAIFSISASDSSRTSTISSMVILPMSFLFSSTTGAVTKSX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243          70      80      90      100     110
GANRSSSSCKPAMFNISASDSSRTSTISSMVILPMSFLFSSTTGAVTKSX

```


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70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCTCT
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTGTGTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSEFL
101 SSTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLETESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSEFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagcccggcc ggcgggttca gacggcattg ccgctttact
51  tcgacgggtt tatacgcaaa acgcgccttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatattc
251 ggatcgagct tatcgcccgc tttaggattg atttccttga tttgcgtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatcgaa attacgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttccac ggcaaaacttc tgtccggcga acttgtgcgt
451 atcggcaatt tcctgctggt ggcgggcgcg caggttttgc tcgtttgcca
501 aagcgcgcag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctggt cctgtacacc
601 gtccgcattt cctactgtct cgacggtttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgcgtgtctt gttecgctcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgcag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgcgcgc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LPCHRNHSRA
51  QHTVQGQITL LHHTNHGIGF LLTGHLRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRLQILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLLCCLFAH IVSLKTNWKS KSGYYPYSKIR
251 TFSRNFQQRQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

```
m244.seq
```


m244.pcp

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIIPQTSPSGFLLRHRNHSRAQHAVGQRITL					
	:					
g244	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIIPQTSPSGFLPCHRNHSRAQHTVQGQITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	: : : : : :					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m244 . pep	IAALIQRKRFQIILDRQHFHGKLLSGELVRIRNFLLVAAQVLLVCQSAAALLVFQLRFOL					
	: :					
g244	ITALIQRKRFQIILDRQHFHGKLLSGELVRIGNFLLVAAQVLLVCQSAQLFVVFQLRFOL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244 . pep	GNPRLQILISRLCGSLFLTIVRISYCFDGFHRLHIFNRFFTVLLLCLFAHIVSLKTNWKS					
	:					
g244	GNPRLQILISRLGGSLFLYTVRISYCLDGFHRLHIFNRFFTVLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244 . pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKYRRX					
	: : : :					
g244	KSGYYPSKIRTFSRNFKQEQEISHPPNTLPQPKYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGCTG AAGCCCGACA GCGGGTTC GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAAATGCT TTTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACTTC TGTCCGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCGCGATT CTACTGTCT CGACGGTTT CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTTAAACAAA TTGGAAATCA AAATCCAGT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCTA CCGAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

m244.pep	10	20	30	40	50	60
	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
m244.pep	70	80	90	100	110	120
	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
m244.pep	130	140	150	160	170	179
	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
m244.pep	180	190	200	210	220	239
	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	240	250	260	270		
	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgcgcctg aagcccgcc gccgggttc gacggcattg ccgctttact
```



```

51  tcgacggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 ccagacgccc ttccaggcttc cttccgtgcc accgtaacca tagccggggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgctt gcacgccttg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga ttgctgtggc
301 atcaaacgcc ttctgcaact cattcaaatg catctgcaca cccattttca
351 gcgcacgcaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttcac ggcaaaactt tgcggcgga acttgtgcgt
451 atcggcaatt tcctgctggt ggcgccggcg cagggtttgc tcgtttgcc
501 aagcgcgcag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctgtt cctgtacacc
601 gtcgcgattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgcgtgtgtc gttegcctat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgcag caagataagg
751 acattttcaa gaaacttcaa gcaaggcag gaaatttcac atccgccgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

```

1  MPPEARPAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LPCHRNHSRA
51  QHTVGGQGITL LHHTNHGIGF LLTGHRHLRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFFVQLRFQL GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFV TVLLCLFAH IVSLKTNWKS KSGYPSKIR
251 TFSRNFQQRQ EISHPPNTL PQPKYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

```

1  ATGCCGCTG AAGCCCGACA GCGCGTTCA GACGGCATTG CCGCTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCAGACGCCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCTT CTTTCATCACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTGT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTGT ATTTCTTGA TTTGCGTAGC
301 ATCAATGCTT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCTGCTGCTT GCGCGCGGCG CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCTG CTGCTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAATTCCT CATAAGCCGG CTCTGCGGCA GCCTGTTTCT GCACACCGTC
601 CGCATTTTCT ACTGTTTGA CCGTTTCCAC GGCCTCCACA TTTTCAACCG
651 CTCTTCACTT GTTTTGCTGC TGTGCTGTT CGCTCATATC GTATCCCTTA
701 AAACAATG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAACAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCTACCG AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRS
101 IKCFLLQVQS HLHAFQRIE IAAIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPRLQILIS LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFV VLLCLFAH VSLKTNWKS SSYYPRKIRT
251 FSRNFXQXQR ISNSFSNPLP KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEI QIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
g244-1	MPPEARPAGSDGIAALLRSVYTONALQEI QIIPQTPSGFLPCHRNHSRAQHTVGGQGITL					
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLLQVQSHLHAFQRIE					
	70	80	90	100	110	120
g244-1	LHHTNHGIGFLLTGHRHLRLMDIRIELIARFRIDFLDLRGIKRLLQLLIQSHLHAFQRIE					

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	130	140	150	160	170	180
m244-1.pep	IAALIQKRHFQIILDROHFH GKLLSGELVRI RNFLLVAAAQVLLVCQSAALLVFQLR FQL					
g244-1	ITALIQKRHFQIILDROHFH GKLLSGELVRI GNFLLVAAAQVLLVCQSAQLFVFQLR FQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRI SYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLGGSFLYTVRI SYCLDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTF SRNFXQXQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTF SRNFKQRQBISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1  ATGCCGCTCG AAGCCCGACA GCGGGGTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCTT CTTATCAGC CCCACCACGG
201 TATTGGGTTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTCCTTGA TTTGCGTAGC
301 ATCAAAATGCT TCTGCAACT CGTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGCGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAA CTCTATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACGCGCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGTCAT ATCGTATCCC
701 TTTAAACAAA TTGGAATCA AATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AATCCCTTA CCGAAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEI NQIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFQLQVQS HLHAHFQRIE IAALIQKRHF QIILDROHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAQ LLVFQLR FQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFKQRQ RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEI NQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEI NQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRLSIKCFQLQVQSHLHAHFQRIE					
a244-1	LHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRLSIKCFQLQVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQKRHFQIILDROHFH GKLLSGELVRI RNFLLVAAAQVLLVCQSA-LLVFQLR FQL					
a244-1	IAALIQKRHFQIILDROHFH GKLLSGELVRI RNFLLVAAAQVLLVCQSAQLLVFQLR FQL					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244-1.pep	GNPRLQILISRLCGSLFLHTVRI SYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRI SYCLDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240


```
g246.seq
  1  atgtacgggc  ggaacggtag  tactcaagcg  gccgttgcc  tcgttttcga
51  ccagacacag  cgtgcccggt  tcggcaacgg  cgaagtttac  gccgctcaag
101 ccagacatcg  cagtctgta  aatctcgcg  agggctttgc  gggcgaatcc
151 ggtagcttgg  tccagctgt  ctgtaacgg  tgtcccgagg  ttttggtgga
201 acagttcgct  gacctgttct  ttggttttat  ggattgcggg  catcacgta
251 tgggtcgggt  ttctgcctgc  catttggacg  ataaactcgc  ccaagtgcgt
301 ttccaccgcc  ttaatgcctt  ttgcttcaag  ataatggttc  agctcgattt
351 ctctcgtgac  catggatttg  cctttgacca  tcagcttgcc  gtttttggct
401 gtgatgatgt  cgtggataat  ttggcaggct  tcggcagggg  tttccgccca
451 gtgtactttc  acgcccaact  tagtcagggt  ttcttccaac  tgctccagca
501 gcgcgggtaa
```

g246.pep

1	MYGRNGSTQA	AVAFVFDQTO	RARFGNGEVY	AAQADIGSAV	NIAQGFAGES
51	QQLVHVVCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDFFAD	HGFAFDHQLA	VFGCDVVVDN	LAFGFRGFRP
151	VYFHAQLSQV	FFQLLQQRG*			

```
m246.seq (partial)
1 ATGCACGGGC GGTACGGTGG TACTCAAGCG ACCGTTgCTT CGTTTTCCAC
51 CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCATCAAAC
101 CGACATCGGC AGTGTCTGTA ATATCGCGCA GTGCTTTACG GCGCAAGCCG
151 GTCAGTTGGT CTACATCGTC TGTCAGCGGC GTACCCAGGT TTTGGTGGAA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTTGTG GATAGCAGGC ATCACGATAT
251 GGGTCGGTTT TTCGCCTGCC ATTTGGACGA TGAACTCGCC CAAGTCGCTT
301 TCTACCGCTT TAATGcYTTT TGCTTCAAGA TAATGrTTCA GCTCGATTTC
351 CTCGTGACC ATCGATTTC GTTGACCATT CAGCTTGGCC TTTTGGCTG
401 TGATGATGTC GTGGATAATT TGGCAGCCTT CGGTGGGGGT TTCTGCCCCG...
```

m246.pep (partial)

1	MHGRYGGTQA	TVAFVFHQTC	RTCFSGNKVY	ATQTDIGSAV	NIAQCFTEGA
51	GQLVYIVCQR	RTEVLVEQFA	NLFFGFVDSR	HHDMGRFFAC	HLDDLAQVA
101	FYRFNAFCFK	IMXQLDPLAD	HRFAFDHQLA	VFGCDDVVDN	LAGFGRGFCP...

m246/g246

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQ	TQRTCF	SNGKVYATQT	DIGSAVNIAQC	FTGEAGQLVYIV	CQR
	: : : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :
g246	MYGRNGSTQAAVAFVFD	QTRARF	GN	GEVYAAQADIG	SAVNIAQGF	AGESQLVHV
	10	20	30	40	50	60
	70	80	90	100	110	120
m246 . pep	RTEVLVEQFANLFFGF	VD	SRHHD	MGRFFACHL	DD	ELAQVAFYRFNAFCFKIMXQLD
	: : : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :
g246	CAEVLVEQFADLFFGF	MD	CGHHD	MGRFFACHL	DD	DKLAQVAFHRLNAFCFKIMVOLDF

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	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1 ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTTGCCT TCGTTTTCCT
51 CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAAA
101 CCGACATCGG CAGTGCTGTA AATATCGCGC AGTGCTTTAC GGGCGAAGCC
151 GGTCACTTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTTGGTGGA
201 ACAGTTCGCT AACCTGTTCT TTGGTTTAT GGATTGCGGG CATCAGGATA
251 TGGGTCGGTT TTTCACCTGC CATTGGACG ATGAAGTCGC CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATTT
351 CCTCGCTGAC CATCGATTG CCTTTGACCA TCAGCTTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGCAGGCT TCGGCCGGTG TTTCCGCCCA
451 GTGTACTTTT ACGCCCAACT TGGTCAGGTT TTCTTCCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1 MHGRNGGTQA TVAFVFHQQT RTCFSNGEVH ATQTDIGSAV NIAQCFTGEA
51 GQLVYVVR*R CAEVLVEQFA NLFFGFMDCG HHDMGREFTC HLDDELAQVA
101 FHRENAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVDD FAGFGRCFRP
151 VYFYAQLGQV FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQQT RTCFSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQQT RTCFSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHDMGRFFACHLDDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHDMGRFFFTCHLDDELAQVAFHRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVDDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1 atgaaacgta aatgctaaa cgtaccaaag ggcggttatg atggatatgaa
51 gggttttacc attgttgaat ttctggttgc gggcctgctc agtataattg
101 tcctgatagc ggtcgtatcg agttacttta catcccggaa attaaatgat
151 gtggcaaacy agcgtcttgc cattcaacag gatttgcgga atgcggcaac
201 attaatgtc cgcgatgcaa gaatggcggg gagcttcggt tgtttcaata
251 tgtccgagca tactaaagac gatattgttg attcaagtaa tcaaactcaa
301 tctaaccctg caaaacccgg tgccaaacaa gaaaatcccc ttttttccctt
351 aaaaaggagc ggcattggata aacaactgat tcccgttgct gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggttttccaa
451 tacggatcgc atgatcttga tgcgagtgtc gagactgttg tagtcagcag
501 ctgtttccaa atagcaaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatata

```


q247.ppe

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 949>:

m247.seq (partial)

1	ATsAGACGTA	AAATGCTAAA	CGTwsyArAA	GGCAGTTATG	ATGGTATGAA
51	AGGTTTTTACC	ATTATTGAAT	TTTTGGTTGC	GGGCCTGCTC	AGTATGATTG
101	TCCTGATGGC	GGTCGGATGC	AGTTACTTCA	CATCCCGGAA	ATTAAATGAT
151	CGGCGAAACG	AGCGTCTTGC	CGCGCAACAC	GATTTGCGGA	ATGGCGCAAC
201	ATTGATTGTCT	CGCGATGCGA	GAAATGGCAGG	CGCCTTCGGT	TGTTTCAATA
251	TGTCCGAGCA	TCCTGCAACT	GATGTTATTC	CCGATACGAC	GCAACAAAAT
301	TCTCCTTTTT	CCTTAAAAAG	GAACGGTATA	GATAAACTTA	TCCCATAGC
351	GGAATCTTCA	AATATCAATT	ATCAGAATTT	TTTCCAGGTT	GGTAGCGCAT
401	TGATTTTTTCA	ATACGGAATT	GATGATGTTA	ATGCAAGCAC	CGCGACTACC
451	GCTGTCAGCA	GCTGTGCCGC	AATATCGAAA	CCGGCGAAGC	AAATCCCTAC
501	TTTAGAAGAT	GCAAAAAAAG	AATTGAAGAT	TCCGGATCAG	GATAAGGAGC
551	AAAAATGGCAA	TATAGCGCGT	CAAAGGCAATG	TGGTCAATGC	CTATGCCGTC
601	GGCAGGATTG	CCGATGAGGA	AAGTTTGTTT	CGCTTCCAAT	TGGATGATAA
651	GGGCAAGTGG	GGTAATCCTC	AGTTGC		

m247.pep (partial)

1	XRRKMLNVXX	GSYDGMKGFT	IIIEFLVAGLL	SMIVLMVGS	SYFTSRKLND
51	AANERLAAQ	DLRNAATLIV	RDARMAGGFG	CFNMSEHPAT	DVIPDTTQON
101	SPFSLKRNGI	DKLPIAIESS	NINYQNFFQV	GSALIFQYGI	DDVNASTATT
151	VVSSCAAISG	PGKQIPTLED	AKKELKIPDQ	DKEQNGNIAR	QRHVVNAYAV
201	GRIADEESLF	RFQLDDKGKW	GNPOL....		

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/q247

```

      10          20          30          40          50          60
m247.pep    XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTRSKLNDAANERLAAQQ
              :| ||||| |:||||| |:||||| :|||:| | ||||| ||||| :||| |
g247        MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIAVVSSYFTRSKLNDVANERLAIQQ
              10          20          30          40          50          60

      70          80          90          100
m247.pep    DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSLKRKN
              ||||| ||||| ||||| ||||| ||||| :: | :| |||||
g247        DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAKPGAKQENPLFSLKRS
              70          80          90          100          110          120

      110         120         130         140         150         160
m247.pep    GIDK-LIPIAESSNINYNQNFQVGSALIFQYGIDVDVNASTATTVVSSCAAISKPGKQIPT
              |:| | |:| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

```


g247 GMDKQLIPVAESIDIKYPGFIQRLNALVFQYIGIDDLASAETVVSSCSKIAKPGKKIST
130 140 150 160 170 180

m247.ppep 170 180 190 200 210 220
LEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKGNPQL
|::||: |:| ::|| |||||:|:| |||||:|:| ::| ||||| ||||| ||||| |||||
g247 LQEAKSALQITNDDK-QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKGKGNPQLL
190 200 210 220 230

g247 VKKVKRMDVRYIYVSGCPEDEDAGKEEFKRYTNKFDKSKNAVTPAGVEVLLDSGLNAKIA
240 250 260 270 280 290

```

a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCCTGATGGC  GGTCGGATCG  AGTTACTTCA  CATCCCGGAA  ATTAATGAT
151 CGGCAAAACG  AGCGTCTTTC  CGCGCAACAG  GATTTCGCGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTTCAATA
251 TGTCGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAAC
301 CAACATGTCC  CTGTAAAACC  CGGTGCCAAA  CAAGAAAATC  CCCTTTTTTC
351 TTTAGATGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCTATTGC  TGAATCCACA  GATATTAAAT  ATCCGGGTTT  TGCCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAAACAAA  ATGGAAATAT  CACCCGTCAA  AGGCATGTGG  TCAATTGCCTA
651 TGCGGTCCGC  AGGATTGCCG  GTGAGGAAGG  TTTGTTCCGC  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCGTGAA  AAAGATTAGA
751 CATATGAAAG  TGCGGTATAT  CTATGTTTCC  GACTGTCCTG  AAGATGACGA
801 TGCCGGCAAA  GAGGCAAAAT  TCAATATATC  GGGTACATTC  GACAGGTCCA
851 CAAATGCTGT  TACGCCCGCC  GGGGTGGAGT  TTTTATTGAG  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAAT  CATAATTATC  CTTACCGTAT
951 CGATGCGACA  ATACGCGGGG  GAAATGTATG  CGCAAAACAGA  ACACTTTGA

```

```
a247.pep
1  MRRKMLNVPK GNYDGMKGFT IIEFLVAGML SMIVLMAVGS SYFTRSKLND
51  AANERLSAQO DLRNAATLIV RDARMAGGFG CFNMSEHTKN DIIVDPFSQQT
101 QHPVPKPGAK QENPLFSLEW ANTNTNNNT AKLPIAEST DIKYPGFAQA
151 RPALIFQYGI DDLDAEATV VVSSCSKIAK PGKKISTLQE AKSALQITND
201 DKQNGNITRV RHVVNAYAVG RIAGEEGLFR FQLDDKGKWG NPQLLVKKIR
251 HMKVRYIYS DCPEDDDAGK EEKFKYTGTG FSSTNAVTPA GVEVLLSXGT
301 DTKIASSDN HIYAYRIDAT IRGNVCANR TL*
```

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTIIIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAANERLAAQQ					
		:	: :	: :	: :	: :
a247	MRRKMLNVPKGNYDGMKGFTIIIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAAANERLSAQQ					
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSLK-					
			: :		:	:
a247	DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTQHPVVKPGAKQENPLFSLEW					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	-----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDVDNASTATTVVSSCAAISK					
	:		: :	: :	: :	: :
a247	ANTNNTNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDAETVVVSSCSKIAK					
	130	140	150	160	170	180

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	170	180	190	200	210	220
m247.pep	PGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIADEESLFRFQLDDKGKW					
	: :: : : :: : :					
a247	PGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVNAYAVGRIAGEEGLFRFQLDDKGKW					
	190	200	210	220	230	

m247.pep	GNPQL					
a247	GNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKYTGTFDSSTNAVTPAGVEVLLSXG					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

```

1 CCCGGTGCCA AACAAAGAAA TCCCCTTTT TCCTTAAAAA GGAGCGGCAT
51 GGATAAACAA CTGATTCCTCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTGC AGCAGCTGTT CCAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGGTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTGC
401 TCGTGAAAAA GGTAAACGT ATGGATGTGC GGTATATTTA TGTTCCTGGT
451 TGTCTGAAG ATGAAGATGC CGGCAAAGAG GAAAAATTCA GATATACGAA
501 TAAATTCGAC AAATCCAAAA ATGCTGTTC GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TGCACAATA CGCGGGGAA ATGTATGCGC
651 AAACAGAAAC CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

```

1 PGAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYIGDD
51 LDASAETVVV SSSSKIAPG KKISTLQEAK SALQITNDDK QNGNITRQKH
101 VVNAYAVGRF GNNEESLFRF QLDDKGKWN PQLLVKKVKR MDVRYIYVSG
151 CPEDEDAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDSGLN AKIAASSDNS
201 IYAYRINATI RGGNVCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

```

1 ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51 AGGTTTTACC ATTATTGAAT TTTGGTTGCG GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAATGAT
151 GCGGCAACG AGCGTCTTGC CGCGCAACAG GATTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CCGCTTCGGT TGTTCATAA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAT
301 TCTCCTTTT CCTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTACGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAAGT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTTGTTT CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCGGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTCGACAGCG CCCAAATGC
801 TGTACGCCG GCCGGGTGG AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATTT ATGCTTACCG TATCGATGCG
901 ACAATACGCG GGGGAAATGT ATGCGCAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

```

1 MRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CPMNSEHPAT DVIPDTTQQN
101 SPFSLKRNGI DKLIPIAESS NINYQNEFFQV GSALIFQYGI DDVNAATATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEEGLF RFQLDDKGKW GNPQLLVKKV RHMVRYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TDTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*

```


The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 957>:

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

m247-1 / a247-1 80.6% identity in 206 aa overlap

[illegible]


```
g248.seq
1  atgcgcaaac agaacacttt gacaggaatc cgcacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 ttggttgtaac tgcgcgccag tctacaata cccaacagag gatcagtgcg
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggctttgcg
201 ggagggcgaa tttcaggttt tggatttggg atatgctgcg gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaaggtc tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagaggct tttggcaata tcgtggtgca
351 agcgaagccc gccgttgagg cggtgaaacg ttcttgccct gcaagctctg
401 gcaaaaattc taccgcactg tgcattgaca ataaagggat ggaatataat
451 aaaggcgctg caggcgctcg caaaatgccg cgctatatta tcgaatatTT
501 agcgctgaag aacggacaaa atgtttatcg ggttactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 qtaqacaaat aa
```

g248.pep

1	MRKQNTLTGI	PTSDGQGRGSA	<u>LFIVLMVMIV</u>	VAFLVVTAAQ	SYNTEQRISA
51	NESDRKLALS	LAEALREGE	FQVLDEYAA	DSKVTFSENC	EKGLCTAVNV
101	RTMNGSSEA	FGNIVVQGP	AVEAVKRSCP	AKSGKNSTD	CIDNKGMEYN
151	KGAAGVSKMP	RYIIIEYLGK	NGQNVYRVT	KAWGKNANT	VVLQSYVGN
201	DEQ*				

```
m248.seq (partial)
1 ..GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWt
51 gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGtCTT TGGCCGAGkC GkCtwTGCGG
151 GAAGGCGAaC TTCAGGTTTt GGaTTTGGA TATGATACGG ACAGTAAGGT
201 TACaTTTAGC GAAaAGCTTG GAAaAGGTCT GTsTGCCGCA GTGAaTTGtC
251 GGACAAATAA TGATAATGAa GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAa ATTCTACOGa
351 CCTGTGCATT GACaAGAAAG GgwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCaC.AAAAT GCCACGTTAT ATTATCGAaT ATTTTGGGCGT GwAGAACGGA
451 GAAaATGTTT ATCGGGTTAT TGCCaAGGCT TGGGGtAAGA ATGCCAATAC
501 CGTGGTcGtC CTTCAaTCTT ATGTAAAGCAa TAATGATGAG TAA
```

```
m248.pep (partial)
  1  ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXR
51  EGELQVLDL EYDTSKVTF S ENCCKGLXAA VNVRTNNDNE EAFDNIIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXKEYKKG TRSVTKMPRY IIEYLGVMXNG
151 ENVYRVRTAKA WGNKNIANTVVV LOSYVSNNDE *
```

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248.pep

571

```

g248      MRKQNTLTGIPTSDGQGRGSALFIVLMVMIVVAFVLTAAQSYNTEQRI SANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCCKGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| ||| :|||||: :||| |||||
g248      LAEALREGEFQVLDLEYAADSKVTFSENCCKGLCTAVNVRTNNGSEAFGNIVVQGKP
           70      80      90      100      110      120

           110      120      130      140      150
m248.pep  TVEAVKRSCPA----NSTDLCIDKKGXEYKGTSTKMPRYII EYLGXNGENVYRVTA
           :||||||| |||||:| |||: :|:||||||| ||:|||||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYKGAAGVSKMPRYII EYLGXNGENVYRVTA
           130      140      150      160      170      180

           160      170      180
m248.pep  KAWGKNANTVVVLQSYVSNINDEX
           ||||| ||||| ||||| |||||
g248      KAWGKNANTVVVLQSYVGNNDQX
           190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT
101 TGGTGTGAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCAAC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTTGGGCG TGAAGAACGG
501 AGAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCTG CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQGRFA LFIVLMVMIV VAFVLTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCTA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIIE YLGXNGENV YRVTAKAWGK NANTVVVLQS YVSNND*

```

m248/a248 89.4% identity in 180 aa overlap

```

           10      20      30      40
m248.pep  GFALLIVLMVXIVVAFXXVTAAQSYNTEQRI SXNESDRKLAXS
           |||:||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      MRKQNTLTGIPTSDGQGRGALFIVLMVMIVVAFVLTAAQSYNTEQRI SANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCCKGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           |||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      LAEALREGEFQVLDLEYDTSKVTFSENCCKGLCTAVNVRTNNDNEEAFDNIVVQGKPT
           70      80      90      100      110      120

           110      120      130      140      150      160
m248.pep  VEAVKRSCPANSTDLCIDKKGXEYKGTSTKMPRYII EYLGXNGENVYRVTA KAWGK
           ||||| ||:| ||||:| |||||:|:||||| ||||| ||||| |||||
a248      VEAVKRSC TAKSTGLCIDNKGMEYKKGTSVSKMPRYII EYLGXNGENVYRVTA KAWGK
           130      140      150      160      170      180

           170      180
m248.pep  NANTVVVLQSYVSNINDEX

```


|||||
a248 NANTVVVLQSYVSNINDEX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq
1 ATGCGCAAAC AGAACAACCTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51 GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAAGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAGGTC TGTGTGCCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTT GACAATATCG TGGTGCAAGG
351 CAAGCCACCC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep
1 MRKQNTLTGI PTSDGORGFA LFIVLMVMIV VAFVLVTTAAQ SYNTEQRISA
51 NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQKPT VEA VKRSCPA NSTDLCIDKK GMEYKKGTRS
151 VSRMPRIIE YLGVKNGENV YRVTA KAWGK NANTVVVLQS YVSNDE*

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGORGFA	LFIVLMVMIVVAFVLVTTAAQ	SYNTEQRISANESDRKLALS			
g248	MRKQNTLTGIPTSDGORGSA	LFIVLMVMIVVAFVLVTTAAQ	SYNTEQRISANESDRKLALS			
	10	20	30	40	50	60
m248-1.pep	LAEALREGE LQVLDLEYDT	DSKVTFSENC GKGLCAAVNV	RTNNDNEEAF DNIVVQKPT			
g248	LAEALREGE FQVLDLEYA	ADSKVTFSENC EKG LCTAVN	VRTNNGSEEA FGNIVVQKPT			
	70	80	90	100	110	119
m248-1.pep	LAEALREGE LQVLDLEYDT	DSKVTFSENC GKGLCAAVNV	RTNNDNEEAF DNIVVQKPT			
g248	LAEALREGE FQVLDLEYA	ADSKVTFSENC EKG LCTAVN	VRTNNGSEEA FGNIVVQKPT			
	70	80	90	100	110	120
m248-1.pep	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA	-----NSTDLCIDKK	GMEYKKGTRSVSKMPRII	IEYLGVKNGENVYRVTA		
g248	AVEAVKRSCPA	SKGNSTDLCIDNKGMEYN	KGAAGVSKMPRII	IEYLGVKNGQNVYRVTA		
	130	140	150	160	170	180
m248-1.pep	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNINDEX					
g248	KAWGKNANTVVVLQSYVGNDEQX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGORGFA	LFIVLMVMIVVAFVLVTTAAQ	SYNTEQRISANESDRKLALS			
a248	MRKQNTLTGIPTSDGORGFA	LFIVLMVMIVVAFVLVTTAAQ	SYNTEQRISANESDRKLALS			
	10	20	30	40	50	60
m248-1.pep	LAEALREGE LQVLDLEYDT	DSKVTFSENC GKGLCAAVNV	RTNNDNEEAF DNIVVQKPT			
a248	LAEALREGE LQVLDLEYDT	DSKVTFSENC GKGLCAAVNV	RTNNDNEEAF DNIVVQKPT			
	70	80	90	100	110	120
m248-1.pep	LAEALREGE LQVLDLEYDT	DSKVTFSENC GKGLCAAVNV	RTNNDNEEAF DNIVVQKPT			
a248	LAEALREGE LQVLDLEYDT	DSKVTFSENC GKGLCAAVNV	RTNNDNEEAF DNIVVQKPT			
	70	80	90	100	110	120
m248-1.pep	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCIDKK	GMEYKKGTRSVSKMPRII	IEYLGVKNGENVYRVTA	KAWGK		
a248	VEAVKRSCPAKSTGLCIDN	KGMEYKKGTSVSKMPRII	IEYLGVKNGENVYRVTA	KAWGK		
	130	140	150	160	170	180


```
g249.seq
1 atgaagaata atgattgctt gcgcctgaaa aatccccagt ccggtatggc
51 gttgatagaa gtctttggctg ctatgctctg tctgaccatt ggtatttttg
101 ctatgctgtc gctacagttg cggacagtcg ctctcgctcag ggaggcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaattgt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 cccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccgagatgc ggtagctatt cattacctcg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcggtgct
451 tttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 atttggggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagttag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga
```

g249.pep

1	MKNVNDCLRK	NPQSGMALIE	<u>VLVAMLVLT</u>	<u>GILALLSVQL</u>	RTVASVREAE
51	TQTIVSQITQ	NLMEGMLMNP	TIDLDNKKK	YSLYMGKQTL	SAVDGEMFLD
101	AEKSKAQLAE	EQLKRFSHEL	KNALPDAVAI	HYAVCKDSSG	DAPTLSDSGA
151	FSSNCDNKAN	GDTLIKVLWV	NDSAGSDDIS	RTNLEVSGDN	IVYTYQARVG
201	GRE*				

```
m249.seq
1 ATGAAGAATA ATGATTGCTT CCGCCTGAAA TACTCCCAGT CCGGTATGGC
51 GCTGATAGAA GTCTTGGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATT TGCGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCAACAATTGA AGAGATTTTAG
351 TTATGAGCTG AAAAATGCCT TGCCGAGATG CCGCAGCCAT CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCCTCAAATT GCGACAATAA GGCAACGGG GATACTTTAA TTAAGTATT
501 GTGGGTAAT GATTCCGCAG GGGATTCGGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCCGAGGT
601 CGGTAGATGA
```

```
m249.pep
  1  MKKNDCFR LK  DSQSGMALIE VLVAMLV LTI  GILALLSVQL  RTVXXXXXXXX
51  XXXXXXXXXXXX XLMEGMLMNP  TIDSDSNKKN  YNLYMGNHTL  SAVDGFDAID
101 AMKTGQLAE  AQLKRFSYEL  KNALPDAAAI  HYAVCKDSSG  NAPTLSGNAF
151 SSNCDNKANG  DTLIKVLWVN  DSAGSDSISR  TNLEVSGDNI  VYTYQARVGG
201  SN*
```

m249.pep MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXXX
| | | | : | : | | | | | | | | | | | | | | | | | | | : : :

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     120
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNHTLSAVDGDFAIDAMKTKGQLAEQAKRFSYEL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      NLMEGMLMNPTIDSDSNKKNYSLYMGKQTLTSAVDGEFMDAEKSKAQLAEQQLKRFSHEL
           70      80      90      100     110     120

           130     140     150     160     170     179
m249.pep  KNALPDAAAIHYAVCKDSSGNAPTLSGN-APSSNCDNKANGDTLIKVLWVNDSDAGSDSDIS
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      KNALPDAAAIHYAVCKDSSGDAPTLSDSGAPSSNCDNKANGDTLIKVLWVNDSDAGSDSDIS
           130     140     150     160     170     180

           180     190     200
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGCTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCAGTTG CGGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCACGCAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AAACAAAGAC GCAGTTGGCA GAGGCACAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TGGCGCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTCGTCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1   MKNNDCFRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  TOTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLSAGS
151 TFSSNCDGSA NGDTLIKVLW VNDSDAGSDI ARTNLETNGN NIVYTYQARV
201 GGRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

           10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     119
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTKGQLAEQAKRFSYE
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      NLMEGMLMNPTIDSDSNKKNYNLYMGNHHA LSVVDGDFQVDAIKTKTQLAEQAKRFSYE
           70      80      90      100     110     120

           120     130     140     150     160     170
m249.pep  LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVNDSDAGSDSI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVNDSDAGSDSI
           130     140     150     160     170     180

```


m249-1.seq

```
1 ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCACT CCGGTATGGC
51 CTGATAGATA GTCTTGTTG CTATGCTCGT TGTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCG CTTCCGTCAG GGAGGCGGAG
151 ACACAAACCA TCGTCAGCCA AATCACGCCA AACCTGATAG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGACAGCAAA CAAGAAAAAT TATAATCTTT
251 ACATGGGAAA CACATACACTA TCAGCTGTGG ATGGCGATT TCGGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAATGCCT TCGCGGATGC GGCAGCCATC CATTACGCCG
401 CTGCAAGGA TCTCGCGGT AACGCGCCCA CATTGCTCCG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAAAACGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCCGCAG GGGATTCCGA TATTTCCTCG ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTGCGAGGT
601 CGGGAATGA
```

m249-1.pep

1	MKNNDCEFRLK	DSQSGMALIE	VLVAMLVLT	GILALLSVQL	RTVASVREAE
51	TQTIVSQITQ	NLMEGMLMNP	TIDSNSNKKN	YNLYMGNTIL	SAVDGDFIID
101	AMKTKQLAE	AQLKRFSYEL	KNALPDAAAI	HYAVCKDSSG	NAPTLSGNAF
151	SSNCDNKANG	DTLIKVLWVN	DSAGDSDISR	TNLEVSGDNI	VYTYQARVGG
201	RE*				

		10	20	30	40	50	60
m249-1.pep		MKNND	CFLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ				
g249		MKNND	CLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ				
		10	20	30	40	50	60
		70	80	90	100	110	120
m249-1.pep		NLMEGLM	MNPITDSDSNKKNYNLNMGNNHTLSAVDGDFAIDAMKTKGQLAEQLRKFSYEL				
g249		NLMEGLM	MNPITDSDSNKKNYSLYMGKQTL SAVDGEFMDAEKSKAQLAEQLRKFSHEL				
		70	80	90	100	110	120
		130	140	150	160	170	179
m249-1.pep		KNALP	DAAAIH YAVCKDSSGNAPTLSGN-AFSSNCNDKANGDTLIKVLWVND SAGDSDIS				
g249		KNALP	DAVAIH YAVCKDSSGGAPTLS DSGAFSSNCNDKANGDTLIKVLWVND SAGDSDIS				
		130	140	150	160	170	180

```

      180      190      200
m249-1.pep  RTNLEVSGDNIVYTYQARVGGREX
              |||||
g249         RTNLEVSGDNIVYTYQARVGGREX
              190      200

```

Query: 13 QSGMALIEVLVAMLVLITIGILALLSVQLRTVASVREAETQTIVSQITQNLMEGMLMNPTI 72
QSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + ++ NL+E M +P
Sbjct: 12 QSGFSMIEVLVALLISIGVLGMIAMQGKTIQYTADSVERNKAAMLGSNLLESMPASPKA 71

Query: 73 DSDSNKKNYNLYMGNNHALLSVVDGDFQVDAIKTKTQLAEA---OLKRFSYELKNALPDAA 129

576

D + M G A + T L + A + L ++ ++KN LP A
 Sbjct: 72 LYDVKDQ-----MATQSDFFKARGSAFPTAPSSCTPLPDAIKDRLGCVAEQVKNELPGAG 126
 Query: 130 AI---HYAVCKDSSGVAPTLASGSTFSSNCDGSANGDTL-IKVLWVNDASAGDSIARTNL 185
 + Y + C + S + CDG G L I + W + A ++
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLERLAWRGKQACVNAADSSA 172
 Query: 186 ETN 188
 +T+
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLKDSQSGMALIEVLV	AMLVLTIGILALLSVQLRT	VASVREAE	TQTIVSQITQ	
a249	MKNND	CFRLKDPQSGMALIEVLV	AMLVLTIGILALLSVQLRT	VASVREAE	TQTIVSQITQ	
	70	80	90	100	110	119
m249-1.pep	NLMEGMLMNP	TIDSDSNKKNYNLYMG	NH-TLSAVD	GDFAIDAMK	TGQLAE	AQLKRFSYE
a249	NLMEGMLMNP	TIDSDSNKKNYNLYMG	NH-HLSVVD	GDFOVDAIK	TKTQLAE	AQLKRFSYE
	120	130	140	150	160	170
m249-1.pep	LKNALPDAAA	IHYAVCKDSSGNAPT	LS-GNAFSS	NCNKGDTL	IKVLWVND	SAGDSI
a249	LKNALPDAAA	IHYAVCKDSSGVAPT	LSAGSTFSSN	CDGSANGDTL	IKVLWVND	SAGDSI
	180	190	200			
m249-1.pep	SRTNLEVSG	DNIVVYTYQARV	GGREX			
a249	ARTNLETNG	NNIVVYTYQARV	GGREX			
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1 atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaaga
51 aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggtg
101 tgcaggcgcg gcaaaaaggc atgggcccgc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgc ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcggcatat cctgatgggg ggcggcgctt gccacgcaca tgaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1 MHTASPRDE FIRIKESSP MLIGLLPWAL ILGMOGGQKG MGRLEMLLMT
51 GMNFAGGSEF ATVNLAWEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1 ATGCACACCT TCCCCGCATA ACGAATTAT ACGCGGCATC AAAGAAAGTT
51 CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GCGCGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTGTA TGACCAATAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGGCSGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGCGCG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1 MHTPSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51 MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

m250/g250

	10	20	30	40	50	59
m250.pep	MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKMSWLEMLMTSMNFAGGSEF					
	: : : : : :					
g250	MHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKMGRLLEMLMTGMNFAGGSEF					
	10	20	30	40	50	60
	60	70	80	90	100	110
m250.pep	ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRARTVFYVX					
	: : : : :					
g250	ATVNLWAEPLPILLIATVTFMINSRHILMGGGACHAHERNTAEKSRARAVFYV					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 979>:

a250.seq

```

1   ATGACACACA TAAGCTCGCC CCGTAACGAA TTTATACGCG GCATCAAAGA
51  AAGTTCGCCC ATGCTGATCG GGCTTTTGCC TTGGGCATTA ATACTCGGTA
101 TGCAGGGTGG ACAAAAAGGC ATGAGCTGGC TGGAAATGTT GTTGATGACC
151 GGTATGAACT TCGCCGGCGG CTCCGAGTTT GCCACGGTCA ACCTGTGGGC
201 GGAACCTCTG CCGATACTGC TTATCGCCAC CGTAACCTTT ATGATTAATT
251 CTCGGCATAT CCTGATGGGG G.CGGCACTT GCCCCGCACC TGAAAGAAAT
301 ACCGCTGAAA AAAGCCGTGC CCGCACTGTT TTTTATGTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 980; ORF 250.a>:

a250.pep

```

1   MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MSWLEMLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTCAPERN
101 TAEKSRARTV FYV*

```

m250/a250 94.6% identity in 111 aa overlap

	10	20	30	40	50	
59						
m250.pep	MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKMSWLEMLMTSMNFAGGSEF					
	: : : : :					
a250	MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKMSWLEMLMTGMNFAGGSEF					
	10	20	30	40	50	
60						
	60	70	80	90	100	110
m250.pep	ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRARTVFYVX					
	: : : : :					
a250	ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCAPAPERNTAEKSRARTVFYVX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 981>:

g251.seq

```

1   atgcctgacc caatagggat tcttttcgct gccgtcgggg ttgatttttt
51  tgccgttggt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
101 tgataataat aatcctgatg gcggaggtcg gaacacaaac ggtcgtaacc

```


578

```

151 gaggttgacg ctcaggttgt ggcggtatctt ggcggtatcg aaggattttt
201 tgaatgccgc ctgcaagagc ctgtggcttt ccccgtaa at cagcggtcgc
251 gattttgtagt aggaagacgg cttgtcggca ctcggcgggc aatatttgc
301 cgaaccgtcg gcggaacagt gcgtctgctg aaaatgattg tccaaaccga
351 tgccctgccg gtcgtaagag aggcgggcat aatccgcccc agtgtcttta
401 tcggcattgg tatagacata ttccaaaccg tagcggtttt tgggtgtcgt
451 ctgctcgtaa aacacgcccg taccgtattc cgcgccacc tccgaccgt
501 tttcaccgtt ggtaatcagc ccgctgtatt tgcggccgcc cgcgtatttg
551 ccgtagcctc ttatcgatcc gtatttttta ttttcatcaa aaaccgcctt
601 ggtcaggaat gccggaaccg tcatatcgcg cgtgtcgaaa gtttgcgtgcg
651 tgcgttcgag tatgccgcgc atgtagtgcc gtttgttttc aaaacgaaaa
701 ccggggcgga acagccacga ccggctttcg tatga

```

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pep

```

1 MPDPGILFA AVGVDFFAVV LRGRFQRIGA VGMLIIILM AEVGTKTVVT
51 EVDAQVVADF GGIEGFFEER LQEPVAFPVN HAVGFVVGRR LVGTRAAIFV
101 RTVGGTVRLL KMIVQTDALP VVREAGIIRP SVFIGIGIDI FQTVAAFGVR
151 LVVKHARTVF RAHLRTVFTV GNQPAVFAAA RVFAVASYSR VFFIFIKNRL
201 GQECRNRHIA RVESLLRAFE YAADVVPFVF KTKTRAEQPR PAFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

```

1 ATGCGTGCTG CCGTAGTCGT AGCGCAAGCC CGCGCCGACA TCCGCCCACC
51 TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTACCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACGACATTC CCTGCGCTAT GGTGACCAA TAGGGGCTGG
201 TTTCACTGCC GTTGGGGCTG ATTTTITGTC CGTGTGTTTG AGGGGGCGTG
251 TTCGACGAAT AGGCGCGGTT GGCATGTTGA TAATAATAAT CCTGATGGCG
301 GAGATTAGAG CCAAAGCGGT CAAACCGAG ATTACGCTC AGGTTGTGGC
351 GGATTTTGGC GGTATCGAAG GATTTTITGA ATGCCGCTG CAAGAGCCTG
401 TGGCTTTCCC CGTAAATCAC GCGATCGGAT TTGTAATAGG AAAACGGCTT
451 GTCGGCACTC GGGCGGCAAT ATTGTCCGA ACCGTCCGCA GAACAGTGCG
501 TCTGCTGAAA ATGATTATCC AAACCGATGC CCTCCCGTC GTAAGAGAGG
551 CGGGCATAAT CCGCCCAAGT GTCTTTATCG GCATTGGTAT AGACATATTC
601 CAAACCGTAG CGGCTTTTGG TGTGCGTCTC GTCGTAAAAC ACGCCCGTAC
651 CGTATTCGCG GCCCACCAGC GCACCGTTT CGCGGTGGT AAACAGTCCG
701 CCGTATTTGT GGTGCCCCG GTATTGCGG TTACCGGGCA AAGAACCCGC
751 CTGTTTTTTA TTGTCATCAA AAACCGCCTT GGTCAAGAA GCGGGAACCG
801 TCATATCGCG CGTGTGAAA GTTTGTTGCG TGTGTTGAG TATGCCGCCG
851 ATGTAGTGCC GCTTATTCTC AAAACGAAAA CCCGGGCGGA ACAGCCACGA
901 CCGGCTTTCG TATGA

```

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

```

1 MRAAVVVAQA RADIRPPAQT DIVPNCRVIA FTVDAARRAV RISIVAQAAD
51 LPRNDISPAY GDPGAGFTA VGADFFAVVL RGRVRRIGAV GMLIIILMA
101 EIRAKAVKPE IHAQVVADFG GIEGFFEERL QEPVAFPVNH AIGFVIGKRL
151 VGTAAIFVR TVGRTVRLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFGVRL VVKHARTVFR AHQRTVFAVG KQSAVFVVAR VFAVTGQTR
251 LFFICIKNRL GQECRNRHIA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

          40      50      60      70      80      90
m251.pep  TVDAARRAVRISIVAQAADLPRNDISPAYGDPGAGFTAVGADFFAVVLGRVRRIGAVG
          ||||  |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g251      MPDPGILFAAVGVDFFAVVLRGRFQRIGAVG
          10      20      30

```


	100	110	120	130	140	150
m251.pep	MLIIIIILMAEIRAKAVKPEIHAQVVADFGGIEGGFFECRLQEPVAFPVNHAIGFVIGKRLV					
	: : : : : : :					
g251	MLIIIIILMAEVGTKTIVVTEVDAQVVADFGGIEGGFFECRLQEPVAFPVNHAVGVVGRRLV					
	40	50	60	70	80	90
	160	170	180	190	200	210
m251.pep	GTRAAIFVRTVGRTVRLLKMIIQTALPVVREAGIIRPSVFFIGIGIDIFQTVAAFVGRVLV					
	:					
g251	GTRAAIFVRTVGRTVRLLKMIVQTALPVVREAGIIRPSVFFIGIGIDIFQTVAAFVGRVLV					
	100	110	120	130	140	150
	220	230	240	250	260	270
m251.pep	VKHARTVFRAHQRTVFVAVGQSASVFFVARVFAVTGQRTLFFICIKNRLGQECCRNRIAR					
	: : : : : : : : :					
g251	VKHARTVFRAHLRTVFTVGNQPAVFAAARVFAVASYSR-VFFIFIKNRLGQECCRNRIAR					
	160	170	180	190	200	210
	280	290	300			
m251.pep	VESLLRVFEYAADVPLILTKTKTRAEQPRPAFVX					
	: : :					
g251	VESLLRAFEYAADVPPFVKTKTKTRAEQPRPAFVX					
	220	230	240			

```

a251.seq
1  ATGCGTGCTG CGGTAGTCGT AGCGCAACCC CGCGCCGACA TCCGCCACC
51  TGCCCAAACG GACATTGTCC CGAATGCGG CGTAATAGCT TTTGCCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTGTGCCA AGCGGCAGAT
151 TTGTCGCCGTG ACCACATTTT CCCTGCCTAT GCTGACCCAA TAGGGTTTGG
201 CCTTGCCGCC GTTGGGGTTG GCGGTTTTAG GGGGCGTTTT CGACGAATAG
251 GCGCGGTTGG CATGTTGATA ATAATAATCC TGATGCCGGA GATTAGAGTC
301 AAAGCGGTCA AAACCGAGAT TCACGCTCAG GTTGTGGCGG ATTTTGGCGG
351 TATCGAAGGA TTTTGTGAAT GCGCGCTGCA AGAGCCCTGT GCTTCCCCG
401 TAATCAACGC GGTGCGGATTT GTAGTAGGAA AACCGCTTGT GCGCACTCGG
451 GCGGCAATAT TTGTCCGAAC CGTCGGCAGA ACAGTGCCTC TGCTGAAAT
501 GATTGTCCAA ACCGATGCCC TGCCCGTCTG AAGAGAGGCG GGCATAATCC
551 ACCCAAGTGT TCTTATCGCG ATTGGTATAG ACATATTCCA AACCGTAGCG
601 GCTTTTGGTG TCGGTCTCGT CGTAAACAC GCGCGTACCG TATTCCGCGT
651 CCACCAAGCG ACCGTTTTCG CCGTTGGTAA ACAGACCGCC GTATTTGTGG
701 TCGCCCGCGT ATTTGCCGTT GCCTCTTATC GGTCCGTATT TTCTATTTTC
751 ATCAAAAACC GCCTTGGTCA GGAATGCCGG AACCGTCATA TCGCGCGTGT
801 CGAAAGTTTG TTGCGTGTGT TCGAGTATGC CGCCGATGTA GTGCCGTTG
851 TTTTCAAACG TAAACCCCGG GCGGAACAGC CACGATCGGG TTTCGTATGA

```

a251.pep

1	MRAAVVVAQP	RADIRPPAQT	DIVPNCRVIA	FAVDAARRAV	RISIVAQAAD
51	LPRNHISPAY	ADPIGLVLAA	VGVGGRFRGF	<u>RRIGAVGMLI</u>	<u>IIILMAEIR</u>
101	KAVKTEIHAQ	VVADFGGIEG	FFECRLQEPV	AFPVNHAVGF	VVGKRLVGTR
151	AAIFVRTVGR	TVRLKLMIVQ	TDALPVVREA	<u>GIHPSVFIG</u>	<u>IGIDIFQTV</u>
201	<u>AFGVRLVVKH</u>	ARTVFRAHQR	TVFAVGKQTA	VVFVVRVFAF	ASYRSVSFIF
251	IKNRLGOECR	NRHITARVESL	LRVEFYAADV	VPFVEFKTKR	AEOPRSFAF*

```

      10      20      30      40      50      60
m251.pep  MRAAVVQAQARADIRPPAQTDIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      MRAAVVQAQPRADIRPPAQTDIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPA
          10      20      30      40      50      60

      70      80      90      100     110     120
m251.pep  GDPIGAGFTAVGADFFAVLRRGRVRRIGAVGMLIIIIILMAEIRAKAVKPEIHAQVVA
          :|||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```


580

```

a251      ADPIGLVLAAVGVGGF----RGRFRRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVVADFG
              70          80          90          100         110

m251.pep      130          140          150          160          170          180
GIEGFFECRLQEPVAFPNHAIQFVIGKRLVGTRAAIFVRTVGRVRLMKMIQTDALPV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECRLQEPVAFPNHAIQFVIGKRLVGTRAAIFVRTVGRVRLMKMIQTDALPV
              120          130          140          150          160          170

m251.pep      190          200          210          220          230          240
VREAGIIRPSVFIGIGIDIFQTVAAGFVRLVVKHARTVFAHQRTVFAVGKQSAVFVVAR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIRPSVFIGIGIDIFQTVAAGFVRLVVKHARTVFAHQRTVFAVGKQSAVFVVAR
              180          190          200          210          220          230

m251.pep      250          260          270          280          290          300
VFAVTGQTRLFFICIKNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VFAVASYRS-VFSIFIKNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR
              240          250          260          270          280          290

m251.pep      PAFVX
              ||||
a251      SAFVX
              300

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 987>:

```

g253.seq
1  atgatcgaca gggaccgtat gttgcgggac acgttggaaac gtgtgcgtgc
51  ggggtcgttc tggttatggg tgggtggggc atcgatgatg tttaccgccg
101 gattttcagg cacttatctt ctgatggaca atcaggggct gaatttcttt
151 ttagttttgg cgggagtgtt gggcatgaat acgctgatgc tggcagtatg
201 gttggcaacg ttgttcctgc gcgtgaaagt gggacggttt ttcagcagtc
251 cggcgacgtg gtttcggggc aaaggccctg taaatcaggc ggtgttgctg
301 ctgtatgcgg accagtggcg gcaaccttcg gtacgatgga aaataggcgc
351 aacggcgcac agcttgtggc tctgcacgct gctcggaatg ctggtgtcgg
401 tattgctgct gcttttgggt cggcaatata cgttcaactg ggaaagcacg
451 ctgttgagca atgccgcttc ggtacgcgcg gtggaaatgt tggcatggct
501 gccgtcgaaa ctccgtttcc ctgtccccga tgcgcgggcg gtcacgaag
551 gtcgtctgaa cggcaatatt gccgatgcgc gggcttggtc ggggctgctg
601 gtcggcagta tcgtctgcta cggcctcctg ccgcgcctct tggcttgggt
651 agtgtgtaaa atccttttga aaacaagcga aaacggattg gatttgaaa
701 aaacctatta tcaggcggtc atccgcgcgt ggcagaacaa aatcacgat
751 gcggatacgc gtcgggaaac cgtgtccgcc gtttcgccga aaatcgtctt
801 gaacgatgcg ccgaaatggg cgctcatgct ggagaccgag tggcaggacg
851 gccaatggtt cgagggcagg ctggcgcagg aatggctgga taaggcggtt
901 gccccaatc gggaacaggt tgccgcgctg gagacagagc tgaagcagaa
951 accggcgcaa ctgcttatcg gcgtacgcgc ccaaaactgtg ccggaccggg
1001 gcgtgctgcg gcagattgtg cggctttcgg aagcggcgca gggcggcgcg
1051 gtggtgcagc ttttggcgga acaggggctt tcagacgacc tttcggaaaa
1101 gctggaacat tggcgtaacg cgctgaccga atgcggcgcg gcgtggcttg
1151 agcctgacag ggtggcgag gaaggccgtt tgaaagacca ataa

```

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

```

g253.pep
1  MIDRDRMLRD TLERVRAGSF WLWVVASMM FTAGFSGTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVLAT LFLRVKGRF FSSPATWFRG KGPVNQAVLR
101 LYADQWRQPS VRWKIGATAH SLWLCTLLGM LVSVLLLLLV RQYTFNWEST
151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRINGNI ADARAWSGLL
201 VGSIVCYGIL PRLLAWVCK ILLKTSENGL DLEKTYQAV IRRWQNKITD
251 ADTRRETUSA VSPKIVLNDK PKWALMLETE WQDQWFEGR LAQEWLDKGV

```


m253.seq

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253 . pep

1	MIDRNRMLRE	TLERVVAGSF	WLWVVAATFA	FFTGFSTVYL	LMDNQGLNFF
51	<u>LVLGVLGMN</u>	<u>TLMLAVWLAM</u>	LFLRVKVGRF	PSSPATWFRG	KDPVNQAVLR
101	LYADEWRQPS	VRWKIGATSH	<u>SLWLCTLLGM</u>	<u>LVSVLLLLLV</u>	RQYTFNWEST
151	LLSNAASVRA	VEMLAWLPSK	LGFPVPDARA	VIEGRNLNGNI	ADARAWSGLL
201	<u>VGSIACYGIL</u>	<u>PRLLAWVVCK</u>	ILLKTSVLEL	DLEKPPYQAV	IAQWKNKITD
251	ADTRRETVSA	VSPKILNDA	PKKAWMLETE	WQDGEWFEGR	LRQEWLDKGV
301	ATNREQVAAL	ETELQKCPAQ	LILGVRAQTV	PDGRVLQIV	RLSEAAQCGA
351	VVQLLAEQGL	SDDLSEKLEH	WRNALAECGA	AWLEPDRAAQ	EGRLKDO*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/q253

		10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRVAGSFWLVVVAAFFAFTGFSVTYLLMDNQGLNFFVLVLAVLGMN						
	: :						
g253	MIDRDRMLRDTLERVRAGSFWLVVVASMMFTAGFSGTYYLLMDNQGLNFFVLVLAVLGMN						
		10	20	30	40	50	60
		70	80	90	100	110	120
m253.pep	.TLM LAVWLAMLF LRVKVG RFSSPATWFR GKDPVNQAV LRLYADEWR QPSVRWKIGATSH						
g253	TLM LAVWLATL FLRVKVG RFSSPATWFR GKGPVNQAV LRLYADQWR QPSVRWKIGATAH						
		70	80	90	100	110	120
		130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVS VLLLLLV RQYTFNWESTLLSNAAS VRAVEMLAWLP SKLGFPVPDARA						
g253	SLWLCTLLGMLVS VLLLLLV RQYTFNWESTLLSNAAS VRAVEMLAWLP SKLGFPVPDARA						
		130	140	150	160	170	180

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	190	200	210	220	230	240
m253 .pep	VIEGRNLNGNIADARAWSGLLVGSIAICYGILPRLLAWVVCILLKTSENGLDLEKPYQAV					
	: : : : :					
g253	VIEGRNLNGNIADARAWSGLLVGSIVCYGILPRLLAWVVCILLKTSENGLDLEKTYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 .pep	IRRWQNKITDADTRRETVSASVSPKIIILNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	: : : : :					
g253	IRRWQNKITDADTRRETVSASVSPKIVLNDAPKWALMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 .pep	ATNREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGA VVQLLAEQGL					
	: : : : : :					
g253	AANREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGA VVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253 .pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
	: : :					
g253	SDDLSEKLEHWRNALTECGAAWLEPDRAVAQEGRLKDQX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a253 .seq
1  ATGATCGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51  GGGGTCGTTC TGTTGTGGG TGGCGGCGGC GACGTTTGCG TTTTACCAG
101 GTTTTTCAGT TACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
151 TTGTTTGGG CGGGCGTGT GGGCATGAAT ACGCTGATGC TGGCAGTATG
201 GTTGGCAATG TTGTTCCCTG CCGTGAAAGT GGGGCGTTT TTCAAGCAGT
251 CGGCGACGTG GTTTCGGGGC AAAGACCCCTG TCAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTCCG
401 TATTGTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAGCAGC
451 CTGTTGGGCG ATTCTGCTTC GGTACGGCTG GTGGAATGT TGGCATGGCT
501 GCCTGCCGAA CTGGGTTTTC CCGTGCCTGA TGGCGGGCGG GTCATCGAAG
551 GTCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGCTC GGGGCTGCTG
601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTCT TGGCTTGGGC
651 GGTATGCAAA ATCCTTTTGA AAACAAGCGA AAACGGCTTG GATTTGGAAA
701 AGCCCTATTA TCAGGCGGTC ATCCGCGCT GGCAGAACAA AATCACCAGT
751 CCGGATACGC GTCGGGAAAC CGTGTCCGCC GTTTCGCGCA AAATCGTCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAA TGGCAGGACG
851 CGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT
901 GCCGCCAATC GGAACAGGTT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGGCGCAA CTGCTTATCG GCGTGCGCGC CCAAACGTG CCCGACCGCG
1001 GCGTGTGCG GCAGATCGTC CGACTTTCGG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTGGGAAAA
1101 GCTGGAACAT TGGCGTAACG CGCTGACCGA ATGCGGCGCG GCGTGGCTGG
1151 AACCCGACAG AGCGGCGCAG GAAGGCCGTC TGAAAACCAA CGACCGCACT
1201 TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a253 .pep
1  MIDRNRMLRE TLERVRAGSF WLWVAATFA FFTGFSVTYL LMDNQGLNFF
51  LVLAVLGMN TLMLAVWLAM LFLRVKVRGF FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSVLLLLLV RQYTFNWEST
151 LLGDSSSVRL VEWLAWLPK LGFPVPDARA VIEGRNLNGNI ADARAWSGLL
201 VGSIAICYGIL PRLLAWAVCK ILLKTSENGL DLEKPYQAV IRRWQNKITD
251 ADTRRETVSA VSPKIVLND PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGA
351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRAAQ EGRLKTNDR
401 *

```


583

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVAGSFWLVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
a253	MIDRNRMLRETLERVAGSFWLVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVVRQYTFNWESTLLSNAASVRVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVVRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m253.pep	VIEGRLNGNIADARAWSGLLVGSIAACYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRLNGNIADARAWSGLLVGSIAACYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRETSAVSPKIIILNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWQNKITDADTRRETSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVALETELKQKPAQLLIGVRAQTVPDGRVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVALETELKQKPAQLLIGVRAQTVPDGRVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAWLEPDRAAQEGRLEKDOX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLEKTDNRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcagggttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcttc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactggttt ctttgagaaa cgggcccggc
301 tggacgggat tttcactgtc ctggctgctg gcggtgcag gaatcgaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 ttatatcgt aatgggctgg atggtccttg cggtaatgaa atccctgaca
451 gcctcactcc cgcggcagg actggcttgg ctggcgagc gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtatttg gcggcagcat aaccaatatt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```


51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMY VLIAGSYTPF ALVSLRNGPG
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYIVMGW MVLAVMKSLT
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
 201 VSVYGYVI*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTGA GTTCCTGGCT
 51 GTACCACGGA ATTGCAGCCG GAAAACTGAA AAGCATTTTG AAAAAAACCG
 101 ACCACTGCAT GATTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
 201 GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATC GGACGGAAAA
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG
 301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
 351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTGGC ATTTACTGGT
 401 TTGTAAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTC
 451 GTATTGGGCG GCAGCATCAC CCAATTGTC AGCGTGTACG GTTACGTAAT
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSIL KKTDHCMYV LIAGSYTPFA
 51 LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IVIYVVMGWM
 101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF
 151 VLGGISITQFV SVYGYVI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254.pep				10	20	30
				VSVYGISLLL	LYLSSWLYHGIAAGKLKSIL	
g254						
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KKTDHCMYVLIAGSYTPF	ALVSLRNGPGWTVFSLSWLLA	AAGIAQELTIGRKSEKRLLS		
g254						
	80	90	100	110	120	130
m254.pep		100	110	120	130	140
		IVIYVVMGWMVLAVMKSLT	ASLPSAGLAWLAAGGMLYSVG	IYWFVNDEKIRHGHGIWHLF		
g254		: :				
	140	150	160	170	180	190
m254.pep		160				
		VLGGISITQFVSVYGYVIX				
g254						
		VLGGISITQFVSVYGYVIX				
		200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTTGA GCGGTTTGAT
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
 151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAAC
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTTAT GTGCTGATTG
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CCGGCCGGGG

585

```

301 TGGACGGTAT TTCTACTGTC CTGGCTGCTG GCGGCTGCAG GAATCGCACA
351 AGAACTCACC ATTGGACGGA AAAGCGAAAA ACGACTGCTG TCTATTGCGA
401 TTTATATCGT AATGGGCTGG ATGGTCTTGG CCGTAATGAA ATCCCTGACA
451 GCCTCACTCC CGCCGGCAGG ACTGGCTTGG CTGGCGGCAG GCGGTATGCT
501 GTACAGCGTC GGCATTTACT GGTTTGTAAA CGATGAAAAA ATCCGACACG
551 GGCACGGAAT CTGGCATCTG TTCGTATTGG GCGGCAGCAT CACCCAATTT
601 GTCACCGTGT ACGGTTACGT AATCTGA

```

This corresponds to the amino acid sequence <SEQ ID 998; ORF 254.a>:

a254.pep

```

1  MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLL SIAIYIVMGW MVLAVMKSLLT
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

m254/a254 97.6% identity in 167 aa overlap

```

                                     10                20
30
m254.pep
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL
                                     |||||
|||||
a254
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL
                                     20        30        40        50        60
70
                                     40        50        60        70        80
90
m254.pep
KKTDHCMYIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
|||||
a254
KKTDHCMYIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
                                     80        90        100       110        120
130
                                     100       110       120       130        140
150
m254.pep
IVIIYVVMGWMVLAVMKSILTASLPSAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
|:|:|
|||||
a254
IAIYIVMGWMVLAVMKSILTASLPPAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
                                     140       150       160       170        180
190
                                     160
m254.pep  VLGG SITQFVSVYGYVIX
|||||
a254      VLGG SITQFVSVYGYVIX
                                     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

g255.pep

1	<u>MVGQEARL</u> <u>RGQ</u>	<u>FVAVFAA</u> <u>ALR</u>	YAVKTCADFH	AFDGVDAHHR	VGDFGIEAVE
51	NGFAQTGDV	GGFDMQFRAD	GIQGFAHTVH	IVFQFEDLAL	VGGKKRILGN
101	VFAAFKPDPF	FADLGNVGGD	FRAEFFFQPF	FGNGSGGNAG	CGFAGGTPAA
151	APVVARTVFV	PIGIVGVSGA	EGGGDVAVVF	AALVGVD*	

m255.seq						
1	GTGGTTGGAC	AGGAAGCCTT	GCGGGGTCAG	TTCGTCGCCG	TGTTCCGCTGC	
51	C CGCTTGCGT	TACGCTGTCA	AAACCTGCGC	CGATTTCAC	GCCTTTGACG	
101	GCGTTGATGC	CCATCATCGC	GTAGGCGATT	TCGGCATCGA	GGCGGTCAA	
151	AACAGGTTTC	CCC AAGCCGA	CAGGACACTT	GGCTGCTTCG	ATATGCAGCT	
201	TCGCGCCGAC	GGAATCCAAG	GATTT GCGCA	CGCTGTCCAT	ATAGTTTTTC	
251	AGCTCGGC AA	TTTGGCTATG	GTTGCGCGCA	AAAAAAGGAT	TTTGGGAAAT	
301	G GTGTTCCGAC	CTTCAAAACC	GGATTTCTTT	TCGCCCGACT	TGGGTAACGT	
351	AGGCGGTGAT	TTTCGTGCGC	AATTTTCTT	TCAACCAATT	TTTGGCAACG	
401	GCTCCGGCAG	CAACGCGGGC	GGCGGTTTCA	CGGGCGGAGC	TCCTGCCGCC	
451	GCCGCGGTAG	TCGCGCGTGC	CGTATTGTG	CCAATAGGTA	TAGTCGCGGT	
501	GGCCGGGGCG	G AAGCTGGTG	GCGATGTTGC	CGTAGTCTTT	GCTGCGCTGG	
551	TCGGTATTGC	GGATTAA				

m255.pep

1	VVGQEALRGQ	FVAVFAAALR	YAVKTCADFH	AFDGVDAHHR	VGDFGIEAVK
51	NRFAQADRI	GCFDMQLRAD	GIQGFAHAVH	IVFQLGNLAM	VGGKKRILGN
101	VFAAFKPDPF	PADLGNVGGD	FRAEFFFQPF	FVNGSGSNAG	GGFTGGAPAA
151	AAVVARAVFV	PIGIVGVAGA	EAGGDVAVVF	AAIIGVTAD*	

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

[illegible]

587

	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255.seq
1  GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTGCGTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GCGGTCGAA
151 TACGGGTTCG CCCAAGCCGA CGGGACGTT GCGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTTC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTTGCGAG CCTTCAAACC GGATTCTTT TCGCCGACT TGGTAACGT
351 AGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATT TTTGGCAACG
401 GCTCCGGCGG CAACGCGGCG GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCGGCTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGCGCT
501 GGCCGGGCGG GAAGCTGGT GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```

a255.pep
1  VVGQALRGE FVAVFAAALR YAVKTCADFH AFDGVDAHHG VGDFGIEAVE
51  YGFAQADGDV GGFNMQLRAD GIQGFAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDEF FADLGNVGGD FRAEFFQPF FGNGSGGNAG GGFAGGTPAA
151 APVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*

```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255.pep	VVGQ AL RGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVKNRFAQADRDI					
a255	VVGQ AL RGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVEYGFAQADGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGF AVH IVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
a255	GGFNMQLRADGIQGF AVH IVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAE FF QPF FG NGSGSNAGGGFTGGAPAAA AV VARAVFVPIGIVGVAGAEAGGDVAVVF					
a255	FRAE FF QPF FG NGSGSNAGGGFTGGAPAAA AV VARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```

g256.seq
1  atgctcgcgg tacgcaatcg ggggtggcac ggcgcagtcg tccatttcg
51  cagctgcggc ggcgtagcga acaccgcccc ggtgttctac cacttggggtg
101 ataccgcca aatcgccctt gctttggaca cgctcaccgc gcgttaccgt
151 gaaatatacg ccgtcgcggt atcgctgggc ggcaacgcgc cggcaaaata
201 ttggggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgcggtat
251 ccgccccggt tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301 acgcggtgc tctacacgcg ctacttcttc cgcacactga taccctaaagc

```


588

```

351 acgttcgctc caaggttttc agacggcatt tgccgcaggg tgcaaaacac
401 tgggagagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451 cggcacgact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501 tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgccgc
551 ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601 caacctgcac acggcgggca cgccggcctt gtcagcagca ccggcggcag
651 gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttgacagct
701 tccgcacaaa caggcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

```

g256.pep
1 MLAVNRNGWH GAVVHFRSCG GVANTAPVIFY HLGDTAEIAF ALDTLTARYR
51 EIYAVGVSLG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNAANDP FLPPALPRA DEASEAVTLF
201 QPAHGGHAGF VSSTGGRHL QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

```

m256.seq
1 ATGCTTGCGG TACGCGATCG GGGTTGGCAC GCGGTAGTCG TCCATTTCGG
51 CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTGGCG
101 ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTGCGCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAATA
201 TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTCATCT
251 CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTCGA CAGCGGCATC
301 ACGCGGCTGC TCTACACGCG CTACTTCCTC CGCACCTGA TACCCAAAGC
351 AAAATCGCTC CAAGGTTTT AGACGGCAIT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451 CGGCACGACT ACTACGCGCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCCCT GCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCCTGTTT
601 CAGCCGGCAT ATGGTGGTCA TGTCGGCTTT GTCAGCAGCA CCGGCGGCAG
651 GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

```

m256.pep
1 MLAVRDRGWH GVVHFRSCG GIANTAPVIFY XLGDTAEIAF TLDTFAARYR
51 EIYAVGVSLG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRRFDSGI
101 TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNAVNDP FLPPALPRA DEVSEAVTLF
201 QPAYGGHVG FVSSTGGRHL QWLPQTVLSY FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

```

m256/g256
      10      20      30      40      50      60
m256.pep MLAVRDRGWHGVVHFRSCGGIANTAPVIFYHLGDTAEIAFTLDTFAARYREIYAVGVSLG
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256      MLAVNRNGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAFALDTLTARYREIYAVGVSLG
      10      20      30      40      50      60

      70      80      90      100     110     120
m256.pep GNALAKYLGEQGKKALPQAAVISAPVDAEAAGRRFDSGITRLLYTRYFLRTLIPKAKSL
      || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256      GNAPAKYLGEQGKKALPHASAAVSAPVDAEAAGSRFDSGITRLLYTRYFLRTLIPKARSL
      70      80      90      100     110     120

      130     140     150     160     170     180
m256.pep QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNAVNDP
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256      QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNAANDP

```


589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

a256.seq

```

1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGTAGTCG TCCATTTCCG
51  CAGCTGCGGC GGCGTAGCGA ACACGCCCCC GGTGTTCTAC CACTTGGGCG
101 ATACCGCCGA AATTGCCTTT ACTTTGGACA CGTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GCGAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGCTGCG TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCCTGTTC
601 CAGCCGACAC ACGGTGGTCA TGTCGGCTTT GTCGGCAGCA CCGGGCGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

a256.pep

```

1  MLAVRDRGWN GVVVHFRSCG GVANTAPVfy HLGDTAEIAF TLDTLAARYR
51  EIIYAVGVS LG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFD SGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHG FAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG F VGSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVHFRSCGGIANTAPVfyXHLGDTAEIAFTLDTFAARYREIYAVGVSLG					
a256	MLAVRDRGWNGVVHFRSCGGVANTAPVfyXHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGKKALPQAAVISAPVDAEAAAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAAAGNRFD SGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHG FADRH DYYRQTSC KPLLKHVAKP LLLNNAVNDP					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHG FADRH DYYRQTSC KPLLKHVAKP LLLNNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVG FVGSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

g256-1.seq

```

1  ATGATTTTGA CACGCGCCGA CAGGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACA CCCCGCACCC GCATACCGCC

```


590

```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTCGCC CGATGCGCGC CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTGCAACTG ATGCTCGCGG
251 TAGCGAATCG GGGTTGGCAC GCGCGAGTCG TCCATTTCGG CAGCTCGCGG
301 GCGGTAGCGA ACACCGCCCC GGTGTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACC GC GTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCTCG GCGCCGTAT CCGCCCCGT
501 TGATGCGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGGCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCCTGCCG CCGAAGCCCT
801 GCGCCGTGCA GACGAAGCGT CCGAAGCCGT TACCTGTTC CAACCTGCAC
851 ACGGCGGGCA CGCCGCTTT GTGAGCAGCA CCGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVNRNGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EIYAVGVSLG GNAPAKYLGE
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFD RHDYRQTSK KPLLKHVAKP
251 LLLNAANDP FLPEALPRA DEASEAVTLF QPAHGHHAGF VSSTGGRLHL
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCGCGCGCCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTCCGCCGA TCGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCAGCC ATTACCGCGT CGAACTGATG CTTGCGGTAC
251 CCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCCGCAG CTGCGCGGCG
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACCGCTGG CAAAATATTT GGGCGAACAG
451 GGCAAAAGAG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCGCCGTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAGC CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGC ACCCTGATAC CCAAAGCAAA ATCGCTCCAA
601 GGTTTTCAGA CGGCATTTCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGTCTA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CCTGTTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCGC AGACCGTCTT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTRVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVRDRGWHG VVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPIKASLQ
201 GFQTAFAAGC KTLGEFDDR FTAPLHGFA DR HDYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVGFV SSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

          10      20      30      40      50      59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
          |||||
g256-1      MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
          10      20      30      40      50      60

          60      70      80      90     100     110     119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVRDRGWHGVVHFRSCGGIANTAPVYFHLGDTAEIAF

```


591

```

|||||
g256-1  LVVLFHGLEGSSRSYAVELMLAVNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
          70      80      90      100     110     120

120      130      140      150      160      170      179
m256-1.pep  TLDTF AARYREIYAVGVSLGGNALAKYLGEQKKALPQAAVISAPVDAEAAGRFDSDGI
          :|||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      ALDTLTARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVSAPVDAEAAGRFDSDGI
          130      140      150      160      170      180

180      190      200      210      220      230      239
m256-1.pep  TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSC
          :|||||:|||||:|||||:|||||:|||||:|||||
g256-1      TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSC
          190      200      210      220      230      240

240      250      260      270      280      290      299
m256-1.pep  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHGVFVSSSTGGRLHL
          :|||||:|||||:|||||:|||||:|||||:|||||
g256-1      KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSSTGGRLHL
          250      260      270      280      290      300

300      310      319
m256-1.pep  QWLPQTVLSYFDSFRTNRRX
          :|||||
g256-1      QWLPQTVLSYFDSFRTNRRX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA CACCGCCGGA CACACCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACG CTCGCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAACCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGCGGT CGAAGTATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGGCGGC
301 GTAGCGAACA CCGCCCGGT GTTCTACCAC TTGGCGGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACAGCG TCGCCGCGCG TTACCGTGAA ATATACGCGC
401 TCGCGCTATC GCTGGGCGGC AACCGCTGG CAAATATTT GGGCGAACAG
451 GGGCAAAACG CGCTGCCGCA AGCCGCGGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGGCTTA CTCCTCCGC AACTGATAC CCAAGCAGC GTCGCTCCAA
601 GGTTTTCAGA CGGCATTGCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTTC ACCGCACCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCTCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCGCTGCC
801 CCGCGCAGAG GAAGTGTCAG AAGCCGTTAC CCTGTTCCAG CCGACACAG
851 GTGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCCG AGACCGTCTT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.pep
1  MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVRDRGWNG VVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSDGI RLLYTRYFLR TLIPKARSLQ
201 GFQTAFAAGC KTLGEFDDRFTAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHGVGFV GSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

10      20      30      40      50      60
a256-1.pep  MILTPPDTPFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
          |||||
m256-1      MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
          10      20      30      40      50      60

70      80      90      100     110     120
a256-1.pep  VVLFHGLEGGSGSHYAVELMLAVRDRGWNGVVHFRSCGGVANTAPVFYHLGDTAEIAFT
          :|||||:|||||:|||||:|||||:|||||:|||||
m256-1      VVLFHGLEGSSRSYAVELMLAVRDRGWNGVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```


592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVS	LGGNALAKYLGEQ	GENALPQAAVISAP	VDAAAGNRFD	SGIT	
m256-1	LDTF	AARYREIYAVGVS	LGGNALAKYLGEQ	GKALPQAAVISAP	VDAAAGRRFD	SGIT
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPK	ARSLQGFQTAFAAG	CKTLGEFDDRETA	PLHGFADRH	DYYRQTSCK	
m256-1	RLLYTRYFLRTLIPK	ARSLQGFQTAFAAG	CKTLGEFDDRETA	PLHGFADRH	DYYRQTSCK	
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNA	VNDPFLPPEALPRA	DEVSEAVTLFQP	THGGHVGFVGST	GGRHLHQ	
m256-1	PLLKHVAKPLLLNA	VNDPFLPPEALPRA	DEVSEAVTLFQ	PAYGGHVGFVS	STGGRHLHQ	
	250	260	270	280	290	300
a256-1.pep	310	319				
	WLPQTVLSYFDS	FRTNRRX				
m256-1	WLPQTVLSYFDS	FRTNRRX				
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

```
g257.seq
1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggg gcgccgggtt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaaggtgtcg cgctgggttc cggcgcgagg ctgcgcctgt tcggcgtgga
201 cgacagacag gcggcggatt tggtaataa ggttttggcg gaagtggcgc
251 gtttggaata aatgttcagc ctttaccgtg aagacagcct gatcagccgt
301 ctgaaccgcg acggttatct gacttcgcct ccggcggatt ttttgaact
351 gttgagcctg gccgcgatat tcacgcgctg a
```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

```
g257.pep
1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDNVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIETR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

```
m257.seq
1  ATGGGCAGGC ATTTCGGGCG .CAGCGTTT CTGACGTTG CCGCCGTTGC
51  GCGCGGGaC. GCGGcGGTTT CTTTCCTGCC GAATCCTTTT GCCCGCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151 AAAGGTGTG CACTGGGTTC CGGTGCGGa. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCCG TCGGCGGATT TTTTGGAACT
351 GKTGAGCCTG GCCGCGATAT TCACGCKCTG A
```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

```
m257.pep
1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRNVFFW
51  KGVALGSGAX LRLFGVDDRR AADLVNKLVA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLELXSL AAIETX*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10 20 30 40 50 60

593

```

m257.pep      MGRHFGRQRFLTVAAVAAGTAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVGALGSGAD
               |||||:||||:||||: ||||| ||| |:|:|||||:|||||:
g257          MGRHFGRRRRFLTAAAVAVAGA AVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVGALGSGAE
               10      20      30      40      50      60

               70      80      90      100     110     120
m257.pep      LRLFGVDDRRRAADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLELXSL
               |||||:|||||:|||||:|||||:|||||:|||||: ||||| ||
g257          LRLFGVDDRQAADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
               70      80      90      100     110     120

m257.pep      AAIFTXX
               |||||
g257          AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC  ATTTCCGGCGC  CAGGCGTTTT  TTGACAGTTG  CCGCCGTTGC
51 GCGGCGGGGC  GCGGCGGTTT  CTTTCCTGCC  GAATCCTTTT  GCCGCCGATG
101 ATGAAAACG  CAATAAAGAT  GAAAACGCA  ATGAAAATGT  GTTTTCTGG
151 AAAGGTGTCG  CACTGGGTTC  CGGTGCGGAG  CTCCGTCTGT  TCGGTGTGGA
201 CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTTGGCG  GAAGTGGCGC
251 GTTTGGAAAA  AATGTTTCAGC  CTTTACCGTG  AAGACAGCCT  GATCAGCCGT
301 CTGAACCGTG  ACGGTTATTT  GACTTCGCCG  CCGGCGGATT  TTTTGGAACT
351 GTTGAGCCTG  GCCGTGATAT  TCACGCGCTG  A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF  LTVAAVAAG  AAVSFLPNP  AADDEKRNK  EKRNENVFFW
51  KGVGALGSGAE  LRLFGVDDR  AADLVNKKV  LA EVARLEK  MFSLYRED  SLISRLNR
101  LNRDGYLTSP  PADFLELL  SL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

               10      20      30      40      50
60
m257.pep      MGRHFGXQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVGALGSGAX
               ||||| :|||||: |||||
a257          MGRHFGRRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAE
               10      20      30      40      50
60
               70      80      90      100     110
120
m257.pep      LRLFGVDDRRRAADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLELXSL
               |||||:|||||:|||||:|||||:|||||: |||||
a257          LRLFGVDDRRRAADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
               70      80      90      100     110
120

m257.pep      AAIFTXX
               |||||
a257          AVIFTRX

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1  atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgctgta
51  cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtggt gtccgccggt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcggtgt
201 cggttcgagc attgccaaac gcctttcccg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttcctg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cagcaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggcggcagac aatgccgtca
401 gcaacgccgt tcccgtaacg atagacctca tcggcacccg ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgcccc
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccgaca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaa agcataggcg gcgtattgta
651 cgcgcaggga tggttgtcgg caggtacgca caacgggcgc gattacgcgc
701 tgttcttcgg ccagccgatt cccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gcaaaaaagg
801 tttgcagacc tttttcttg taaccctgct gattgcctcg ctgctgtcga
851 tttttcttgc gctggtaatg gcaactgtatt ttgccgccg tttcgtcgaa
901 cccattctgt cgttgccga gggcgcaaag gcggtggcgc aggggtgatt
951 cagccagacg cgcccgtat tgcgcaacga cgagttcgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcgga ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctctacccc ctctcttgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctcccctct ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51  LARYVILLK DRRNGVFGSQ IAKRLSGMFT LVAVLPLGLF FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVFPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKGLQOT FFLVTLLIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLNRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLDG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1  ATGCGCCGTT TTCTACCGAT CGCAGCCATA TCGCGCGTCG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTCT
101 GGTGGATTGT TCGTTTCAGC GCAATGCTGC TGCTGTTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGTTTGCCG
251 TACTGCCCGG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAAAT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATTT GCGGCGAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAaaaaaATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CCGCGAGGCG TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCC
701 TGTTTTTCGG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAaaaaaAGG
801 TTTGCGAGCC TTTTTCCTGG CAACCCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCGCGCG TTTCTGCGAA
901 CCCGTCCTAT CGTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATT
951 CAGCCAGACG CGCCCCGTGT TCGCAACGA CGAGTTCGGA CGCTTGACCA

```


m258.ppt

from *N. gonorrhoeae*:

m258/q258

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVAFSAMLLLVLSAVLARYVILLK					
	:					
g258	MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVSFSAMLLLVLSAVLARYVILLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLPGVSAQFINGTINSWFGNDTHEALERSINL					
	:					
g258	DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSINL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNVAVPQIDLIGAASLPGDMGRVLEHYAGSGFAQLALYNAASGKIEK					
	: :					
g258	SKSALDLAADNAVSNVAVPQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m258.pep	SINPHKLDQPPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV					
	: : : :					
g258	SINPHQFDQPLPDKHWEQIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI					
	190	200	210	220	230	240

	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAE	LSYSKKG	LQTF	FLATLLIAS	LLSIF	LALVMALYFARRFVE
	:: :			:		
g258	PENVAQDAVLIEKARAKYAE	LSYSKKG	LQTF	FLVTL	LIASLLSIF	LALVMALYFARRFVE
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQ	GDFSQ	TRPVL	RNDEF	GR	LTKLFNHMT
	:					
g258	PILSLAEGAKAVAQ	GDFSQ	TRPVL	RNDEF	GR	LTKLFNHMT
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTT	GGVVVF	DEQ	CLKT	FNKA	AEQILG
	:		:	:	:	:
g258	RHYLECVLDGLTT	GGVVVS	YPL	SCCR	TAVF	STCHSSPLSYFX
	370	380	390	400		

```

a258.seq
1 ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTGC TCTGTGTGTA
51 CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGTGGCGC GATTATTCTT
101 CGTGGATTGT TGCCTTACCG GCAATGCTGC TGCTGTGTGT GTCCGCGGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGCGCGC ACGGCGGTATT
201 CGGTTCCGAG ATTGCAAAC GCCTTTCGGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTTCTG TTCGGCGTTT CCGCACAAGT TATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATAAC CACGAGGCGC TTGAACGCGA
351 CCTCAATTGT AGCAAGTCGG CATTAATCT GGCGCCAGAC AACGCCCTTG
401 GCAACGCCAT CCCCGTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TCATATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCGG TTTCCAGGTA AGCGCGCTTG GCAAAAAATC
601 CAACAGGCGG GTTCGGTCAG GGATTTGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCCG CAGGTACGCA CAACGGGCGC GATTACGCTT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGCGGAA ATATGCTGAG TTGATTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCTGCT GATTGCTCG CTGCTGTCTG
851 TTTTCTTTCG ACTGTCATG GCACTGTATT TCGCCCGCCG TTTCTGCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGCGGAAG GCGGTGCGCG AAGGCGATTT
951 CAGCCAGACG CCACCCGTGT TGCGCCACGA CGAGTTCCGA CGCTTGACCA
1001 AGTTGTTCAA CCACATAGC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGACATTATC TCGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAACAACCT CAACAAAGCG CGGGAACAGA TTTTGGGGAT GCCGCTTACC
1201 CCCCTGTGGG GCACGACCGG GCACGGTTGG CACGCGCTTT CGCGCGACGA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCTTG
1351 CTGGGCAAGG CAACCGTCTT GCCCGAAGC AACGGCAACG GCGTGTGTAAT
1401 GGTGATTGAC GACATCACC TTTTGATACA CGCGCAAAAA TAAGCCCGCT
1451 GGGGCGAAGT GGCAAAACGG CTGGCACACG AAATCCGAA TCCGCTACG
1501 CCCATCCAGC TTTCTGCCGA ACGGCTGGCG TGGAAATTGG GCGGGAAGCT
1551 GGACGAGCAG GACGCGCAAA TCCTGACACG TTCGACCGAC ACCATCATCA
1601 ACAAAGTGGC GGCATATAAA GAAATGGTGC AGGATATTCC CAATTACCGG
1651 CGTTCGCCCT CGCTCAAAAT GGAATAATCAG GATTGTAACG CTTAATTCGG
1701 CGATGTGPTG GCATTGTACG AAGCTGGTCC GTGCCGGTTT GCGGCGGAAC
1751 TTGCCGGCGA ACCGCTGATG ATGGCGGCGG ATACGACCGC CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATCCCGCC GAAGCGGCGG AAGAAGCCGA
1851 TTGTGCCGAA GTCAGGGTAA AATCGGAAGC GGGCGAGGAC GGACGGATTG
1901 TCCTGACAGT TTGCGACAAC GGCAAGGGGT TCGGCAGGGA ATAGCTGCAC
1951 AATGCCTTCG AGCCGTATGT AACGGACAAA CCGGCTGGAA CGGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGCG CGCATCAGCC
2051 TGAGCAATCA GGTAGCGGGC GGGCGGTGTG TCAGAAATCAT CTTGCCAAAA
2101 ACGTAGAAAA CTTATGCGTA G

```


This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLKK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSINL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSSKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGKGLDEQ DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AELAGEPLM MAADTTAMRQ
601 VLHNIFKNAE EAAEEADVPE VRVKSEAGQD GRIVLTVCDN KGKFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIIEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

```

      10      20      30      40      50      60
m258.pep  MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAMLVVLSAVLARYVILLKK
a258      MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAMLVVLSAVLARYVILLKK
      10      20      30      40      50      60

      70      80      90     100     110     120
m258.pep  DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSINL
a258      DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSINL
      70      80      90     100     110     120

      130     140     150     160     170     180
m258.pep  SKSALNLAADNALGNAVPVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK
a258      SKSALNLAADNALGNAIPVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK
      130     140     150     160     170     180

      190     200     210     220     230     240
m258.pep  SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV
a258      SINPHKLDQPFPGKARWEKIQQAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV
      190     200     210     220     230     240

      250     260     270     280     290     300
m258.pep  PKGVAEDAVLIEKARAKYAE LSYSSKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
a258      PKGVAEDAVLIEKARAKYAE LSYSSKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
      250     260     270     280     290     300

      310     320     330     340     350     360
m258.pep  PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA
a258      PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA
      310     320     330     340     350     360

      370     380     390     400     410     420
m258.pep  RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLT PLWGSSRHGW HGVSAQQSLL
a258      RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLT PLWGSSRHGW HGVSAQQSLL
      370     380     390     400     410     420

      430     440     450     460     470     480
m258.pep  AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
a258      AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
```


598

	430	440	450	460	470	480
m258.pep	490	500	510	520	530	540
	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDTIIRKQVAALK					
	490	500	510	520	530	540
m258.pep	550	560	570	580	589	
	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIKNAEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaatctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagAACGAA agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgctc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccc acgacgaaga cgcgcgcacg attgccgccg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgccctc
451 ggcgaaacct atggcgcgct gttcgccgat attttcgagt tgcggcgccg
501 tttggaaagg cgcgcgttca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgtcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAELAKMDM FALGTDAAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKIKHLRRC LPFGNGVGVFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAACTCTG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CCGCGGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTGCGCTCG
451 GGCgAAACCT ATGGACGCGT GTTCGCGGAT ATTTTCGAGT TGTCGGMGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAELAKMDM FALGTDAAVAS

```


599

151 GETYGRVFAD IFELSXALEG RAFKGMMLKT AEYKXHLRRC LPFGNGVGVG
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNE SIHPVLHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNE SIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSXALEGRAFKGMMLKT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALERRAFKGILKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRC LPFGNGVGVGRTQSGVAGDFKNIR					
g259	AEYKXHLRRC LPFGNGVGVGFGRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGCTTCGTG TCGGCGCGTT CAAAGGCTAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCGCCCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAA.CATCT TCGCGCATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCGCTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCG GAAAAGTCCA
651 A

```

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTD AVAS
151 GETYGRVFAD IFELSAALEG RAFKGMMLKT AEYKXHLRRC LPFGNGVGVG
201 RAQSGVAGDF KNIGKVQ

```

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					

600

	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKIFYREKMIQNESIHVPXHASLOHLEHKPQILALLVKNHKGMAEQVRFKAE					
a259	SARSKAKAEKIFYREKMIQNESIHVPVHASLOHLEHKPQMLALLVKNHKGMAEQVRFKAE					
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAELAKMDMFALGTDAVASGETYGRVVFADIFELSALEGRAFKGMLKLT					
a259	VLPDDEDARTIAELAKMDMFALGTDAVASGETYGRVVFADIFELSAALEGRAFKGMLKLT					
	190	200	210			
m259.pep	AEYKXHLRRLPFGNGVGVGRGTQSGVAGDFKNIR					
a259	AEYKXHLRRLPFGNGVGVGRAQSGVAGDFKNIGKVQ					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTGATTTTC TTTGCCGGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGTCGCTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCC ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTGATTTTC TTTGCCGGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGTCGCTT CAAAGGCCAA
201 GCGCGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCC ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG CGGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTC A A A A C A T C G G A A A A G T C C A A
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLAQEIS KTSEKSKRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHKGMAEQVR	FKA		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHKGMAEQVR	FKA		
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDMF	FALGTD	AVASGETYGRVFADIFEL	SAALE		
m259-1	VLPDDEDARTIAAELAKMDMF	FALGTD	AVASGETYGRVFADIFEL	SAALEGRAFKGMLKLT		
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGCTTCGTG TCGGCGCGTT CAAAGGCTAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGCGGAAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCCGCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGCGCATGCC TGCCGTTCGG AAACGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGCGGTTGCA GGAGATTTC AAAAAATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTD AVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQALQEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHKGMAEQVR	FKA		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHKGMAEQVR	FKA		
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDMF	FALGTD	AVASGETYGRVFADIFEL	SAALEGRAFKGMLKLT		
m259-1	VLPDDEDARTIAAELAKMDMF	FALGTD	AVASGETYGRVFADIFEL	SAALEGRAFKGMLKLT		
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELG	ALNQALQEISK	TSEKSKRIFYX			
m259-1	AEYKNIFGDACRSETALELG	ALNQALQEISK	TSEKSKRIFYX			
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

602

```

1  atggggtgcgg gtgtagtatt cgttgctctt cagccgttct tcagcctgtt
51  tcgagcgttg ttcgagggcg gagtccggtat agtcgagggg gcgcacgatg
101 ccgctgaatg cgacttcttg tccgaggaat ttaccctgat ccggatcggg
151 gatgttttta ttgattcggg aggtcagata acggccccgg tctttcaggc
201 ctttggtgta aaccctggcg cctttggtgt acagcagcct gccttccggg
251 cccgagagca ggcgcggcgc ggcagcgggt tctttgctgg aaacgatttg
301 cgggtgctgc ataaagacgc ggtagaagtt gacatcgatg gcgggaatac
351 cgtatccgga cacttcctta tccggactga ttttgacgac ggggatgccc
401 tctgtctgtt ccaagccgag gcgcgggttc cgcacaacgt agcgcaacac
451 caatacctgg cccggataaa tcaggtcggg attgtggatt tgatcccggt
501 tcgcgccccca caggggggga ccattgccac gggctgtaca ggtatttgcc
551 cgaaataccc cacagggtgt cgcctgttt ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1  MGAGVVFVVF QPFFSLFRAL FEGGVGIVEG AHDAAECDLF SEEFTRIRIG
51  DVFIDSVGQI TARFFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVLHKDAVEV DIDGGNTVSG HFLIRTFDGD GDAVCLFQAE ARFAANVAQH
151 QYLARINQVG IVDLIPVRAP QGGTIATGCT GICPKYPTGC RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCCGT AGGTCAGGTA GCGCCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGwTCA sGCGCGGyGC GGCAGCGGTT TCTTTGCGGG AAACGATTG
301 CGGATGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTG CCGTCAACGT GCGCAACAC
451 CAATACCTGG TCCGGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTyCCA CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1  MGAGMVVFVF RPFSSLFRAL FEDRVGIVEG AHDAAECDLF PEEFTRIRIG
51  DVFIDSVGVQ AARLFQAFGV NPGAFGVQQP AFRARXXARX GSGFFAGNDL
101 RMPHKDAVEV DIDGGNTVSG HFLIRTFDGD GDAVCLFQAE ARFAVNVAQH
151 QYLVRINQVG IVDLIPVRVP Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRALFEDRVGIVEGAHDAAECDLFPEEFTRIRIGDVFIDSVGVQV					
	: :					
g260	MGAGVVFVVFQPFSSLFRALFEGGVGIVEGAHDAAECDLSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
	: : :					
g260	TARFFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTFDGDGDAVCLFQAEARFAVNVAQHQYLVRINQVGIVDLIPVRVPQ					
	: :					
g260	HFLIRTFDGDGDAVCLFQAEARFAANVAQHQYLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

603

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

a260.seq
1 ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51 TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGCGCGC GGCAGCGGTT TCTTTCGGG AACGATTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTG CCGTCAACGT GCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTGCCC
551 CGAAATGCCC CACAGGTGT CGCCCTGTTT GA

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

a260.pep
1 MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51 DVFIDSVGQV AARLFQAFGV NPGAQVQFP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGNTVSG HFLIRTHFDD GDAVCLFAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAECDFL PEEFTRIRIG DVFIDSVGQV					
a260	MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAECDFL PEEFTRIRIG DVFIDSVGQV					
	10	20	30	40	50	60
m260.pep	AARLFQAFGV NPGAQVQFP AFRAREQARR GSGFFAGNDL RMPHKDAVEV DIDGNTVSG					
a260	AARLFQAFGV NPGAQVQFP AFRAREQARR GSGFFAGNDL RVPHKDAVEV DIDGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDD GDAVCLFAE ARFAVNVAQH QYLVQINQVG IVDLIPVRVP Q					
a260	HFLIRTHFDD GDAVCLFAE ARFAVNVAQH QYLVQINQVG IVDLIPVRVP QAAXIATGCT					
	130	140	150	160	170	180
m260.pep	GICPKCPTGCRPVX					
a260	GICPKCPTGCRPVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

g261.seq
1 atggagcttg ggcatacgt attccttggtg ctttgccgcg gttcagacgg
51 cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctccggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctgttcgctg atgtagtcca acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtac atcagcggcg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcag gatttgacga acacgccgcg
301 gcagtcggga tagcccga aaatcggttc gcacacgccc gcgatgatgt
351 gccgataacc ctgccctttg gcaaaaatgg cggcgtaaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc
451 gatggcggcg gtttcgatgg cggcggtttc gtccatcagg gcgttgtagc
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttcagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgccgtag gtttgatttg

651 cctgaatcag gcaggtggtc gaatcctgac cgcccagaaa gatgaccaag
701 gcttttttggg ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep
1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG
51 LFADVVQHAH FVRQRPRLRL GQVHQRRLDL KIVVHRQIKG NVHGFDEHAA
101 AVGIARKIGF AHARDDVPDT LPPGKNGGVK QEKRVTPVHK GIGNAVVGGF
151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP
201 VSEGDLGVF APVGLDCLNQ AGGRILTARE DDQGLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq
1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTCCGC CAAGATACAG
101 CTCGGGCATT CGCGcCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCCACG
201 TTGCGCCTT GGTGAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA AATTAAGGGT AACGTTTCATC GATTGACAA ACACGTCGCG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 gCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GgCTcAAGTC GAGTACGTT TGTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep
1 MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51 LLADIVQHAH FVRQRPRLRL GQIHQRRLDL KIIVHRQIKG NVHRFDKHVA
101 AVGIAGEVGF AHARDDVPYP LPPGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFPVGL DCLNQAGGRI LTARKDDQGL LV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

m261.pep	10	20	30	40	50	60
	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVVQHAH					
	10	20	30	40	50	60
m261.pep	70	80	90	100	110	120
	FVRQRPRLRLGQIHQRRLDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
g261	FVRQRPRLRLGQVHQRRLDLKIVVHRQIKGNVHGFDEHAA AVGIARKIGFAHARDDVPDT					
	70	80	90	100	110	120
m261.pep	130	140	150	160	170	
	LPPGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGV----VHQGIVRNLPHQAVEYGLF					
g261	LPPGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAEYGLT					
	130	140	150	160	170	180
m261.pep	180	190	200	210	220	230
	DAQILRNPAFTFQLDGMALPVLESNGLDVFPVGLDCLNQAGGRILTARKDDQGLLVX					
g261	DTQILRDPLCAFLDGMALPVSEGDLGVFAPVGLDCLNQAGGRILTAREDDQGLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCTGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTCTAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTTTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGC CGTAGGTTT GATTGCCTGA ATCAGGCAGG
651 TGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTT TTGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFQKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPQAAQV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQRAH					
	10	20	30	40	50	60
m261.pep	FVRQRPRRLRGQIHQRRVDLKIIVHRQIKGNVHREDFKHVAAVGIAGEVGFHARDDVPYP					
a261	FVRQRPSLRLRGQIHQRRVDLKIIVHRQIKGNVHGFQKHVTAVGIAGEVGFHARDDVPYP					
	70	80	90	100	110	120
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPQAAQVEYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPQAAQVEYGLFDAQIL					
	130	140	150	160	170	180
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGFVLX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgccaa
51  accgcgcgta gaggccgtac ccaaaaacaa cggctttatc cccaacctca
101 tcggcgattt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgccgccaa cagcctgacc gccggcgaa tcgaagtgat
201 ccggtatcat gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccgc ctttggcggc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctggaagcgg gctacaaccg gcagcaggca
```


g263 . pep

```

1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIQVLANA PEALAFYQEV
51 GKLNAANSLT AGEVEVIRII AVR TNQCSFC VAGHTKLATL KKL LSEQSLN
101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDDELNAF LEAGYNRQQA
151 VEVVMGVALA TLCNYANNLA OTEINPKLOA YA*

```

m263.seq (partial)

1 GCAGCAGGCG AATTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101 CATTTTTCGA TGCGGGCTAC AACCAGACAG AGCGAGTCTGA AGTCGTGATG
151 GGGCT. AsyC TgGCAACCTT GTGCAACTAC GTCAACAACC TCGGACAAAC
201 CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

m263.pep (partial)

```

1      GCAGCAGGGG AATTTGACGA TGCCAAACTC GGC GCGCTCG CCGCCTTCAC
51     CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101    CATTTTTCGA TCGGGGCTAC AACCAGACAG AGGCAGTCTGA AGTCGTGATG
151    GGGCT. AsyC TgGCCAACTCT GTGCAACTAC GTCAACAACC TCGGACAAAC
201    CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

```

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/g263

m263.pep
AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
|||::|||||||
g263 QCSFCVAGHTKLATLTKLLSEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSDD
80 90 100 110 120 130

m263.pep
ELKAFFDAGYNQQQAVEVVMGVXLATLCNYVNNLGQTEINPELQAYAX
||:::||:|||||
g263 ELNAFLEAGYNRQQAVEVVMGVVALATLCNYANNLAQTETNPQLQAYAX
140 150 160 170 180

a263.seq

1	ATGGCAGCTT	TAACCGTACA	CACCCTCGAA	ACCGCCCCCG	AAGCCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAACAA	CGGCTTTATC	CCCAACCTTA
101	TCGGCGTATT	ATCAAACGCG	CCCGAGAGCT	TGGCGTTTTA	CCAAGAAGTC
151	GGCAAGCTCA	ACGCCGCCAA	CAGCCTGACC	GCCGCGCAAG	TGCAAGTAAT
201	CCAGATTATT	GCCGCGCGCA	CCAACCAATG	CGGCTTTCTG	CTGGCAGGGC
251	ACACCAAAC	CGCAACCGTG	AAAAAAGTCC	TTTCCGAACA	ATCCGTCAAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GCTCGCGGCT	TTTACCCAAG	CCGTAATGGC	AAAAAAGGC	GCGGTATCCG
401	ACGAGGAATC	CAAGGACATTT	TTTGATGCGG	GCTACAACCA	GCAGCAGGCA
451	GTCGGAATCG	TGATGGCGGT	AGCCTTGGCA	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCACATCCGA	ATTGCAAGCT	TACGCTGA

a263.pep

1 MARLTVHTLE TAPEAAKARV EAVLQNNGFI PNLIGVLSNA PEALAFYQEV
51 GKLNAANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KKLLEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA
151 VEVVMGVALA TLCNYVNNLG QTEINPELOA YA*

607

m263/a263 97.4% identity in 77 aa overlap

					10	20	30
m263.pep					AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
a263	QCGFCVAGHTKLATLKKLLSEQSVKAA	80	90	100	110	120	130
		40	50	60	70		
m263.pep	ELKAFFDAGYNQQQAVEVVMGXLLATLCNYVNNLGQTEINPELQAYAX						
a263	ELKAFFDAGYNQQQAVEVVMGVALATLCNYVNNLGQTEINPELQAYAX	140	150	160	170	180	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

g264.seq

```

1   ttgacttttaa cccgaaaaaac ccttttcctc ctcaccgccc cggtcggcac
51  acactccctt cagacggcat ccgcccacgc agtgggtcaag ccggaataaac
101 tgcacgcctc cgccaaccgc agctacaaag tcgcccgaatt cacgcaaac
151 ggcaacgcct cgtgtgtacgg cggcagggtt caccggcgca aaacttcagg
201 cggagaccgc tacgatatga acgcttttac cgccgcccac aaaaccctgc
251 ccatcccccag ccatgtgcgc gtaaccaaca ccaaaaacgg caaaagcgtc
301 atcgtccgcg tcaacgacgc cggccccttc caccggcaacc gcatcatcga
351 cgtatccaaa gccgcccgcg aaaaattggg ctttgtcagc caagggacgg
401 cacacgtcaa aatcgaacaa atcgtccagg gccaatccgc accggttgcc
451 gaaaaaaaag acatctttat cgacttgaaa tctttcggta cggaacacga
501 agcacaagcc tatctgaacc aagccgcccc aaatttcgcc gcttcgtcat
551 caagcccga cctctcgggt gaaaaacgcc gttacgaata cgttgtcaaa
601 atgggcccgt ttgcctcgca ggaacgcgcc gccgaagccg aagcgcaggc
651 acgcggtatg gttcgggagg tactgacctc cggttga

```

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

```

1   LTLTRKTLFL LTAAPGTHSL QTASADAVVK PEKLHASANR SYKVAEFTQT
51  GNASWYGGFR HGRKTSGGDR YDMNAFTAAH KTLPIPSHVR VTNTKNGKSV
101 IVRVNDRGPF HGNRIIDVSK AAAQKLGFSV QGTAHVKIEQ IVPQGSAPVA
151 ENKDIFIDLK SFGTEHEAQA YLNQAAQNFA ASSSSPNLSV EKRRYEYVVK
201 MGPFSQERA AEAEQAQARG VRAVLTS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

```

1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACCGCCG CATTCCGGCAC
51  ACACGCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGAAC ACGCTACACG
151 CCGAAAAACC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCCT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAA CCGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAATTT GGGCTTTGTC AACCAGGGA CCGCACACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCAGTT GCCGAAAACA AAGACATCTT
501 TATCGACTTG AAATCTTTTC GTACGGAACA CGAAGCACA GCCTATCTGA
551 ACCAAGCCGC CCAAACTTC GCCGTTTCGT CATCGGTAC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTACCTC
651 GCAGGAACGC GCCGCGAAG CCGAAGCTCA GCGCGCGGT ATGTTTCGGG
701 CGGTATTGAC CGCCGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

```

1   LTLTRKTLFL LTAAPGTHSL QTASADAVVK AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGF FHGRKTSGGE RYDMNAFTAA HKTLPIPSYV
101 RVTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAAQKLGFSV NQTAHVKIE
151 QIVPQGSAPV AENKDIFIDL KSFGEHEAQA AYLNQAAQNF AVSSSGTNLS
201 VEKRRYEYVV KMPFSTQER AAEEQAQARG MVRAVLTAG*

```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKEKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTS GGERYDMNAFTA AHKTLPIPSYRVVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTS GGDYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQA QKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLSFGTEHEAQ					
g264	FHGNRIIDVSKAAQA QKLG FVVSQGT AHVKIEQIVPGQSAPVAENK DIFIDLSFGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRY EYVVKMGPF TSQERAAEAEQA RGMVRAVLTAGX					
g264	AYLNQAAQNFAASSSPNLSVEKRRY EYVVKMGPFASQERAAEAEQA RGMVRAVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

```

1  TTGACTTTAA CCCGAAAAC CCTTTTCCTC CTCACCGCG CATTCGGCAT
51  ACATTCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAGG GCAGAAAAAC
101 TGCACGCCCTC CGCCAACCGC AGCTACAAAG TCGCCGAAA ACGCTACACG
151 CCGAAAAACC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CGCGCGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCGC
401 CGCAAAATT GGGCTTTGTC AACCAAGGGA CGGCGCACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCGGTT GCCGAAACA AAGACATCTT
501 CATCGACTTG AAATCTTTCG GTACGGAACA CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CCAAAACCTG GCTTCATCGG CATCAAACCC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTGCCTC
651 GCAGGAACGC GCCGCCGAGG CCGAAGCTCA GCGCGCGGGT ATGGTTCGGG
701 CGGTATTAAC CGCCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

```

1  LTLTRKTLFL LTAAFGIHSF QTASADAVVR AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGR FHGRKTS GGE RYDMNAFTA AHKTLPIPSYV
101 RVTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAQAQKLGFV NQGT AHVKIE
151 QIVPGQSAPV AENKDIFIDL KSFGEHEAQ AYLNQAAQNL ASSASNPNLS
201 VEKRRY EYVV KMGPFASQER AAEAEQA RGMVRAVLTA G*

```

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLGFEVNGTAHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
a264	FHGNRIIDVSKAAQKLGFEVNGTAHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEVVVMGPFTSQERAAEAEQAQGMVRAVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEVVVMGPFTSQERAAEAEQAQGMVRAVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```
m265 . seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGCGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151 ATGCTCAGCA GTGCGGTTGC GCGCGAGGTC AAGAGAAGGT GTTTGATGTT
201 CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTGCGCTTC GCGGCGCGCT TCCTGCGAGG TAAACGGTCC
351 CATTTTGACG ACGTATTCGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```
m265 . pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAEMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFVNRGLENVDINKVSNNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

a265.seq

```

1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GGCGGCGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... . . . . GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GGCGCGTTCC TGCAGAGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

a265.pep

```

1   MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDKVAGHQ PAVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*

```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANAFA SAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
a265	MSVILPPTRANAFA SAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMPISAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFIXFAFVN RGLNVDINKVSNNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
	: : :					
a265	KRRRLKFI---FAPAKYLXCLKDV KAGHQPAVNTARTIPRAXASASAARSCEANGPILT					
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

g266.seq

```

1   agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccatcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tgctcgcggt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgatc gagctggcgg cagggttcgc gctgaccgcc
201 tctcttgect acatcctcga atcccgtgcg ggagcggtag acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttcc
301 cgtgtttcgt gcggcggtat ttttggcaca cgcgcaacag ggaataa

```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

g266.pep

```

1   MQFRRHRRRQ CPNRKPIMTA SMYILLVLAL IFANAPFLT RLFVGAALKR
51  KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGW EYFA TVVCLYLIFA
101 FPCEVRRYFW HTRNRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

m266.seq

```

1   ATGCCGTTCC GCAACGCGT CAGACGGCAT CGCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGCCAC
101 TCATCTTTCG CAACGCCCC TCCCTACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATT CCGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAGGAT
251 CGGTACACGA TCAGGGTTGG GAGTTTATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTTC CGTTTCCATG TTTTGTGTGG CGGTATTTT GGCAACGCGC
351 CAACAGGGAA TAG

```


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This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101 LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

m266/g266

	10	20	30	40	50	60
m266.pep	MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH					
g266	MQFRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH					
	10	20	30	40	50	
	70	80	90	100	110	120
m266.pep	MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX					
	:					
g266	LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX					
	60	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTG CTGCTTGCTT
101 TGATTTTTC CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151 CCGCTCAAGC GCAAACATT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TGCCTACAT CCTCGAATCC CGTGGGGAG
251 CGGTACACGA TCAGGGTTGG GAGTTTTACG CCACCGTCGT CTGCCTGTAC
301 CTGATTTTTC GTTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351 CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTKLFGIV
51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101 LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

	10	20	30	40	50	60
m266.pep	MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH					
a266	MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKLFIVPLKRKHFGHH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m266.pep	MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE					
	:					
a266	LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE					
	70	80	90	100	110	120
m266.pep	X					
a266	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

g267.seq

q267.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1077>:

m267.seq

This corresponds to the amino acid sequence <SEQ ID 1078; ORF 267>:

m267.pep

Computer analysis of this amino acid sequence gave the following results:

ORF 267 shows 82.7% identity over a 127 aa overlap with a predicted ORF (ORF 267.ng) from *N. gonorrhoeae*:

m267/q267

		10	20	30	40	50	60
m267.pep		VQVAFFLAVVFQNMGFHNRI	SRACLFAETAEDALGQVDV	VTLGAARTVFTFFRFDVNRHC			
		:					
g267		MQVAFFLAVVFQNMGFHNRI	IGRAGLFAETAEDALGQVDV	VTLGAAGAVFAFFRFDVDRHC			
		10	20	30	40	50	60
		70	80	90	100	110	120
m267.pep		RTHCLTQLTRDTPLFAVRIP	PLRVQTAETHGLRRFLG	EINCVFAGEKVFERYAHT	FPYQF		
			: : : :	: : :	: : :	: : :	:
g267		RTHRLAQFTRDAAFLSVR	KTALRVQTAETHGLRRFL	PGKINCVFAGKKVFERYA	HAFTDQF		
		70	80	90	100	110	120
m267.pep	AKQKGIFYX						
g267	AKQKGIFYX						

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1079>:

a267.seq

```

1   GTGCAAGTCG CCTTTTTTCT CGCCGTGGTA TTCAAAAATA TGGGTTTCCA
51  CAATCGCATC  GGTGCGGCAG GCTTCTTCGC AGAAACGCGA GAAGATGCAC
101 TTGTCGAGTG CGATGTCGTG ACGCTTGGTG CGGCGCGTGC CGTCTTCGCG
151 TTCTTCCGAT  TCGATGTTGA TGCGCATTGC GGGGCAACAG GCTTCACACA
201 ATTTACACGC  GATGCAGCGT TCCTCGCCGT TTGGATAACG GCGTTGCGCG
251 TGCACGATCC GGAACGCAC  GGATTGCGCG GTTTCTCTT  CGGGAAATAA
301 AATCGTGTC  TTGCGGGCAA AAAAGTTTTT GAGCGTTACG CCCATACCTT
351 TTACCAATTC  GCCAAGCAGA AAGGTTTTTA CTA

```


This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
  1 VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGOVDVV TLGAARAVFA
 51 FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGOVDVV	TLGAARTVFTFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGOVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLFAVRIP	PLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFGK	INRVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
  1 atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
 51 gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101 cctgcggaag cgaagagact aaagagattt tggcacaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251 gtttgggcat aaccgtcgat gaagtcgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgcgca
351 tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgaggga
651 ggcagaagaa gcggcggcgc aggaggcatt gggtcgggag caggaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcagaaaa acatggaaaa gcggtatgga caagatctgt gccaacaatg
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
  1 MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVDRD
 51 NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101 SSKLKCEAAL KLDVPDDVVD YAVAAQSIG NSHKKTPDFF EPYYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAEEA TAQEAEEAE AAAQEAALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301 CKTAETEAREL EELHNKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
  1 ..ATGGCACTGA TTAAGAGCC GTTGGACAAA GTGAAACAAA GGAACGAAGA
```


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```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCCGCG
151  AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCh TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTTCAGC
301  GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   ..MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAAARVS EWEERYKLSR
51  XQFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

```

m268/g268

m268.pep                               10      20
                               MALIKEPLDKVKQRNEELEAAE-----
                               |||||:||||:|||||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
          160      170      180      190      200      210

m268.pep                               30      40      50      60      70      80
--EAAAQEALGREQEAAARVSEWEERYKLSRSQFEQFWKGLPQTQVQNKLPQSQTWKSMD
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g268      AEEAAAQEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTQVQNKLPQSQTWKSMD
          220      230      240      250      260      270

m268.pep                               90      100     110     120     130     140
KICANNAKAEGETPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g268      KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCCGCG
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTTCAGC
301 GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

m268.pep      10      20      30      40      50      60
MALIKEPLDKVKQRNEELEAAEAAAQEALGREQEAAARVSEWEERYKLSRXQFEQFWKGL
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a268      MALIKEPLDKAKQRNEELEAAEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```


615

	10	20	30	40	50	60
	70	80	90	100	110	120
m268.pep	PQTVQNKLPQSQKTKWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
a268	PQTVQNKLPQASQKTKWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	70	80	90	100	110	120
	130	140				
m268.pep	KALIDEMXREADXKELSKRLX					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHK FKHCSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLPQASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

	10	20	30	
m268-1.pep	VQSRDGLHKFKHCSAAMALIKEPLDKVKQRNE			
g268	KEGAYVYKTISSVQPTDDKSKIFAELSQANDIHLSELVLS--MALIKEPLDKAKQRNE			
	150	160	170	
	40	50	60	
m268-1.pep	ELEAAE-----EAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN			
g268	KLEAAEATAQEAREAEAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN			
	210	220	230	
	90	100	110	
m268-1.pep	KLQASQKTKWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE			
g268	KLQASQKTKWKSMDKICANNAKAEGKTPNGIKVSELACKTAKTEARLEELHNRKKALIDE			
	270	280	290	
	150	159		
m268-1.pep	MAREADKKELSKRLX			
g268	MVREEDKKELPKRLX			
	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```


616

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AAATGGCCAG GGAAGCGGAC
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHICSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR
 51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI
 101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLDEMAREAD
 151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHICSAAMALIKEPLDKAKQRNEELEAAE	EAEEAAAEALGREQEVDRVSEW				
m268-1	VQSRDGLHKFKHICSAAMALIKEPLDKVQRNEELEAAE	EAEEAAAEALGREQEAARVSEW				
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETP	NGIKFSEL				
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGKTP	NGIKFSEL				
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKALLDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggtttggc gtgtgaattg cgcggaacg gcggcgctga ttttttcgtc
 51 cagcccttgg atttgggcgg tggtgtgggt gtggtcgcgg tcggcttttt
 101 cctgcaaac ttgcgccagc cttgacgcgt ccagtgcgcg ggcgttggcg
 151 gtttcgccgt gggactttat ccggaacacg gtttcgcca aggtgtcggc
 201 ggctttgatg cacagtttta aaaccaggcg tttggggcgg tttctgcgc
 251 cggccgttgc cattttgctg tccaatcgcg gggttaaaa accgttgctg
 301 ttaagtgcg cgtccgtcca agtcgatac agcgcgcttc tttgccttc
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MVWRVNCAAT AALIFSSSPW IWAUVVWSR SAFSCKPCAS LDASSAPALA
 51 VSPWDFIRNT ASPKVSALM HSPKTRALGR FSAPPVAILL SNRGVKKPLS
 101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
 51 CAGCCCTTGG ATTGCGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTTGT
 101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCCTGC GTTGATGGTT
 151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTCGGCGGC
 201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGCGGTTT TCGTCGCGGC
 251 CTGTCGCCAT TTGCTGTCC GAGCGCGGG TTA AAAAGCC GTTGTGTTT
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGTCTCTCT GCCTTTCGTT
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MVWRVNCAAT AVLIFSSSPW IWAUVVWSR SALSCKPCAT CPRPAPALMV
 51 SPWDFIQNTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
 101 KFSSVQVDT SALLCLSLRS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng)

from *N. gonorrhoeae*:

m269.pep	MVWRVNCAATAVLIFSSSPWIWA	AVVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT	59
g269	MVWRVNCAATAALIFSSSPWIWA	AVVWWSRASFCKPCASLDASSAPALAVSPWDFIRNT	60
m269.pep	ASPKVSAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT	SALLCLSLSRS	119
g269	ASPKVSAALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDT	SALLCLSLSRS	120
m269.pep	SX	121	
g269	SX	122	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

a269.seq

1	ATGGTTTGGC	GTGTGAATTG	CGCGGCAACG	GCGGTGCTGA	TTTTTTCGTC
51	CAGCCCTTGG	ATTTGGGCGG	CGGTGTGGGT	GTGGGCGCGG	TCTGCTTTGT
101	CTTGGAGGTT	TTGCGCCAGC	GTGCCCGCGT	CCAGCGCGCC	GGCGTTGACG
151	GTTTCGCCGT	GGGACTTTAT	CCAGAACACG	GCTTCGCCCA	AGGTGTCGGC
201	GGCTTTGATG	CACAGTTTTA	AAACCAGGGC	TTTGGGGCGG	TTTCGTCGCG
251	CGCCTGTCGC	CATTTTGCTG	TCCGGGCGCG	GGGTTAAAAA	GCCGTTGTCTG
301	TTTAAATTTT	CGTCCGTCCA	AGTCGATACG	AGCGCGCTTC	TCTGCCTTTC
351	GTTGTGGTCT	TCGTAA			

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

a269.pep

1	MVWRVNCAAT	AVLIFSSSPW	IWA	AVVWAR	SALSWRFCAS	VPASSAPALT
51	VSPWDFIQNT	ASPKVSAALM	HSFKTRALGR	FSSPPVAILL	SGRGVKKPLS	
101	FKFSSVQVDT	SALLCLSLS	WS	S*		

m269/a269 90.1% identity in 121 aa overlap

m269.pep	10	20	30	40	50	59
	MVWRVNCAATAVLIFSSSPWIWA					
a269	10	20	30	40	50	60
	MVWRVNCAATAVLIFSSSPWIWA					
m269.pep	60	70	80	90	100	119
	ASPKVSAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT					
a269	60	70	80	90	100	120
	ASPKVSAALMHSFKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDT					
m269.pep	120					
	SX					
a269	SX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

g270.seq

1	atgaataaaa	accgcaaatt	actgcttgcc	gcactgctgc	tgactgcctt
51	tgccgccttc	aagctcgttt	tggtgcaatg	gtggcaggcg	cagcagccgc
101	aagccgtggc	ggcgcaatgc	gatttgaccg	agggttgac	gctgccggac
151	ggaagccgtg	tccgcgcgcg	cgccgtttca	acaaaaaac	cgtttgatat
201	ttatatcgaa	cacgcgccc	cggcacgga	acaggtcagc	atcagcttca
251	gtatgaaaaa	tatggatatg	ggtttcaacc	gctatatgtt	cgagcgcaa
301	ccgtcgggga	cttggcaggc	agcacgcata	cgctgcccc	tctgtgtcga
351	aggcaggcgc	gattttacgg	cggacattac	aatcggcagc	cggacatttc
401	agacggcatt	taccgccgaa	taa		

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

618

g270.pep

```

1  MNKNRLLLLL ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG Ca.CAGCCGC
101 AAGCTGTGGC GGC GCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTC
401 AGACGGCATT TACCGCCGAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep

```

1  MNKNRLLLLL ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRLLLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPD GSRVRAAAVS					
g270	MNKNRLLLLLAALLLTAFAAF KLVLLQWWQA QQPQAVAAQCDLTEGCTLPD GSRVRAAAVS					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRI RLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARI RLPVCVEGRR					
	70	80	90	100	110	120
	130 140					
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG CAGCAGCCGC
101 AAGCTGTGGC GGC GCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTC
401 AGACGGCATT TACCGCCGAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep

```

1  MNKNRLLLLL ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

```


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101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKLALLAALLLIAFAAVKLVLLOWWQAXQPQAVAAQCCLTEGCTLPDGSRRVRAAAS					
a270	MNKNRKLALLAALLLIAFAAVKLVLLOWWQAXQPQAVAAQCCLTEGCTLPDGSRRVRAAAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
a270	TKKPFDIYIEHAPAGTEQVSISFSMKNMMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
a270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1  atgttcagtt  cgcggatggc  gaggatttgg  gcgacggggg  taacgttgtg
51  tatggtcagt  cctgttccgg  cgttgacgac  caagcccaaa  tcgccggcga
101  aatgcgcgcc  gttttggatg  cgctcgaact  gcctgatttg  ttcggcgtgg
151  ctttgtgcgt  cggcatatgc  gccgggtgtg  agctcgacaa  cgggcgcgcc
201  gacatcacgg  gcggcttgga  ttgcctgtc  gtcggcatcg  ataaacaagg
251  acacgcgtat  gcccgctcg  gtcaggattt  tggcgaattc  ggcgattttt
301  tcctgttgcg  ccaatacgtc  caaacgcct  tcggtcgtga  tttcctgccg
351  tttttcaggc  acgatgcaca  cgtcttccgg  catcacttta  agcgcgtttt
401  cgagcatttc  ttccgtcaac  gccatttcaa  gggtcaggcg  cgtgcggatg
451  gcggttttga  cggcaaatac  atccgcgtct  ttgatgtggc  ggcggctctc
501  gcgcaggtgc  atggtaatca  ggtctgcacc  gtgcgtttcg  gcaaccagtg
551  ccgcctccac  ggggctggga  taa

```

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

```

1  MFSSRMARIW  ATGVTLCMVS  PCPALTTKPK  SPAKCAPFWM  RSNCLICSAW
51  LCASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKOTRMPAS  VRILANSAIF
101  SCCANTSKEP  SVVISCRFSG  TMHTSSGITL  SAFSSISSVN  AISRFRRVRM
151  AFLTANTSAS  LMWRRSSRRC  MVIRSAPCVS  ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1  AwGTTTCAGTT  CGCGGATGGC  GAGGATTGGG  GCGATGGGGG  TAACGTTGTG
51  TATGGTCAGT  CCGTGTCCGG  CGTTGACGAC  CAAGCCCAAA  TCGCCGGCGA
101  AATGCGCGCC  GTTTTGGATG  CGCTCGAACT  GCCTGATTGG  TTCGGCGTGG
151  CTGCGCGCGT  CGGCATACGC  GCCTGTGTGC  AGCTCGACAA  CGGGCGCGCC
201  GACATCACGG  GCGGCTTGGA  TTTGCCTGTC  GTCGGCATCG  ATAAACAAAG
251  ACACGCGTAT  GCCTGCGTCG  GTCAGGATT  TGGTGAACCC  GGCgATTtTT
301  TCCTGTGTGC  CCAATACGTC  CAAACCGCCT  TCGGTCTGTA  TTTCTGACG
351  TTTTTCAGGC  ACGATGCACA  CGTCTCCGG  CATCACTTTC  AAAGCGTTTT
401  CCAACATTTT  TTCCGTCAAC  GCCATTTCAA  GGTCAGGCG  CGTGCGGATG
451  GCGTTTTTGA  CGGCAAACAC  GTCCGCGTCT  TTGATGTGGC  GGCgGTCTTC
501  GCGCAGGTGC  ATGGTAATCA  AATCCGCACC  GTGCGTTTCG  GCAACCAGTG
551  CCGCCTCCAC  GGGGCTGGGA  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

```

1  XFSSRMARIW  AMGVTLCMVS  PCPALTTKPK  SPAKCAPFWM  RSNCLICSAW
51  LRASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKOTRMPAS  VRILVNPAIF
101  SCCANTSKEP  SVVISXRFSG  TMHTSSGITF  KAFSNISSVN  AISRFRRVRM
151  AFLTANTSAS  LMWRRSSRRC  MVIKSAPCVS  ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:

620

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng)

from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTL CMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTL CMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTS SKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANS AIFFSCCANTS SKPPSVVIS CRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVKSAPCVS					
g271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

```

1  ATGTTCAAGT  CGCGGATGGC  GAGGATTGCG  GCGATGGGGG  TAACGTTGTG
51  TATGGTCAGT  CCGTGTCGGG  CGTTGACGAC  CAAGCCCAA  TCGCTGGCAA
101 AATGCGCGCC  GTTTTGGATG  CGCTCGAACT  GCCTGATTG  TTCGGCGTGG
151 CTGCGCGCGT  CGGCATACGC  GCCTGTGTGC  AGCTCGACAA  CGGGCGCGCC
201 GACATCACGG  GCGGCTTGGA  TTTGCCTGTC  GTCGGCATCG  ATAAACAAGG
251 ACACGCGTAT  GCCCGCGTCG  GTCAGGATT  TGGTGAATC  GGCAATTTTG
301 TCTTGTTGCG  CCAATACGTC  CAAGCCGCCT  TCGGTCGTGA  TTTCTTGACG
351 TTTTCCGGC  ACGATGCACA  CGTCTCCGG  CATCACTTA  AGCGCGTTTT
401 CGAGCATTTT  TTCCGTCAAC  GCCATTCAA  GGTTCAGCG  CGTCCGGATG
451 GCGTTTTTGA  CAGCAAACAC  GTCCGCGTCT  TTGATGTGGC  GGCGGTCTTC
501 GCGCAGGTGC  ATGTAATCA  GGTCCGCACC  GTGCGTTTCG  GCAACCAGTG
551 CCGCTCCAC  GGGCTGGGA  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

```

1  MFSSRMARIW  AMGVTLCMVS  PCPALTTKPK  SLAKCAPFWM  RSNCLICSAW
51  LRASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKDTRMPAS  VRILVNSAIL
101 SCCANTSKPP  SVVIS*RFSG  TMHTSSGITL  SAFSSISSVN  AISRFRVRM
151 AFLTANTSAS  LMWRRSSRRC  MVIRSAPCVS  ATSAASTGLG  *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTL CMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTL CMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTS SKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTS SKPPSVVISXRFSG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVKSAPCVS					
a271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcatgg ctgcgccata tgaacaaaaa
51  caaaggttcc gacctgtttg tgacgaccca tttcccgccc gctatgaagc
101 tggacggcaa aatcacccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgacc aacgagtga atttcgccat cagcctgccg gacaccagcc
251 gcttcgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggcttgaag gatgttgcgc tgaaaaaacg cgggctggtt attttgtcg
401 gcggcaccgg ctcgggcaaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgc gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgt gcgtcaggcg
601 ccgatgtga tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgtgcacg
701 ccaacagcac caatcaggcg. ctcgaccgca tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatttcgcaa cgcctcgttc cgcgagacgg cggcaagggc aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcgt
1051 ttggcggtac agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKEELFAW LRHMKNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RAITSKIPKF ESLNLPPALK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIQ FAETGHLQMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTCG TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCCTGAC GCGGAAAAA
151 TGTATGAAAT TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTTCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGCGCG

```


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```

551 TGGATACGGA AACTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCGGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGA TTTCGGAGTT GATTCAACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCGCGCG CAAAGTTyCA GCCCCGATTT
1101 GGnACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272 . pep

```

1  MTAKEELFAW LRHMxQXKGS DLFVTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RTITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMOF DQHLQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272 . pep	10	20	30	40	50	60
	MTAKEELFAWLRHMxQXKGS DLFVTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
g272	MTAKEELFAWLRHMKNKXKGS DLFVTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272 . pep	70	80	90	100	110	120
	AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRTITSKIPKFESLNLPPVVK					
g272	AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIPKFESLNLPPALK					
	70	80	90	100	110	120
m272 . pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180
m272 . pep	190	200	210	220	230	240
	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAI FAETGHLCMATLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAI FAETGHLCMATLHANSTNQA					
	190	200	210	220	230	240
m272 . pep	250	260	270	280	290	300
	LDRIINFFPEERREQLLTDLSNLQAFISQRLVPDGGKGRVAAVEVLLNSPLISELIHN					
g272	LDRIINFFPEERREQLLTDLSNLQAFISQRLVPDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
m272 . pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMOF DQHLQLYE KGDISLQEALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMOF DQHLQLYE KGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

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```

          370
m272.pep  QSXSPDLXLLX
          || :||| |||
g272      QSSDPDLELLX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCG TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCCTGACG GCGGAAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCGG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCCGGC
551 TGGATACGGA AACTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCATT
801 TATTTGCAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAAATGCC ATTCCGCACA CGATTTCGCT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATT
1101 GGAAGTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RAITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETM DYIA FAETGHL CMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLYQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272.pep  MTAKEELFAWLRHMKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEKCM EIAFSIMS
          ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
a272      MTAKEELFAWLRHMKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEKCM EIAFSIMS
          10      20      30      40      50      60

          70      80      90      100     110     120
m272.pep  AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRTITSKIPKFESLNLPVVK
          ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
a272      AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIPKFESLNLPVVK
          70      80      90      100     110     120

          130     140     150     160     170     180
m272.pep  DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a272      DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          130     140     150     160     170     180

```


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	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DYAI AFAETGHLCMATLHANSTNQA					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DYAI AFAETGHLCMATLHANSTNQA					
	190	200	210	220	230	240
m272.pep	250	260	270	280	290	300
	LDRIINFPEERREQLTDLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFPEERREQLTDLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
m272.pep	310	320	330	340	350	360
	GNIHEIKEVMKRKSTTLGMQTFDQHL YQLYEKGDISLQ EALKNADSAHDLRLAVQLRSRA					
a272	GNIHEIKEVMKRKSTTLGMQTFDQHL YQLYEKGEISLQDALKNADSAHDLRLAVQLRSRA					
	310	320	330	340	350	360
m272.pep	370					
	QSSXSPDLXLLX					
	:					
a272	QSSGPDLELLX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

```

g273.seq
1  atgagtccttc aggcgggtatt tatatacccc ccaagccgta ccgcacaata
51  caacgaaaaat caggaaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacacac cgaccgccgt caggatatac gcgtattcga ggccgggaact
151 ccattcaccg ttttcctgcc gtttcttgct gcttttgaaa taaaggatga
201 tgccggcaag cagcgcggca gccgcgccc acattggcat tgtgttcatt
251 gttgttcctt aacgggtaaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcggggcg gtgccgctga aatcaaggcg
351 gtttgagaag tgttccnac gcgccgccg tatgtgccga aatattattt
401 gtgcgtcacc tgcaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgcctg ctttttgctt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

```

g273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPLV AFEIKDDAGK QRGSRARHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

```

m273.seq
1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAAACACG CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAACT
151 CCATTCCCCG TTTTCCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCC ACATTAGCAT TGTGTTCATT
251 GTTGTTCCCTT AATGCTTAAA AACC CGCCTG TCCGTGCAAC CGTTTAAAGG
301 CGGCAAATTG CAAAATTTGT TTGCGGGGCG GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTTCCTGAC GCGCGCCCT GTGTGCCGA GTTATTGTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTTGTkTwTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

```

m273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFTVFLPLV AFEIKDDAGK QRGSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

625

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGSQGHADRCQDIGVFKAGTPFPVFLPLL					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGSQGHADRRQDIGVFEAGTPFTVFLPFLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFEG					
g273	AFEIKDDAGKQGRSRARHWHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRA-ALCAGVICRSPAKSPRTREAFEPHCPLVSYGVLPFVXQAVFSYAX					
g273	CFXRARPMCRNIICRSPAKSPRTREAFEPHCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

```

1  ATGAGTCTTC AGGCGGTATT TGTATACCCC CCAAGCCGTA CCGCACAAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCATAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCCGT CAGGATATAG GCGTATTCCA GACCGGAAC
151 CCATTACCGG TTTTCCTGCC GCTTTTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT AATGTTTATT
251 GTTGTTCCTT AACGGTTAAA AACCCGCCCC TCCGTGCAAC CGTTTTTAAG
301 AGGCGGTAAA TCACAAAGTT TGTGGCGGA CGTGCTCTCT TACAATCAGG
351 GCGGTTTAAG GGGCATGATG CACTGCCCGG TGTGCCGGAT ATTATTTGTC
401 GCTCACCTGC AAAATTGCCA AGAACGCGCT TTGCGGGATT TCCACATTGC
451 CCACTTGTTC CACACGGCGT TTGCCTGCTT TTTGTTTTTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1  MSLQAVFVYP PSRTAQYNEN QENGGAHKQ GSQGHADRR QDIGVFQTGT
51  PFTVFLPLFV AFEIKDDAGK QGRSRARH*H NVHCCSLTVK NPPVRATVFK
101 RR*ITKFVGG RALLQSGRFK GHDALPRVPD IICRSPAKLP RTRFAGFPHC
151 PLVSYGVCLL FVQAVFSYA *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGSQGHADRCQDIGVFKAGTPFPVFLPLL					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGSQGHADRRQDIGVFQTGTPFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRARHXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRRALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRALCAGVICRSPAKSPRTREAFEPHCPLVSYGVLPFVXQAVFSYAX					
a273	GHDALPRV-PDIICRSPAKLPRTREAFEPHCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTTCATCGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTTCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCTGGC ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTgt tcaaAACCTT
351 TCCGCCGGCC AACCACTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AGGCAATGC GGTTCGATTTG
451 ACCCCGATGG ACAAACTTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAACATAT CGACATCCAG CTTTCATCGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCTGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCACTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTTCGATTTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
g274.pep	DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA					
m274	DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNATESKX					
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNATESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCCGG GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCAGCGTCG GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGCGATTG
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQGNVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
a274	DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
a274	DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEA VFKTLSPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNTESKX					
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggacgacg tgaatgccgt gcggttttcc atcaggcggt
101 cgagcgcttg ttggacgagg cgttcggatt cgttgtecaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgctctt ttcaaatgg cgcgggcgat
201 ggcgacgcgt tgcgctgtgc cgcggataaa gttgctgccc ttcgatccga
251 tgggctggtg cagtccgagc ggggatgcgt cgatcaggct ttgcagggtg
301 gcggcttggg ggcgggacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcgacg ttttcaaca ggtgtcgtc aaacaggaat acgtcttggg
401 agacgagggc gaattgggcg cgcaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccgga gacggttcga caaagcgggg
501 cagaagggtg acgacggtgg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgctcg atgtcgaggt tgaagttgtc gagggccttg
601 atgccgtctg aacggtattc gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgaga gcgtgccttt gtctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcgcgga ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct ttgatgggg cgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgcgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

628

```

1  MILPPSMTMM RSADSTVRR WATMPVRF SIRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSILMSAM
151 SIPSMQMLPA DGSTKGRRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMRPSTR CGASVPLSCS GGVS RNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

m276.seq

```

1  ATGATTTTGC CGTCGTCCAT CACGATGATG CGGTCGGCCC CTTGATGGT
51  GGT CAGGCGG TGGCGACGA TGATCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCTAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAGCGCGT TGCCGCTGTC CGCCGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGA GGGCGAACAG GACTTCGGCT TCGCCGCGT CGGGACGGCT
351 GTATCGGACG TTTTCAAACA GGGTGTCTGC AACAGGAAT ACGTCTTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTG ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGTCTG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGTGCGA GCGTGCCCTT GTCCTGTTG GCGGGGTGT
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTTGATGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

m276.pep

```

1  MILPSSITMM RSAPSMVRR WATMPVRF SIRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GELIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSILMSAM
151 SIPSMQMLPA DGSTKGRRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMRPSTR CGASVPLSCS GGVS RNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng) from *N. gonorrhoeae*:

m276/g276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVRRWATMPVRF SIRRSSACWTRRSDSLSNALVASSNNNIGAS					
g276	MILPSSITMMRSADSTVRRWATMPVRF SIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELIRLCRLAVWRANRTSASPASGRLYRT					
g276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
m276.pep	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
g276	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKGRRLTTVDLPLPER					
	130	140	150	160	170	180
m276.pep	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMRPSTRCGASVPLSCSGGVS RNAHTP					
g276	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMRPSTRCGASVPLSCSGGVS RNAHTP					
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```
a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACAGGGG AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATCGGCC
651 TTCGACACGC TCGGGTGCGA GCGTGCCTTT GTCCTGTTTC GCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```
a276.pep
1  MILPSSITMM RSAPSMVRR WATMMPVRF IRRSSACWTR RSDSLSNALV
51  ASSNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRSRL TTVDLPLPER PTRATRSPL MSRLKPSRAL
201 MPSEYSTST LRLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVRRWATMMPVRFIRSSACWTRRSDSLSNALVASSNNIGAS					
a276	MILPSSITMMRSAPSMVRRWATMMPVRFIRSSACWTRRSDSLSNALVASSNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
	: : :					
a276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTRKRSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTRKRSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLMSRLKLSRALMPSEYSTSTLRKLRPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPLMSRLKPSRALMPSEYSTSTLRKLRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

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250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1  ..atggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttgccc
51  aaacgaggtc atagacgttt tccacgcctt gcaggtacat cgccaagcgt
101 tcgatgccgt aggtaatctt gccgagtacg ggcgtgcaat cgataccgcc
151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201 cttcccagcc caaaccaccac gcaccgaggg tgggggtttc ccagtcgtct
251 tcgacaaagc ggatgtcgtg gactttggga tcgatgccc attcgcgcag
301 ggagtcgaga tagaggtctt ggatattggc gggggcgggg ttgagggcga
351 cttggaattg gtaatagtgt tgcaggcggg tgggggtgtc gccgtagcgg
401 ccgtcttttg ggcggcggct ggggtggacg taggcggcaa accaaggtc
451 gggggcgagc gcgcgcaggc aggtggcggg atgggagtgt ccggcaccga
501 cttccatgtc gaagggttg atgacggtgc agcctttgtc tgcccagaag
551 gtttcagatt tgaagatgat ttggttgaag gtaagcatgg cttattgttc
601 gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
51  DLLEIGKLG YFAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101 GVEIEVLDIG GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPRL
151 GAERAQAGGG MGCAGTDFHV EGLDDGAAFV CPEGLQFEDD LLEGKHGLLF
201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTCGTAGTGC GTTGAAC TGG
101 CGCAGCAGCC AGTCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGCTC
151 GACTTCTGTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201 GCGTTTTTTC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301 GTCGATCCCG CCGACTTGTT GGAAATAGGT AAAGTGGGTT ACTTCCATGC
351 CGTTGAGCCA GACTTCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTCGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451 CAATTCCGCG AGAGAGTCGA GATAGAGGTC TTGGATATTG CGGGGAGCGG
501 GCTTGAGGGC GACTTGGAA TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GGCCGTCCTT GGGCGGCGG CTGGGTTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651 TCGCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTTCAG TTTGAAGATG ATTGTTGGA AGGTAAGCAT
751 GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVGI AVFEVVGGLL
51  DFVLVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101 VDAADLLEIG KLG YFHAVEP DFPAQTPRAE GGVFPVVPDK ADVVDFGIDA
151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201 KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30
MVHVAVAYGI AVRRFCPNEV IDVFHALQVH


```
a277.seq
1  ATGCCCCGCT  TTGAGGACAA  GCTCGTAGGC  AGGCAGGGCG  AGGGCGGCGT
51  TTTCTTCGGC  AAGCAGGCCT  TTGGCTTGCG  CTTCGTAGTC  GTTGAAGTGG
101 CGCAGCAGCC  AATCGGCATC  CTTGTATTCC  AAGTTGTAGG  TGGATTGTTT
151 GACTTCGTTT  TGGTGGTACA  GCTCGCCGTA  AGTTACTGTA  TTAACCGTCCA
201 GCGTTTTTGC  CCAAACGAGG  TCATAGACGT  TTCCACGCC  TTCAGGATAC
251 ATCGCCAAGC  GTTCGATGCC  GTAGGTGATT  TCGCCGAGTA  CGGGGGTGCA
301 GTCGATGCCG  CCGACTTGTT  GGAAATAGGT  GAACTGGGTT  ACTTCCATAC
351 CGTTGAGCCA  GACTTCCCAG  CCCAAACCCC  ACGCGCCGAG  GGTGGGGTTT
401 TCCAGTCGT  CTTTCAGAAA  GCGGATGTCT  TGCATTATTG  GGTCGATGCC
451 CAATTCCGCG  AGGGAGTCGA  GATAGAGGTC  TTGGATTTTG  GCGGGAGCGG
501 GCTTGAGGGC  GACTTGGAAT  TGGTAATAGT  GTTGCAGGCG  TTGGGGTTTG
551 TCGCCGTAGC  GACCGTCTTT  GGGGCGGCGG  CTGGGTTGGA  CGTAGGCGGC
601 AAACCAAGGC  TCGGGGCCGA  GTGCGCGCAG  ACAGGTGGCG  GGATGGGATG
651 TGCCGGCACC  GACTTCCATG  TCGAAGGGTT  GGATGACGGT  GCAGCCTTTG
701 TCTGCCCAGA  ATGTTTGCAG  TTTGAAGATG  ATTTGTTGGA  AGGTAAGCAT
751 GGCTTATGA
```

a277.pap

1	MPRFEDKLVG	RQEGGVFFG	KQAFGLRFVV	VELAQQPIGI	AVFEVVGGLF
51	<u>DFVLVVHVAV</u>	SYCITVQRFC	PNEVIDVFHA	LQVHRQAFDA	VGDFAEYGGA
101	VDAADLLEIG	ELGYFHTVEP	DFPAQTPRAE	GGVFPVVFDD	ADVVFHGVDA
151	QFAQGVIEIV	LDIGSGLEG	DLELVIVLQA	VGVVAVATVF	GAAAGLDVGG
201	KPRLGAECAQ	TGGMGCGAGT	DFHVEGLDDG	AAFVCPCECLQ	FEDDLLEGKH
251	GI*				

	10	20	30	40	50	60
m277.pep	MPRFEDKLVGRQGE GGV FFGKQAFGLRFV VV VELAQ Q VPVGIAVFEV V GGLLDFVLV VH VAV					
a277	MPRFEDKLVGRQGE GGV FFGKQAFGLRFV VV VELAQ Q PIGIAVFEV V GG L FD F VLV VH VAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m277.pep	GDGVAVERFCPNEVVDV FF YTLQVH R QAFDAVGDFAEYGRAVDAAD L LEIGKLG Y FHAV E P					
a277	SYCITV R FCPNEVIDV F HALQVH R QAFDAVGDFAEYGGAVDAAD L LEIGELG Y FHTV E P					
	70	80	90	100	110	120
	130	140	150	160	170	180

632

```

m277.pep    DFPAQTPRAEGGVFPVVDKADVDFGIDAQFAQRVEIEVLDDIGSGLEGDLELVIVLQA
a277        DFPAQTPRAEGGVFPVVDKADVDFGIDAQFAQGVVEIEVLDDIGSGLEGDLELVIVLQA
              130      140      150      160      170      180

              190      200      210      220      230      240
m277.pep    VGVVAVAAVFGAAAGLDVGGKPRPGAECAGAGGGMGCAGTDFHVEGLDDGAAFVCPECLQ
a277        VGVVAVATVFGAAAGLDVGGKPRPGAECAGTGGGMGCAGTDFHVEGLDDGAAFVCPECLQ
              190      200      210      220      230      240

              250
m277.pep    FEDDLLEGKHLX
a277        FEDDLLEGKHLX
              250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1   ttgcgtgcaa tcacgcccgg tgcgattttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcacgcacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaaat acggccggta
151 caggtaacgg tgtcgccctt tttaatatgt tcgtactcgc ccaacactac
201 ggcaaccgacg gagtgcgctt ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcattg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgatcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatt aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1   LRAITPGAIF STGAVKVVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSAFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1   TTGCGCGCAA TCACGCCCGG TCGGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTGCGCCTT TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACCT AATTGCTTGT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTGC GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1   LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPQVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRDFD DRDFQLAVET LIQHLHQLAD
201 LFGVQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

633

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng)

from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVVLI	GPLPSIGRPNASTTRPTNSRPTGT	SKIRPVQVTVSPSLIC			
m278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVTVSPSLMC			
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYPNNTAPTESRSR	FIAPKPKVLPGNSSIS	PCIASDKPMMRTIP	SVTEITVPRVLTSAFT		
m278	SYPNNTAPTESRSR	FIAPKPKVLPGNSSIS	PCIASDKPMMRTIP	SVTEITVPRVLTSAFT		
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGL	SCMKTLLIRHSRVQSTQF	ALYRQIQNLITHENF			
m278	DRFSILALIKSLISAGL	SCMKTLLIRHSRVQSTQF	ALYRQIQNLITHENFYAANQLRFDF			
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHQLADL	FVGQRIGTVNDGRFDMVE*				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

```

1  TTGCGCGCAA TCACGCCCGG TCGGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GCGCGCGACG GAGTCGCGCT CCAGGTTTCA CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTGCGCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTGAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

```

1  LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLIC SCSNNTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPMM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFVGQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVTVSPSLMC			
a278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVTVSPSLIC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYPNNTAPTESRSR	FIAPKPKVLPGNSSIS	PCIASDKPMMRTIP	SVTEITVPRVRTSAFT		
a278	SCSNNTAPTESRSR	FIAPKPKVLPGNSSIS	PCIASDKPMMRTIP	SVTEITVPRVRTSAFT		
	70	80	90	100	110	120

g279.seq

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.ppe

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	I T R I C G C L I S T V F R A S A S L S A A G F I R L Q W E G T D T G S G R A R L A P A S L A A A M A R P T A A A L P A					
:	: :					
g279	M T R I C G C L I S T V L S V S A S L S A A G F I R L Q W E G T D T G S G R A R L A P A S L A A A M V R P T A A A L P A					
	10	20	30	40	50	60
	70	80	90	100	110	120


```

m279.pep      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g279          ITTCPGELKLTASTTSPCADSAQICLTCCSSSKPKMAAIAPTPCGTADCISSARRRTSLTA
              70      80      90      100      110      120

              130      140      150
m279.pep      SAKFNAPAATSAVYSPRLCPATAAGVLPASXK
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g279          SAKSNSAATSAVYSPRLCPATAAGVLPPTSXK
              130      140      150

```

```
a279.seq
  1  ATGACNCNGA  TTTGCGGCTG  CTTGATTTCa  ACGGTTTNNa  GGGCTTCGGC
51  GAGTTTGTCG  GCGGCGGGTT  TCATGAGGCT  GCAATGGGAa  GGTACNGACA
101  CNGGCAGCGG  CAGGGCGCGT  TTGGCGCCGG  CTTCTTTGGC  GGCAAGCATA
151  CGCGCTCGA  CGGCGGCGGT  ATTGCTGTCA  ATCACGACTT  GTCCGGGCGA
201  GTTGAAGTTG  ACGGCTTCAa  CCACCTCATC  CTGTGCGGAT  TCGGCGCAAA
251  TTTGTTTTAC  CTGTTTCATC  TCCAAGCCGA  GAATCGCCGC  CATTGCGCCC
301  ACGCCTTGCG  GTACGGCGGA  CTGCATCAGT  TCGGCGCGCa  NGCGCACGAG
351  TTTGACCGCG  TCGGCAAAAT  CCAATGCGCC  GGCGGCAACN  AGTGCGGTGT
401  ATTGCGCCGaN  GCTGTGTCCG  GCAACGGCGG  CAGGCGTTTT  GCCGCCCGCT
451  TCCGAATAG
```

a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	<u>ARSTAAALPA</u>	<u>ITTCPGELKL</u>	<u>TASTTSSCAD</u>	<u>SAQICFTCSS</u>	<u>SKPRIAIAIP</u>
101	<u>PCGTADCIS</u>	<u>SARXRTSLTA</u>	<u>SAKSNAPEAT</u>	<u>SAVYSPXLCF</u>	<u>ATAAGVLPPA</u>
151	SE*				

[illegible]

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Ouakvi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcgga
151 gccaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgccgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagcaccacg atcatgacca cgaaggacac caccacgacc
401 acggcggaata tgacccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccaaa acgtcgctga aacctgata aaggccgac cgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaatgcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtccctga ccggggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtag cagcgaagcc gagccgtccg
701 ccaaacaagt cgccgccatc atccggcaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcacgcg
801 caaagaacc ggcgtaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTIA ALLATAATAA PLPVVTSFSI LGDVAQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EEGGHHHDHH HDHDHDHEGH HHDHGEYDPH VWNDPVLMDS
151 YAQNVATLI KADPEGKVYY QQLGNVYQMQ LKKLHSDAQA AFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQVSSEA EPSAKQVAI IRQIKREGIK
251 AVFTENIKDT RMVDRIAKET GVNVSGLYS DALGNAPADT YIGMYRHNVE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACAC CTTATTGCC GCATTGCTGA CCGCTCCGC
51  AACTGCCGCC CCCCTGCCG TTGTAACCAG CTTAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTGGTCCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAACTCG TCCTGCTCAA CGGCTTAGGA CTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTA TGCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CTTTTCTTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCGCAA GCGTGAGCA GCGAAGCCGA GCCTTCGCC AAACAAGTCG
701 CCGCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGCG AACCGGCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTIA ALLTASATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EEGGHHHDHD HDHEGHHHDH GEYDPHVWND PVLMSAYQN
151 VAKALIKADP EGKVYYQRL GNYQMQLKKL HSDAQA AFNA VPAKRKVL

```


201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAARIQI KREGIKAVFT
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN
 301 AMKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng)
 from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTSPFSILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
	::					
g280	MKHLKLTLIAALLATAATAAPLPVVTSPFSILGDVAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
m280.pep	70	80	90	100	110	119
	TSGDIKKIRSACLVLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EEGHHHDH-					
	::					
g280	TSGDIKKIRSACLVLNGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAE EEGHHHDH					
	70	80	90	100	110	120
m280.pep	120	130	140	150	160	170
	---DHDHEGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQQLGNYQMQ					
	::					
g280	HDHDHDHEGHHHDHGEYDPHVWNDPVLMSDYAQNVAETLIKADPEGKVYYQQLGNYQMQ					
	130	140	150	160	170	180
m280.pep	180	190	200	210	220	230
	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSAEPSAKQVAAI					
	::					
g280	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGVSSAEPSAKQVAAI					
	190	200	210	220	230	240
m280.pep	240	250	260	270	280	290
	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	::					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNV					
	250	260	270	280	290	300
m280.pep	300					
	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

```

1  ATGAAACACC CCAAACAC CCTTATCGCC GCATTGCTGA CCACTGCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTACAGCAT TTAGCGCACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGCGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGATTAA CGGCTTAGGA CTTGAAGCTG
251 CGGACATCCA ACGTGCCGTC AAACAGAGCA AAGTATCCTA TGCCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGCGG GACACCATCA
351 CGACCACGAT CATGACCACG ACCATGACCA CGAAGGACAC CACCACGACC
401 ACGGCGAATA TGACCCCCAC GTCTGGAACG ACCCCGTCCT TATGTCCGCC
451 TATGCCCAAA ACGTCGCCGA AGCCCTGATA AAGGCCGACC CCGAAGGCAA
501 AGTTTATTAT CAACAACGCT TGGGCAACTA CCAAATGCAG CTCAAAAAAC
551 TGCACAGTGA CGCACAAGCC GCATTTAATG CCGTCCCTGC CGCCAAACGC
601 AAAGTCCTGA CCGGGCACGA TGCTTTTTC TATATGGGCA AACGTTACCA
651 TATCGAATT CCGCCCCAC AAGGTGTGAG CAGCGAAGCC GAGCCTTCAG
701 CCAAACAAGT CGCCGCCATC ATCCGACAAA TCAAACGCGA AGGCATCAAA
751 GCCGTATTTA CCGAAAATAT CAAAGACACC CGCATGGTTG ACCGCATCGC

```


638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHPKLTLLIA ALLTTAATAA PLPVVTSFSI LGDVAQKIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE EEGHHHDHD HDHDHDHEGH HHDHGEYDPH VWNDFVLSA
 151 YAQNVAEALI KADPEGKVYY QORLGNYQMQ LKKLHSDAQA AFNAVPAKR
 201 KVLTHGDAFS YMGKRYHIEF IAPQGVSSA EPSAKQVAI IRQIKREGIK
 251 AVFTENIKDT RMDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLLIAALLTASATAAPLPVVTFSILGDVAQKIGGERVSIQSLVGANQDTHAYHM					
a280	MKHPKLTLLIAALLTTAATAAPLPVVTFSILGDVAQKIGGERVSIQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m280.pep	TSGDIKKIRSAKLVLLINGLGLAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280	TSGDIKKIRSAKLVLLINGLGLAADIQRAVKQSKVSYAEATKGIQPLKAE EGGHHHDHD					
	70	80	90	100	110	120
	130	140	150	160	170	
m280.pep	HDH----EGHHHDHGEYDPHVWVNDPVLMSAYAQNVAKALIKADPEGKVYYQORLGNYQMQ					
a280	HDHDHDHEGHHHDHGEYDPHVWVNDPVLMSAYAQNVAEALIKADPEGKVYYQORLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA AFNAVPAKRKVLTHGDAFSYMGKRYHIEF IAPQGVSSA EPSAKQVAI					
a280	LKKLHSDAQA AFNAVPAKRKVLTHGDAFSYMGKRYHIEF IAPQGVSSA EPSAKQVAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
a280	IRQIKREGIKAVFTENIKDTRMDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq
 1 atgcactacg ccctcgcacg cgtcttctgc ctgtccctca gcgcgcgacc
 51 cgtcggcgta ttcctcgtca tgcgcgctat gagcctgata ggcgacgcat
 101 tgagccacgc cgtcctgccc ggtgccgccc tcggctacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtggcgggg tttgccgccc gtagctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgtctccg
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa
 451 agcatagacc ccttttctct caagtccgtc aacggcaaaag gcgggctttg

501 gcacgtcatt ttcctcatcc tcgtcgttat gaacctcgta tccggtctcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccgtt tatgggcaag aaatatgggg acgctcattc tgtgtccgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tctaccaca
701 tcgaaatccc ttccggcccc gccattcatcc tctgttgag cgtcctttat
751 cttttttccg tcatactcgg caaagaagcg ggcattctgc ccaaatgggt
801 caaaaaccac qcaccacaca ccactcga

g281.pep

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

1	ATGCGCTACG	CCCTCGCATC	CGTCTTCTGC	CTGTCCCTCA	GTGCCGACC
51	CGTCGGCGTA	TTCCTCGTCA	TGCGCCGTAT	GAGCCTGATA	GCGCAGCAT
101	TGAGCCACGC	CGTCCTGCCC	GGTGC CGCG	TCGGCTACAT	GTTTGCCGGC
151	TTGAGCCTGC	CCGCGCATGG	TTTGGGCGCG	GTAGCCCGAG	GCATGCTGAT
201	GGGACTGCTT	CGCGGACTCG	TCAGCCGCGT	CACCAACCTG	AAGAAGATG
251	CCAACTTTGC	CGCCTTTTAT	CTCAGCAGCC	TCGCCATCGG	CGTAGTCTCT
301	GTCAGCAAAA	ACGGGAGCAG	CGTCGATTTG	CTCCACCTCC	TTTTCGGCTC
351	TGTACTTGCC	GTCGATATTCT	CTCGCCCTGA	GCTCATCGCC	GCCGCTCCCA
401	GCCTCACGCT	CATTACCCCT	CGCGTCATCT	ACCGCCCGCT	CGTACTCGAA
451	AGCATCGACC	CCCTGTTTCT	CAAAATCCGT	GGCGGCAAAG	CGGGGCTTTG
501	GCACGTCTCT	TTTCTCGTCC	TGGTCGTGCT	GAACCTCGTA	TCCGGCTTTT
551	AAGCCCTCGG	CACACTCATG	TCCGTCGGAC	TCATGATGCT	GCCAGCCATT
601	ACCGCCCGCC	TGTGGGCGAA	GCATATGGGC	GCACTCATCC	TCTTATCCGT
651	TCTGACAGCC	CTGCTGTGCG	GCTTGAGCGC	ACTGCTCAT	TCTTACCACA
701	TCGAATTTCC	TTCCGGTCCC	GCCATCATCC	TCGTGTCAG	CGCTCTTTAT
751	CTCTTTTCCG	TCATACTCGG	CAAAGAAGGC	GGCAATCTGA	CC. .

m281.pep (partial)

1 MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGVMFAG
51 LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTLTITL AVIYRPLVLE
151 SIDPLFLKSV GKGGLLWHVL FLVLVVMNLV SGFQALGTLN SVGLMLMLPAI
201 TARLWAKHMG AGILLSVLTA LLCGLSGLLI SYHIEIPSGP AII LCSSVLY
251 LFSVLQKAG GALT..

Homology with a predicted ORF from *N.gonorrhoeae*

from *N. gonorrhoeae*:

m281/g281

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVGVLV	MRRMSLIGDALSHAVLP	GAAVGYMFAGLSLP	PAMGLGG		
	:					:
g281	MHYALASVFCLSLSAAPVGVLV	MRRMSLIGDALSHAVLP	GAAVGYMFAGLSLP	PAMGVGG		
	:					:
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRFTTL	KEDANFAAFYLSSLAIGV	VLVSKNGSSVDLHL	LFGSVLA		
				:		
g281	FAAGMLMALLAGLVSRFTTL	KEDANFAAFYLSSLAIGV	ILISKNGSSVDLHL	LFGSVLA		
				:		
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSSLTLIT	LAVIYRPLVLESIDPLFL	KS	VG	GGKGLLHW	HLVFLVVMNL


```

g281      |||||::|||||::|||::|||::|||
          VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGLWHVIFLLVMNLV
              130           140           150           160           170           180

                190           200           210           220           230           240
m281.pep  SGFQALGTILMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIETPSGP
          |||||::|||||::|||::|||::|||::|||::|||::|||::|||
g281      SGFQALGTILMSVGIMMLPATARLWARNMGTLLLSVLIALFCGLIGLLISYHIETPSGP
              190           200           210           220           230           240

                250           260
m281.pep  AIILCCSVLYLFVSILGKEGGILT
          |||||::|||||::|||::|||
g281      AIILCCSVLYLFVSILGKEGGILPKWFKNHRHHTTX
              250           260           270

```

```
a281.seq
1 ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51 CGTCGGCGTA TTCCTCGTCA TGGCGCGTAT GAGCCGTGATA GGCGCAGCAT
101 TGAGCCACGC CGTCTCGCC GGTGCCGCGG TCGGCTACAT GTTTGCCGGC
151 TTAAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCGAG GTATGCTGAT
201 GGCAC TGCTT GCCGGA CTG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG TGTAGTCCTC
301 GTCAGCAAAA AGGCGAGCAG CGTCGATTTC CTCACCTCC TTTTCGGCTC
351 CGTACTTTGCC GTCGATATTC CTGCCCTGCA ACTCATCGCC GCGGTATCCA
401 CCCTCACACT GCTTACCCTT GCCGTCATCT ACCGCCCCTG CGTACTCGAA
451 AGCATCGACC CCTGTTTCT CAAATCTGTC GCGGCGAAAG GCGGGCTTTG
501 GCACGCTCCT TTTCTCGTCC TGGTCGTGAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGCGGAA GCACATGGGC GCACCTATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CCAATGGCT
801 CAAAACCAC CGCACCACA CCACCTGA
```

a281.pep

1	<u>MRYALASVFC</u>	<u>LSLSAAPVGV</u>	<u>FLVMRRMSLI</u>	<u>GDALSHAVLP</u>	<u>GAAVGYMFAG</u>
51	<u>LSLPAMGLGG</u>	<u>VAGMLMALL</u>	<u>AGLSRFTTL</u>	<u>KEDANFAAFY</u>	<u>LSSLAIGVVL</u>
101	<u>VSKNGSSVDL</u>	<u>LHLFLGSVLA</u>	<u>VDIPALQLIA</u>	<u>AVSTLTLLTL</u>	<u>AVIYRPLVLE</u>
151	<u>SIDPLFLKSV</u>	<u>GGKGGLVHVL</u>	<u>FLVLVVMNLV</u>	<u>SGFQALGTLN</u>	<u>SVGLMLMLPAI</u>
201	<u>TARLWAKHMG</u>	<u>ALILLSVLTA</u>	<u>LLCGLSGLLI</u>	<u>SYHIEIPSGP</u>	<u>AIILCCSVLY</u>
251	<u>LFSVILGKEG</u>	<u>GILTKWLKNH</u>	<u>RHHHTT*</u>		

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVG	VFLVMRRMSLIGDALSHAV	LPGA	AVGYMFAGLSL	PAMGLGG	
a281	MRYALASVFCLSLSAAPVG	VFLVMRRMSLIGDALSHAV	LPGA	AVGYMFAGLSL	PAMGLGG	
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVS	RFTTLKEDANFAAFYLSS	LAIGVVLVSKNGSSVD	LHLLFGSVLA		
a281	VAAGMLMALLAGLVS	RFTTLKEDANFAAFYLSS	LAIGVVLVSKNGSSVD	LHLLFGSVLA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSS	LTLLTAVIYRPLVLES	IDPLFLKSVGGKGL	LWHVFLVLVVMNLV		
a281	VDIPALQLIAAVSS	LTLLTAVIYRPLVLES	IDPLFLKSVGGKGL	LWHVFLVLVVMNLV		
	130	140	150	160	170	180

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1   atgggattgg gtatggaaat cggcaagctg atttgtgctc ttttgggtgct
51  gatcaatccg tttagcgcgt tgcgcgttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgacg ggcggtgcgc tattgaaggt
201 tttgggcattc agcgtcgggt cgtttcaggt cggcggcggtg attttgggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcgggtccgg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggcggtttg gtggtcagtg cgatttgtaa
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggcgtgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattcccgc aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1   MGLGMEIGKL IVALVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKO
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYS
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAAYS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1   ATGGGATTGG GCATGGAAAT CCGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GCGCGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CCGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTGCTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CCGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GCGCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1   MGLGMEIGKL IVAFLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKO
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAAYS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng)

from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	:					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFFQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFFQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GCGCGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGCGGCGGGA ATTTTGGTGT
251 TGCTGATTGC CATTTGCATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GTGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGTGCGACGG
551 GGCTGACGAT TTAAACCGT ATCATGGGTA TGATGCTGGC GCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAATG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282.pep

```

1  MGLGMEIGKL IVAFVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ VRPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRL GATGLTILNR IMGMLAAVS
201 VEIIVSGLKM IFFQLAG*

```

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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```

              70      80      90      100     110     120
m282.pep      GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI
a282          GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI
              70      80      90      100     110     120

              130     140     150     160     170     180
m282.pep      AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL
a282          AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL
              130     140     150     160     170     180

              190     200     210
m282.pep      GATGLTILNRIMGMLAAVSVETIIVSGLKTIFFQLAGX
a282          GATGLTILNRIMGMLAAVSVETIIVSGLKMIFFQLAGX
              190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1  atgaactttg ctttatccgt catcacattt accctcgcct ctttctgccc
51  cgtcccgcct gccggaaccg ccgtctttac ttggaaagac ggcggcgcca
101 acagctattc ggatgtgccg aaacagcttc atcccgaacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaaccg gcggtcaagc ccaaacctgc
201 cgctgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaaacaagga tgatttgatc cgtaaataca
401 ataacgccgt aaacaaatac tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1  MNFALSVITF TLASFLPVPP AGTAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTLTQTKP AVKPKPAVDT NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNNAVNY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1  ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTG GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGCG CGGATTTCAA AAATGAACCT
351 GAAGCGGTG GGAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1  MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTLTQTKP AVKPAQADAG KRTDGAQEN NPDTAEKNRQ LEEKKRIAE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

```

              10      20      30      40      50      60
m283.pep      MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLTQTKP
g283          MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLTQTKP
              10      20      30      40      50      60

```


	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAENRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
		:	:	:	:	:
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKKIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	
		130	140			
m283.pep	GNSNAKNKDDLIRKYNNNAVNYKCRX					
g283	GNSNAKNKDDLIRKYNNNAVNYKCRX					
	120	130	140			

a283.seq

a283.pep

m283/a283 100.0% identity in 144 aa overlap

		10	20	30	40	50	60	
m283.pep		MNFALSVM	LTLASFLPVP	PAGAAVFTWKD	GGNSYS	SDVPKQLHPD	QSQILNLR	TRQTKP
a283		MNFALSVM	LTLASFLPVP	PAGAAVFTWKD	GGNSYS	SDVPKQLHPD	QSQILNLR	TRQTKP
		10	20	30	40	50	60	
		70	80	90	100	110	120	
m283.pep		AVKPAQADAG	KRTDGA	AQENNPD	TAENRQ	LEEEKK	RIAETER	QNK
a283		AVKPAQADAG	KRTDGA	AQENNPD	TAENRQ	LEEEKK	RIAETER	QNK
		70	80	90	100	110	120	
		130	140					
m283.pep		GNSNAKNK	DDLIRKYNN	AVNKYCRX				
a283		GNSNAKNK	DDLIRKYNN	AVNKYCRX				
		130	140					

q284.seq.

```

. 1 atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttacgcggc
51 aggttggggc ttacgggtct ttgtaacggc attcgctttt gcctgcaaaa
101 gagtcgccgg ctttgcggtt gcctttgaag ccttcgccgg tttttttgaa
151 actgtctttt ttaaaagcct ctttcttgaa accttcgccg cgcgttttgc
201 cgccgaagcc ttctttgccg ggtttatgat cgcgcgcgcg cgcgcgggat
251 ttctatcgcc ccagccgcgc tttgccttcc ggcttgccgc ctgcgggatt
301 gcgtttgcgg gccgcttcca tgccttcgat ggtcagttcg ggcagtttgc
351 ggttaatgta ttttttcgatt ttgtggacct tgacgtatcc gttcacttcg
401 gcaaacgtaa tcgcaatacc cgtgcggcct gcgcgcgcgg tgcgcccgat
451 cgggtggacg tagtcttcgg cctgtttcgg caggtcgtaq tttatgaact

```


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```

501 gggtaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaattttgc agcggccttt acgcaaattcc gtcagcgtgc ggttgcgcca
601 gccctgcggc atatcgccgt gcaggcagtt ggcggcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggtcatcg ctttggtgga cgtgaaaatc
701 acacattggt cgatgttggc atcgcgcagg atgtggtcga gcaggcgggt
751 tttgtggcgc atatcgctgc agtacaaca ctgctcttcg attttgcctt
801 ggcggtccac gcgttcgact tcgataattt cagagtcttt ggtcagtttg
851 cgcgccagtt tgccgactgc gccgtcccaa gtggcggaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
  1 MPSETRNRFQ TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
 51 TVFLKAFFLE TFAARFAAEA FFAREMIAAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD QFGQFAVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVYDVNGG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHRFGG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LFDFAALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
  1 ATGCCGCTCTG AAACGCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
 51 AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTGTGAA
151 ACCGTCTCTC TTAAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CCGCGAAGCC TTCTTTGCTC GGTTCATGAT CGCGCGCCCA ACCGCGGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATT
301 GCGTTTGGCG GTCGGTTCCA TGCCTTCGAT GGTCAAGTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCT GCGCGGCCGG TGCGCCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CCGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TGCGGCGAAA CCTTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGTCATGG CTTTGGTGGA CGTGAATAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATTT CAGGGTCTTT GGTCAAGTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGGCGTTG CTTCCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTTGCC GCTTTCATC AGGTCCATCA GACGCCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTGGTAGC
1101 CGAAAGACGC GCGCCGACG ATGCTGACGG TGCGGAACCA ACGCATATTT
1151 TTGGCATACG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGCCTTT GCCCGGTTT TCGCTGCGTT
1251 TGGTCAAGTT TTGCAAAGTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
  1 MPSETRNRFQ TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
 51 TVSLKAFFLE TFAARFAAEA FFAREMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD QFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVNGG RYVDTACGNI GGNQNFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFGG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFDFAALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTFKINFA ALHQVHQATAR
351 RGNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQRV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAAGFPIAPAAFAFRLAACGFAFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVFVHFGKRNRRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVDTACGNI					
g284	FFDFVDFDVFVHFGKRNRRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAFTQIHRVAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHFRFGGRENHTLVDSG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFDRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLLDFALAVHAFDFFDRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQFQTFKINFAALHQVHQTARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284.seq
1  ATGCCGCTCTG  AAACGCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTGCGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101  GAATCGCCGG  CTTTGCCTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTTTTGAA
151  ACCGCTCTCT  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTCG
201  CGCCGAAGCC  TTCTTTGCTC  GGTTCATGAT  CGCCGCGCCA  ACCGCCGGAT
251  TTACGATCGC  CCCAGCGGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301  GCGTTTGGCG  GTCGGTTCCA  TGCCTTCGAT  GGTCAGTTCG  GGCAGTTTTC
351  GGTAAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401  GCAAAACGTA  TCGCAATACC  CGTGCGGCCT  GCGCGGCCGG  TGCGCCCGAT
451  GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501  GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551  AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTGCGCCA
601  GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GCGCGCGAAA  CCTTTTTCGT
651  ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701  ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751  TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCTTT
801  GGTTCGTCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCACTTTC
851  CGCGGCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901  CTGACGGTCT  TCCGGCGTGG  CTTGACGAT  GGTTCGATG  TCGTCGATAA
951  AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAAATCAG  CACTTCCAAG
1001  CGGGCGAAAT  CGACTTTGCC  GCTTTGCATC  AAGTCCATCA  GACGGCCCGG
1051  CGTGCGGACA  ATCAGATCGA  CCGGTTGCT  CAGGGCGCGG  GTTTGGTAGC
1101  CGAACGATGC  ACCACCGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151  TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  ATTCGCGGGT
1201  CGGCGTCAAC  ACCAACGCGC  GCGGGCCTTT  GCCCGGTTTT  TCGCTGCGTT
1251  TGGTCAGTCG  CTGCAAGTC  GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284.pep
1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE

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51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRHFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFLRLFR QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQO LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVNQ HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDSLRFQFAG
401 RRQHQRRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

	10	20	30	40	50	60
m284.pep	MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSVNV					
a284	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNGRYVDTACGNI					
a284	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNGRYVDTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAAFQIHRQAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	GGNQNFAAAFQIHRQAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
a284	IAQDMIEQAVFVAHIVAVQQLFFDFALVVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVNQHFQTFKINFAALHQVHQTARRGDNQIDRFA					
a284	LTVFRRGFDDGFDVVDKAHIQHTVGFVNQHFQAGEIDFAALHQVHQTARRGDNQIDRFA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m284.pep	QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDSLRFAGRGQHQSTRAFFAAGFQF					
a284	QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDSLRFAGRRQHRARAFARFFAAGQS					
	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

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g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat ttggcagta

```


151 tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct
 201 ttaccaaatc ccgtcctggg tcggcgtaaa catttcctcc caaaacctca
 251 aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
 301 gagggggcag acctaaaaat cagccgcttc cgcttcgcgt ggaaaccgtc
 351 cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
 401 tcgccatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa
 451 ggccctgccg acagcataga cctgcccgcg gctgtctatc tcgaccgctt
 501 cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaaccgtct
 551 atctcgaaacg cctcaacgcg gcataccgtt acgaccgtaa agggcacccg
 601 ctcgacatga aggcgcgcga cacgcggtgg agcagttcgt cggggtcagc
 651 ctccgtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
 701 aaggcggatt cgaaggcgaa accatacaca gtacggcgcg gctgagcgcg
 751 agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
 801 cctctcggga aaatccgtca tccacccgtt tgccgaatca ttggataaaa
 851 cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
 901 ttgccttccc tgcccgatgc cgggctgaat ttcgacctga ccgccatccc
 951 gtcgttttca gacggcatcg cgctggaagg ctgcgtcgat ttggaaaaca
 1001 ccaaagccgg ctttgcggac cgcaacggca tccccgtccg tcaggttttg
 1051 ggccgctttg tcatccggca ggacggcacg gtgcataatc gcaatacgtc
 1101 ccgcgccttg ctccgacggg gcggcatcag gctgtcgggc aaaatcgaca
 1151 ccgaaaaaga catccttgat ttaaatatag gcatcaactc cgtcggcgcg
 1201 gaagacgtgc tgcaaacgcg gttcaaaggc aggttggacg gcagcatcgg
 1251 catcggcggc acgaccgcct cgcccaaat ctcttggcaa ctccggcaccg
 1301 gcacggcacg cacggacggc agcctcccca tcgcaagcga ccccgcaaac
 1351 gaacagcgga aactggtgtt cgacaccgtc aacatctccg ccggggaagg
 1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgtctca
 1451 agctggacat ccgttcccgc gcattcgacc ctccgcgat cgatccgcaa
 1501 tttccggcag gcaatatcaa cggttcgatt catcttgcg gtgaactggc
 1551 aaaagagaaa ttacgggca aaatgcgtt ttgcccgg acgttcaacg
 1601 gcgtgccgat tgccggcagc gccgacattg ttacgagtc ccgccacct
 1651 ccgcgcgccg ccgtcgattt gcggttgggg cggaacatcg tcaaaacaga
 1701 ccggcgcttc ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
 1751 ccgatttatc ccgtttcggg ttccgactcg cggggtcttt aaatgtacgc
 1801 ggacaccttt ccggcgattt ggacggcggc atccgaacct ttgaaaccga
 1851 cctttccggc acggcgcgca acttacacat cggcaaacgc gcagacatcc
 1901 gttcgctcga ttttacctc aaaggctcac ccggcacaaag ccgcccgatg
 1951 cgcccgata tcaagggcgg ccgcctttcc ctgtcgggcg gcgcgcggt
 2001 ttcgataacc gccggcctga cgctggaagg tacggcgcg cagcaccgca
 2051 tccgcacaca cgccgccatg acgtggacg gcaaacgtt caaactcgat
 2101 ttggacgctt caggcgcat caacaggga cttaccgat ggaaaggcag
 2151 catcggcatc ctgcacatcg gcggcgatt caacctcaag ctgcaaaacc
 2201 gtatgacgct cgaagccggg gcggaacacg tggcggaag tcgcgcaaat
 2251 tggcaggcaa tggcgcgag cctcaacctg caaacctttt ctgggacag
 2301 gaaaaccggc atatcggcaa aaggcgcgcg acgcgccctg cacatcgccg
 2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac
 2401 ggcgactggg atgtcgccca cgggcacaac gcgcgcggct acctcaatat
 2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
 2501 tgaacgcatt ttccctgaaa acgcgcttcc aaaacgaccg catcgggaatc
 2551 ctgcttgacg gcggcgcgcg tttcgacgg attaacgcg atttgggcat
 2601 cggcaacgcc ttccggcgca atatggcaaa tacaccgctc ggcggcagga
 2651 ttacagcctc ctttcccgc ttgggcgcac tgaagccctt tctgcccgcc
 2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcgcgcg
 2751 acgggtaggc tctccgtccg tcaatgcgcg cgtcaacggg agcagcaact
 2801 acgggaaaaat caacgcgaat atcaccgtcg ggcaaacgg ctcttcgat
 2851 accgcacctt tggcgcgag gctcaacctg accgttgcg atgccgaagc
 2901 attccgcaac ttctaccgg tcggacaac cgtaaaagg agcctgaatg
 2951 ccgccgtaac cctcgcgcg acgatcgccg acccgactt ggcgcgagc
 3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt
 3051 ggacaacggc tcgctcggtt cgcataattg aggcaggaaa tgggtaatcg
 3101 acagcctgaa attccggcac gaaggacgg cggaactctc cggcacggtc
 3151 agcatggaaa acagcgtgcc cgatgtcgat atcgcgcgcg gtttcgacaa
 3201 ataccgcac cgttcccgc ccaaccgccg cctgacgggt tccggcaaca
 3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
 3301 aaaactgac aggggtctgt cggttcgcaa aaatcctcga tgccgtccgt
 3351 cggcgacgat gtcgtcgat tggcggaagt caagaaagag gcggcggcg
 3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

649

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3451 ttctccggct acggcgcgga cgttaccata ggcggcaaac tgacctgac
3501 cgcgcaaccg ggcggaaatg tgcgtggggt ggcacggtc cgcgtcatca
3551 aagggcggtta caaagcatac ggcagagatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgcct caacgacccc aacctgaaca tccgcgcccga
3651 acgccgcctt tccccgcgtg gtgcgggctg ggaatatatt ggagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcgga gcagcggtga
3801 caatgccgct ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgct tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacgcaaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

g285.pep

```

1 MDTTPTD TD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGNWSIET
101 EGADLKISRF RFAWKPSSELM RSLHITDIS AGDIAIVTKP TPKKEERPPQ
151 GLPDSIDLPA AVYLDREFETG KISMGKTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGFEFE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451 EQRKLVFDTV NISAGEGLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTGGF GKKGDRLNLN ITAPDLRFRG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRLS LSGGAADVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKGSGI LDIGGAENLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSNLN QHFSWDRKTG ISAKGGARGL HIAELHNFFK PFEHNLVLN
801 GDWDVAYGHN ARGYLISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNTGSLN ASAQIGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSEF
951 TAPLGGRLNL TVADAEAFRN FLPVGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
1051 SMENSVPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPVGGD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GGKLTLTAPQ GGNVRGVGTV RVIKGRYKAY GQDLIDITKT
1201 VSFVGPLNDP NLNIRAERRL SPVAGVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLIILNR GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRLFSGDKK DSAGNGKKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

m285.seq

```

1 ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51 CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCCGCG GCACTGCTGT CTGTCTTGAT TTGGCAGTA
151 TGTTCCTCG GCTGCTCGC CGGTACGGA GCAGGTTTC GCTTCGGGCT
201 GTACCAAATC CCGTCTGGT TCGGCGTAAA CATTTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGACGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AGAAGAAGC CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAAGC GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CAGCCGCTGG AGCAGTTCTG CGGGGGCGGC
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

```


801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
 851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC
 901 GTGCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
 951 GTCGTTTTC ACGGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAACA
 1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCGG TCAGGTTTTA
 1051 GGCGGCTTTG TCATCCGGCA GGACGGCAGC GTGCATATCG GCAATACGTC
 1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCCGGC AAAATCGACA
 1151 CCGAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
 1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
 1251 CATCGGTGGC ACGACCGCCT CGCCAAAAT CTCTTGCCAA CTCGGCATCG
 1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
 1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
 1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCTGCTCA
 1451 AGCTGGACAT CCGTTCGCCG GCATTGACCC CTTCCGCGCAT CGATCCGCAA
 1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
 1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGCG ACGTTCAACG
 1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
 1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACAACAG
 1701 CGCGGCGCTT GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC
 1751 CCGATTATAT CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
 1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA
 1851 CCTTTCGGG CCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
 1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA
 1951 CGCGCGGACA TCAAAGCGAG CCGCCTTCG CTGTCCGGCG GAGCGGCGGT
 2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA
 2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
 2101 TTGGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAGGCGAG
 2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
 2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TCGCGCAAA
 2251 TGGCAGGCAA TGGGCGGCGC CCTCAACCTG CAACACTTTT CTTGGGATAA
 2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
 2351 AGTTGCACAA TTTCTTCAAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
 2401 GGCGACTGGG ATGTGCGCTA CCGGCGCAAC GCGCGCGGCT ACCTCAATAT
 2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
 2501 TGAACGATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
 2551 CTGCTTGACG CCGGCGCGCG TTTCGGGCGG ATTAACGCGG ATTTGGGCAT
 2601 CGCCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GGCGGCAGGA
 2651 TTACCGCCTC CCTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
 2701 GCCGCGCAAA ACATTACCGG CAGCCTGAAT GCCCGCGCGC AAATCGGCGG
 2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
 2801 ACGGGAAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
 2851 ACCGCGCCTT TGGGCGGCGC GCTCAACCTG ACCGTTGCGG ATGCCGAAGT
 2901 ATTCCGCAAC TTCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
 2951 CCGCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCGAGC
 3001 ATCAACGGCG ACAAACTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT
 3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
 3101 ACAGCGTGAA ATTCGGCAC GAAGGGACGG CGGAACCTCT CGGTACGGTC
 3151 GGTATGAAA ACAGCGGACC CGATGTGAT ATCGGCGCGG TGTTGACAAA
 3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGCTT TCCGGCAACA
 3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CGGGATGATT
 3301 AAAACGGATC AGGGGCTGTT CGGTTGCAA AAATCCTCGA TGCCGTCCGT
 3351 CGGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCGC
 3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC
 3451 TTCCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCGCAAC TGACCCTGAC
 3501 CGCCCAATCG GGCGGAAGCG TACGGGCGGT GGGCACGGTC CGCGTCATCA
 3551 AAGGCGGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
 3601 GTCTCTTTG TCGGCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
 3651 ACGCGCCTT TCCCCGTCG GTGCGGCGGT GGAAATATTG GGCAGCCTCA
 3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAGAAAGC
 3751 AAGCTCTCTT GGCTCATCTT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA
 3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAATCA
 3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
 3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT
 3951 CGGCAAAACA CTGACGGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
 4001 CCAGCGCGGA ACAGTCCGTC AAAGTATTTT ACCGGCTGAC CCGCGCCATA
 4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTCT TCGGGCGGCG AGCTGACATA

651

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACGGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
1 MTDTAPTDT PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPELMM RRSLLHITEIS AGDIAIVTKP TPPKEERPPPL
151 SLPDSIDLPA AVYLDREFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
301 VPSLPDAGLN FDLTAIPSF S DGIALEGS LD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTDGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRSL LSGGAAVVDT ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHL HIAELHNFFK PPFENHLVLN
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIANA FGNMANAPL GGRITASLPD LGALKPFLPA
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSPD
951 TAPLGGRLNL TVADA EVFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKE AAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GKKLTTLTAQS GGSVRGVGTV RVIKGRYKAY QQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKD
1251 KLSWLILNRA GSGSSGDNA LSAAAGALLA QQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
g285	MTDTTPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRFAWKPELMM					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRFAWKPELMM					
	70	80	90	100	110	120
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDREFETGKISMKGAFDK					
g285	RRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDSIDLPAAVYLDREFETGKISMKGTFDK					
	130	140	150	160	170	180
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
g285	QTVYLERLNAAAYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
m285.pep	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
g285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
	250	260	270	280	290	300
m285.pep						
g285						

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|||||:|||||
g285      AAQNITGSLNAsAQIGGRVGSpsvNAAVNGSSNYGKINGNITVGQSRsFDtAPLGGRlNL
          910      920      930      940      950      960

          970      980      990      1000     1010     1020
m285.pep  TVADAEVFRNfLPVgQTVKGSlnAAVtLGGSiADPhLGGSINGDKLYYRNQtQGIIlDNG
          970      980      990      1000     1010     1020
g285      TVADAEAFRNfLPVgQTVKGSlnAAVtLGGSiADPhLGGSINGDKLYYRNQtQGIIlDNG
          970      980      990      1000     1010     1020

          1030     1040     1050     1060     1070     1080
m285.pep  SLRSHIAGRKwVIDsLKfRHEGTAElsGTVGMENSGPDVDIGAVFDKYRILSRPNRRLtV
          1030     1040     1050     1060     1070     1080
g285      SLRSHIAGRKwVIDsLKfRHEGTAElsGTVSMENSVPDVDIGAVFDKYRILSRPNRRLtV
          1030     1040     1050     1060     1070     1080

          1090     1100     1110     1120     1130     1140
m285.pep  SGNTRLRYsPQKGISVtGMiKTDQGLFGsQKSSMPsVGDDVvVLGEVKKEAAAPLpVNMN
          1090     1100     1110     1120     1130     1140
g285      SGNTRLRYsPQKGISVtGMiKTDQGLFGsQKSSMPsVGDDVvVLGEVKKEAAASLpVNMN
          1090     1100     1110     1120     1130     1140

          1150     1160     1170     1180     1190     1200
m285.pep  LTLDLNDGIRfAGYgADVTIGGKLtLTaQSGGSVRGvGTVrVIKGRYKAYGQDLdITKGT
          1150     1160     1170     1180     1190     1200
g285      LTLDLNDGIRfAGYgADVTIGGKLtLTaQPGGNVRGvGTVrVIKGRYKAYGQDLdITKGT
          1150     1160     1170     1180     1190     1200

          1210     1220     1230     1240     1250     1260
m285.pep  VSFVGPLNDPNlNIRAErRLsPVgAGVEILGSlnSPRITLTANePMSEKDkLSWlILNRA
          1210     1220     1230     1240     1250     1260
g285      VSFVGPLNDPNlNIRAErRLsPVgAGVEILGSlnSPRITLTANePMSEKDkLSWlILNRA
          1210     1220     1230     1240     1250     1260

          1270     1280     1290     1300     1310     1320
m285.pep  GSGSSGDNAALsAAAGALLAGQINDRIGLVDDLGfTSKRsrNAQTgELNPAEQVlTVGKQ
          1270     1280     1290     1300     1310     1320
g285      GSGSSGDNAALsAAAGALLAGQINDRIGLVDDLGfTSKRsrNAQTgELNPAEQVlTVGKQ
          1270     1280     1290     1300     1310     1320

          1330     1340     1350     1360     1370     1380
m285.pep  LTGKLYIGYEYSISSAEQsVKLIYRLTRAIQAVARIGSRSSGgELTYtIRfDRfSGSDKK
          1330     1340     1350     1360     1370     1380
g285      LTGKLYIGYEGISSAEQsVKLIYRLTRAIQAVARIGSRSSGgELTYtIRfDRfLFGSDKK
          1330     1340     1350     1360     1370     1380

          1390
m285.pep  DSAGNGK GKX
          |||||
g285      DSAGNGK GKX

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

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a285.seq
1  ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGCTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTTCTGAT TTTGGCAGTA
151 TGTTTCTCTG GCTGGCTCGC CGGCACGGAA GCGGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCTCTC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGAGCC TGCACATTAC CGAAATTTC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTA AAGAAGAACG CCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTCGACCTGA AGGCTGCCA CACGCCGTGG AGCAGTTCGT CGGGGTCAGC

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651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
 701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
 751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
 801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
 851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCCTTC
 901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
 951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGGAACA
 1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGTCCG TCAGGTTTTA
 1051 GGCAGCTTTG TCATCCGGCA GGACGGCAG GTGCATATCG GCAATACGTC
 1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTGCGG AAAATCGACA
 1151 CCGAAAAAGA CATCTCGAT TTAATATAG GCATCAACTC CGTCGGCGCG
 1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
 1251 CATCGGTGGC ACGACCGCCT CGCCAAAAT CTCTGGCAA CTCGGCATCG
 1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCCAGAAAC
 1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCG CCGGGCAAGG
 1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
 1451 AGCTGGACAT CCGTTCCCGC GCATTGACC CTTGCGCAT CGATCCGCAA
 1501 CTTCCGCGAG GCAATATCAA CGGCTCAATA AACCTTGCGG GCGAACTGGC
 1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
 1601 GCGTACCGAT TGCCGGCAGT GCCGACATG TTTACGAGTC CCGCCACCTT
 1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACAGAGA
 1701 CCGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACCACAC
 1751 CCGATTATC CCGTTTCGGT TTCGGAATCG CCGGGTCTTT AAATGTACGC
 1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
 1851 CTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
 1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA
 1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGAGGT
 2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCAGC
 2051 TCCGACACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
 2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAGGCGAG
 2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
 2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAT
 2251 TGGCAGGCAA TGGGCGGCG CTTCAACCTG CAACACTTTT CTTGGGATAA
 2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
 2351 AGTTGCACAA TTTCTTCAAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
 2401 GCGGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGCGGCT ACCTCAATAT
 2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAT GCTTTGGGTT
 2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
 2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCGC ATTTGGACAT
 2601 CGGCAACGCC TTCGGCGGCA ATATGGCAA TGACCCGCTC GCGGCGAGGA
 2651 TTACCGCCTC CCTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC
 2701 GCGCGCGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
 2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
 2801 ACGGGAAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
 2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCGG ATGCCGAAGT
 2901 ATTCCGCAAC TTCTTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
 2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCG ATCCGCACTT GGGCGGCGC
 3001 ATCAACGGCG ACAAACTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT
 3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
 3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
 3151 GGTATGGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTCGACAA
 3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
 3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CGGGATGATT
 3301 AAAACGATC AGGGGCTGTT CGGTTGCGAA AAATCCTCGA TGCCGTCCGT
 3351 CGGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
 3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC
 3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCCTGAC
 3501 CGCCCAATCG GCGGGAAGCG TCGGGGCGT GGGCACGGTC CCGTCATCA
 3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
 3601 GTCTCCTTTG TCGGCGCGCT CAACGACCCC AACCTCAACA TCCGCGCGGA
 3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAAATATTG GGCAGCCTCA
 3701 ACAGTCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAAAGAC
 3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA
 3801 CAATGCCGCC CTGTCCGCG CCGCGGCGC GCTGCTTGCC GGGCAATCA
 3851 ACAGCGCAT CCGGCTGGT GATGATTGG GCTTTACCAG CAAGCGCAGC
 3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

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3951 CCGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTATT ACCGGCTGAC CCGCGCCATA
4051 CAGCGGGTTG CCCGTATCGG CAGCGGTCG TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
1  MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPPL
151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLECK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPPAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSF S DGIALEGLSD LENTKAGFAD RKGIPVRQVL
351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQSSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTGDFG GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEVVDL ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKGSIIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSNLN QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLNLN
801 GDWDVAYGRN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFLPA
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSRSEF
951 TAPLGGRNLN TVADAEVFRN FLVPGQTVKG SLNAAVTLLG SIADPHLGG
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKEE AAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGLTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTITGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGDDK DSAGNSKKG*

m285/a285 99.4% identity in 1389 aa overlap

10 20 30 40 50 60
m285.pep MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
a285 MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
10 20 30 40 50 60

70 80 90 100 110 120
m285.pep AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
a285 AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
70 80 90 100 110 120

130 140 150 160 170 180
m285.pep RRSLLHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAVYLDRFETGKISMKGAFDK
a285 RRSLLHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAVYLDRFETGKISMKGAFDK
130 140 150 160 170 180

190 200 210 220 230 240
m285.pep QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLECK
a285 QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLECK
190 200 210 220 230 240

250 260 270 280 290 300
m285.pep TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF

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a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPPAESLDKTL EEVLVKGFNINPSAF
	250 260 270 280 290 300
m285.pep	310 320 330 340 350 360
	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
a285	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
m285.pep	370 380 390 400 410 420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
a285	VHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
m285.pep	430 440 450 460 470 480
	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
a285	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
	430 440 450 460 470 480
m285.pep	490 500 510 520 530 540
	RLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
a285	RLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	490 500 510 520 530 540
m285.pep	550 560 570 580 590 600
	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRNLNITAPDLSRFGFGLAGSLNVR
a285	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRNLNITAPDLSRFGFGLAGSLNVR
	550 560 570 580 590 600
m285.pep	610 620 630 640 650 660
	GHLSGDLGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGS P DTSRPIRADIKGSRLS
a285	GHLSGDLGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGS P DTSRPIRADIKGSRLS
	610 620 630 640 650 660
m285.pep	670 680 690 700 710 720
	LSGGAUVDTADLMLDGTGVQHRIRTHAAMTLDGKPKFDFLDASGGINRELTRWKSGSIGI
a285	LSGGAUVDTADLMLDGTGVQHRIRTHAAMTLDGKPKFDFLDASGGINRELTRWKSGSIGI
	670 680 690 700 710 720
m285.pep	730 740 750 760 770 780
	LDIGGA FN LKLQNRMTLEAGAERVAASAANWQAMGGS LN LQHFSWDKKTGISAKGGAHGL
a285	LDIGGA FN LKLQNRMTLEAGAERVAASAANWQAMGGS LN LQHFSWDKKTGISAKGGAHGL
	730 740 750 760 770 780
m285.pep	790 800 810 820 830 840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	790 800 810 820 830 840
m285.pep	850 860 870 880 890 900
	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
a285	TRFQNDRIGILLDGGARFGRINADLDIGNAFGGNMANAPLGGRITASLPDLGTLKPFLPA
	850 860 870 880 890 900
m285.pep	910 920 930 940 950 960
	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
a285	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN

657

a285	AAQNITGSLNAAQIGGRVGSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRLNL
	910 920 930 940 950 960
m285.pep	TVADAEVFRNFLPVGQTVKGSLSNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
a285	TVADAEVFRNFLPVGQTVKGSLSNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
	970 980 990 1000 1010 1020
m285.pep	SLRSHIAGRKWWIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRRLTV
a285	SLRSHIAGRKWWIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRRLTV
	1030 1040 1050 1060 1070 1080
m285.pep	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
	1090 1100 1110 1120 1130 1140
m285.pep	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
a285	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
	1150 1160 1170 1180 1190 1200
m285.pep	VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
a285	VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
	1210 1220 1230 1240 1250 1260
m285.pep	GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
a285	GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
	1270 1280 1290 1300 1310 1320
m285.pep	LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
a285	LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
	1330 1340 1350 1360 1370 1380
m285.pep	DSAGNGKGKX
a285	DSAGNSKGKX
	1390

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

```

1  CTGAAGCTGT CGGCCGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGCCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATT CTCCCAAAA CCTCAAAGGC
151 AACTGCTCG ACGGCTTCGA CGGCACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGAAA CCGTCCGAAC
251 TGATCGCCG CAGCCTGCAC ATCACCACA TCTCCGCCG CGACATCGCC
301 ATCGTAACCA AACCAGCTCC GCCTAAAGAA GAACGCCCGC CTCAAGGCCT
351 GCCCGACAGC ATAGACCTGC CGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTG ACAAACAAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACAGC CGTGAGCAG TTCGTCGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGACGATCGA CGCGGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTGCGCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTGCA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTGAGG TTTTGGGCGG
951 CTTTGTCTATC CCGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGACCCCG CAAACGAACA
1251 GCGGAAACTG GTGTTTCGACA CCGTCAACAT CTCGCGCGGG GAAGGCAGCC
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1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGcgt atCAACGTT CGATTCTCTT TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTGC CCGGTACGTT CAACGGCGTG
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1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTCCGGC GATTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
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2151 GGCATGGGG GCGAGCCTCA ACCTGCAACA CTTTCTTGG GACAGGAAA
2201 CCGGCATATC GGCAAAAGGC GCGCAGCGG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAAACGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
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3001 CTGAAATTC GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTGAGCAT
3051 GGAACACAGC GTGCCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCTCTGT CCGCCCCAAC CGCCGCCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAAAC
3201 TGATCAGGGG CTGTTGCGGT CGCAAAAATC CTCGATGCCG TCCGTGCGG
3251 ACCATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC
3301 CCCGTCATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CGGCTACGGC GCGGACGTTA CCAAGGCGG CAAACTGACC CTGACCGCGC
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3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAT TATTGGGCGG CCTCAACAGC
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3651 CTCTTGCTC ATCCTCAACC GTGCCGGCAG CCGCAGCAGC GCGCAATG
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3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGCAAAACC GCGCAACTCA ACCCGCGCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACTGAC CCGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC GATTACCGG CTGACCGCGC CCATACAGGC
3951 GGTGCGCGT ATCGGCAGCC GTTCGTGCGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTCTTC GTTCGGGACA AAAAAGACTC CGCAGGAAC
4051 GGCAAGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pep


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1  LKLSAALLSV LILAVCFGLW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAYVLD RFETGKISMG KTFDKQTVYL
151 ERLNAAARYD RKGHRLDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGDN IRLSGKSVIH PFAESLDRTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSILTAQYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKSGPG TSREMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRI
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
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751 HNEFFKPFEEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGAQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNASAQI GGRVGSPPVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRNLTLVADA EAFRNFLPVG QTVKGSLNAA
951 VTLLGSIADP HLGGSSINGDK LYRNRQTQGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
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1201 PRITLTANEP MSEKDLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKDSAGN
1351 GKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGCTCTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGCTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGCT TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACCCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAC CCGTCCGAAC
251 TGATCGCCCG CAGCCTGCAC ATTACCGAAA TTTCGCCCGG CGACATCGCC
301 ATCGTTACCA AACCAGCTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAGGAC ACCGCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG CGCGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTGA CACCAAAGGC
601 GGAATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAATAAT CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 CAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGAC TGAATTTTGA CCTGACCGCC ATCCGCTCGT
851 TTTCAGACGG CATCGCGCTG GAAGTTTCGG TCGATTTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCGG
951 CTTTGTTCATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAAT TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAACCGGACA
1251 GCGGAACTG GTGCTCGACA CCGTCAACAT CGCCGCGCGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA -CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTCCGA CAATTGTTTAC GAGTCCCGCC ACCTTCCGCG
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1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
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660

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3551 GCCTTTCCCG CGTCGGTGGG GCGTGGGAA TATTGGGCG CCTCAACAGC
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3951 GGTGCGCGCT ATCGGAGCC GTTCGTCGGG CGGCGAGCTG ACATACACCA
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4051 GGCAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.psp

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101 IVTKPTPPKE ERPLSLPDS IDLPAAYLDR FETGKISMG KAFDRQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGGKTIHST ARLSGSLKDV RAELAIDGNN IRLSGKSVIH PFAESLDKTL
251 EEVLVRGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLNTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
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451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGRM RFLPGTFNGV
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601 LDFTLKSPD TSRPIRADIK GSRLSLSGGA AVVDATDML DGTGVQHRIR
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901 KINGNITVGO SRSFDTAPLG GRNLTVADA EVFRNPLPVG QTVKGSNLAA
951 VTLLGSIADP HLGGSSINGDK LYRNTQTQGI ILDNGLSLRSH IAGRKWVIDS
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1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDVVVLG EVKKEAAAPL
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1351 GKGR*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

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661

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70 80 90 100 110 120
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m285-1 WSIETEGADLKISRFRFAWKPSLMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS
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670 680 690 700 710 720
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662

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	850	860	870	880	890	900
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m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAEISGTVGMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTTGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTTGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVVVKGRYKAYQDLDTKGTVSFVGPLNDPFLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVVVKGRYKAYQDLDTKGTVSFVGPLNDPFLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANPEMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAQINDRIGLVDDLGF					
m285-1	PRITLTANPEMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGKGK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

```

1  CTGAAGCTGT CCGCGGCACT GCTGTCTGTT CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGCGA CGGAAGCGGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCAGCTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGGCTTGA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CCGCGGCAAT ATCCGCTCT
701 CGGGAATAAT CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCG GATGCCGGGC TGAATTTCGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAA
901 GCCGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTATC CCGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CCCTGCTCG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAAT TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAG CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCCGACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 GCGGAACCTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATT CCGCCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCGCGC ACCTTCCGCG
1551 TGCCGCCGTC GATTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGC GATTTGGACG GTGGCATCCG AACCTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGCGCGCAGA CATCCGTTCC
1801 CTCGATTICA CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGGCG
1851 GCAGATCAAA GCGAGCCGCC TTTCGCTGTC GGGCGGAGCG GAGGTTGTCG
1901 ATACCGCCGA CCTGATGCTG GACGGCAGCG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCCG CCATGACGCT GGTATGGCAA CCGTTCAAAT TCGATTGGA
2001 CGCTTTCAGG GGCATCAACA GGGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACCTCTCGAAG CCGGTGCGGA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2151 GGCATGCGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAAACCGCC CTTCGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAGACCGG CGATGCCGTA TTGCCCGCGG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAAC GACCGTATCG GAATCTTGCT
2451 TGACGGCGCG GCGCGTTTCG GCGCGATTAA CGCCGATTTC GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAATGCAAC CGCTCGCGCG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTTCTGC CGCCCGCCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CCGGCAATC GCGCGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCCGCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CGGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGAAC
2951 ACGGCTCGCT GCGTTGCGAT ATCGCGGGCA GGAAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCCGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CCGCGTGTTC GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCTTGA CCGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAAAC
3201 GGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTGCGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGCGCGC GGCACCGCTC
3301 CCCGTCATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGCGCG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGCGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATAAGGGCA GGATTGGAAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCCAACCT CAACATCCGC GCGAAACGCC
3551 GCCTTTCCCG CGTCGGTGCG GGCGTGGAAG TATTGGGCGC CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCTTCAACC GCGCCGGCAG TGGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGCG TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGGCAAAAC GCGCAACTCA ACCCCGCGGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACCTGAC GCGCAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTTCGCCGT ATCGGCAGCC GTTCGTGCGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC GCGCGGAAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

a285-1.pep

1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDFGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPEK ERPLSLPDS IDLPAAYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAEALIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGSILAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSREFGFLAG SLNVRGHLGS DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPP TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWOAMG GSNLQHFWS DKKTGISAKG GAHGLHIAEL
751 HNFEPKPFEPH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGAQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGM ANAPLGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSLNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVQG SRSFDTAPLG GRNLNTVADA EVFRNFPVG QTVKGSNLAA
951 VTLGGSIADP HLGGSINGDK LYRNQTOGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFSGQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1151 RYKAYQDLDL ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGOIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIREDFRS GSDKKDSAGN
1351 SKGK*

a285-1/m285-1 99.3% identity in 1354 aa overlap

a285-1.pep	10	20	30	40	50	60
m285-1	10	20	30	40	50	60
a285-1.pep	70	80	90	100	110	120
m285-1	70	80	90	100	110	120
a285-1.pep	130	140	150	160	170	180
m285-1	130	140	150	160	170	180
a285-1.pep	190	200	210	220	230	240
m285-1	190	200	210	220	230	240
a285-1.pep	250	260	270	280	290	300
m285-1	250	260	270	280	290	300
a285-1.pep	310	320	330	340	350	360
m285-1	310	320	330	340	350	360
a285-1.pep	370	380	390	400	410	420
m285-1	370	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	SLTAQGYLE	LFKDRLLK	LDIRSR	AFDPSRID	PQLPAGNINGS	SINLAGE
m285-1	VLDTVNIAAGQGS	SLTAQGYLE	LFKDRLLK	LDIRSR	AFDPSRID	PQLPAGNINGS	SINLAGE
	430	440	450	460	470	480	
a285-1.pep	490	500	510	520	530	540	
a285-1.pep	LAKEKFTG	KMRFLPG	TENGVP	PIAGSAD	IVYESR	HLPRAA	VDLRLGRNI
m285-1	LAKEKFTG	KMRFLPG	TENGVP	PIAGSAD	IVYESR	HLPRAA	VDLRLGRNI
	490	500	510	520	530	540	
a285-1.pep	550	560	570	580	590	600	
a285-1.pep	RLNLNITAP	DLSRFG	FLAGSL	NVRGHL	SGDL	DGGIRT	FETDLSGA
m285-1	RLNLNITAP	DLSRFG	FLAGSL	NVRGHL	SGDL	DGGIRT	FETDLSGA
	550	560	570	580	590	600	
a285-1.pep	610	620	630	640	650	660	
a285-1.pep	LDFTLKGS	PDTSRPI	RADIKGS	RLSLSG	GAEVVD	TADLMD	GTGVQHR
m285-1	LDFTLKGS	PDTSRPI	RADIKGS	RLSLSG	GAEVVD	TADLMD	GTGVQHR
	610	620	630	640	650	660	
a285-1.pep	670	680	690	700	710	720	
a285-1.pep	PFKFDLD	ASGGIN	RELTRW	KGSIGI	LDIGGA	FNKLQNR	MTLEAGA
m285-1	PFKFDLD	ASGGIN	RELTRW	KGSIGI	LDIGGA	FNKLQNR	MTLEAGA
	670	680	690	700	710	720	
a285-1.pep	730	740	750	760	770	780	
a285-1.pep	GSLNLQH	FSWDKKT	GISAKG	GAHGLH	IAELHN	FFKPPF	EHNLVL
m285-1	GSLNLQH	FSWDKKT	GISAKG	GAHGLH	IAELHN	FFKPPF	EHNLVL
	730	740	750	760	770	780	
a285-1.pep	790	800	810	820	830	840	
a285-1.pep	NISRQSG	DAVLP	GGQALG	LNFA	SLKTRF	QNDRI	GILLD
m285-1	NISRQSG	DAVLP	GGQALG	LNFA	SLKTRF	QNDRI	GILLD
	790	800	810	820	830	840	
a285-1.pep	850	860	870	880	890	900	
a285-1.pep	ANAPLGG	RITASL	PDLGTL	KPFLP	AAQNIT	GSLNAA	QIGGRV
m285-1	ANAPLGG	RITASL	PDLGTL	KPFLP	AAQNIT	GSLNAA	QIGGRV
	850	860	870	880	890	900	
a285-1.pep	910	920	930	940	950	960	
a285-1.pep	KINGNIT	VGQSR	SFDTAP	LGGR	LNLTVA	DAEVR	NFLPV
m285-1	KINGNIT	VGQSR	SFDTAP	LGGR	LNLTVA	DAEVR	NFLPV
	910	920	930	940	950	960	
a285-1.pep	970	980	990	1000	1010	1020	
a285-1.pep	HLGGSIN	GDKLY	RNQTQ	GII	LDNGS	LRSHI	AGRK
m285-1	HLGGSIN	GDKLY	RNQTQ	GII	LDNGS	LRSHI	AGRK
	970	980	990	1000	1010	1020	
a285-1.pep	1030	1040	1050	1060	1070	1080	
a285-1.pep	GPVDIG	AVFDK	YRILSR	PNRRL	TVSGN	TLRYS	PQKGIS
m285-1	GPVDIG	AVFDK	YRILSR	PNRRL	TVSGN	TLRYS	PQKGIS
	1030	1040	1050	1060	1070	1080	
a285-1.pep	1090	1100	1110	1120	1130	1140	
a285-1.pep	SVGDDV	VVLGE	VKKEA	AAPLP	VNMNLT	LDLND	GIRFAG
m285-1	SVGDDV	VVLGE	VKKEA	AAPLP	VNMNLT	LDLND	GIRFAG
	1090	1100	1110	1120	1130	1140	
a285-1.pep	1150	1160	1170	1180	1190	1200	
a285-1.pep	GVGTVR	VIKGR	YKAYG	QDL	DITKGT	VSFVG	PLNDP
m285-1	GVGTVR	VIKGR	YKAYG	QDL	DITKGT	VSFVG	PLNDP

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANPEMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANPEMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQTGELNPAEQVLTGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYTIRDFRSGSDKKDSAGNSKKGX					
m285-1	IGSRSSGGELTYTIRDFRSGSDKKDSAGNSKKGX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

```

1 atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51 ggctttatatt ttctttccgc acgcatacgc gcctgccgcc gacctttccg
101 aaaacaaggc ggcgggtttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtc aattaaacc caaattcccc gtccgcatcg acacgcagga
201 cagtgaatc aaagatatgg tcgaagaaca cctgccgctc atcacgcagc
251 agcaggaaga ggttttggat aaggaacaga cgggattcct tgccgaagaa
301 gcaccggaca acgttaaaac aatgctccgc agcaaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacggtg cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501 ctggcagcag ccggtaggca gcgatttcca tcaggacagt tgggaaaaa
551 gcaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta ccgcttgcc
601 aagctcggca acaccgggc ggccgtcaac cccgataccg ccaccgccga
651 tttgaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcacagg cacacagcgt taccccaagc aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgtgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcatattc cggcgcgctc gtacaagccg
851 acttcgaccg cctccaagc ggaccgcgtc cccgtcaaag tcagcgtaac
901 cgagggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcggtcgt ctgggatatg gacaaatagc aaaccacgct
1051 tgccgcgggc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaacgcgcc
1151 tctcggcg gcatctggtg tgtgcgcgac cgcgcggggc tcgatgccag
1201 gctggggcg gaatttctcg cagaaggccg gaaaatcccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaaacgc
1301 cagctgctca acaacgtgct gcaccccga aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtccctcacc gcgctaattc
1401 gcacctctgc ccgcgcaggt tatttcttca cgcccgaata caaaaaactc
1451 ggcacgttca tcatacgcg acaagcgggt tacaccgttg cagcgacaa
1501 tgccgatgtc cctcggggc tgatgttccg cagcgcgggc gcgtcttccg
1551 tgcgcggtta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

```

1 MONTGTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51 ESVKLKPFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAITV HITPGPRTKI ANVGVAIIGD
151 ILSGDLAEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201 KLGNTAAVN PDTATADLV VVDSGRPIAF GDFEITGTQR YPEQTVSGLA
251 RFQPGTFYDL DLLLDFOQAL EQNGHYSAS VQADFDRLEP GPRPRQSQRN
301 RGQTPQTRNR HPPRFGIRFG RQNRLLRLQ LQORLYRLGR LGYGQIRNHA
351 CRRHQPAQAL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRQC
401 AGGGISRRRP ENPRLGCRFG QPRHDADRL LETPAAQORA APRKRPLPRR

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667

451 QNRDDFGHIP VLHRANPHLC PRRLEFLHARK QKTRHVHHTR TSGLHRCTRO
501 CRCPLGADVP QRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq

```

1  ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51  GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GGCGGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACAC
151 GAATCAGTCA AATTAAAACC CAAATCCCCG GTCCTCATCG ACACGCAGGA
201 CAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTACAGC
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGAAAAA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAAACA
551 GCAAACTTC CGTCTCGGC GCGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGCTCGGCA ATACGCAGGC GGCGTCAAC CCGGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGCCGCCCC CATCGCCTTC GCGACTTTG
701 AAATCACCGG CACACAGCGT TACCCCGAAC AAATCGTCTC CGGCCTTGCG
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAAACT CGAAACCGGC ATCCGCCTCG ATTCCGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCTGC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT
1151 TCTCCGCGCG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGGCGG AATTTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGCTGT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCTCT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCCAGAA ACGGCCATTA CCTCGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCTTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTCA CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGCAAT
1501 GCCGACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGATGCCCG
1701 CGCCAAATTT AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTTGCG CCGTTTTCTT TCGACATCGC CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep

```

1  MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLRPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAITV HITPGPRTKI ANVGVAAILGD
151 ILSGDNLAIE YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLLDFQQAL EQNGHYS GAS VQADFDRLOQ DRVPEKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAIDYYNL FNKGYIGSVV WMDMKYETTL
351 AAGISQPRNY RGNWTSNVV YNRSTTQNLK KRAFSGGVWY VRDRAGIDAR
401 LGAEFLAEGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGTFL SSTALIRTS RAGYFFTPEN KKLGTFFIIRG QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FRTLSTGAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKN	KS	PDTE	SVKLKPKFP	
g286	MQNTGTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKS	KSPDTE	SVKLKPKFP		
	10	20	30	40	50	60
m286.pep	VLIDTQDSEIKDMVEEHLPLITQ	QEEVL	DKEQT	GFLAE	APDNVKTMLRS	KGYFSSKVS
g286	VRIDTQDSEIKDMVEEHLPLITQ	QEEVL	DKEQT	GFLAE	APDNVKTMLRS	KGYFSSKVS
	70	80	90	100	110	120
m286.pep	LTEKDGAYTVHITPGPRTKIANV	GVAILGDILSDGNLAEYYRNA	LENWQQPVGSDF	QQDS		
g286	LTEKDGAYTVHITPGPRTKIANV	GVAILGDILSDGNLAEYYRNA	LENWQQPVGSDF	QQDS		
	130	140	150	160	170	180
m286.pep	WENSKTSVLGAVTRKAYPLAKL	GNTOAAVNPD	TATADLN	VVVDSGRPIAF	GDFEITGTQR	
g286	WENSKTSVLGAVTRKGYPLAKL	GNTRAAVNPD	TATADLN	VVVDSGRPIAF	GDFEITGTQR	
	190	200	210	220	230	240
m286.pep	YPEQIVSGLARFQPGMPYDLD	LLLD	DFQ	QALEQNGHYSGASVQAD	FDRL	-QGDRV
g286	YPEQIVSGLARFQPGMPYDLD	LLLD	DFQ	QALEQNGHYSGASVQAD	FDRL	-QGDRV
	250	260	270	280	290	299
m286.pep	TEV	KRHKLET	GIRLDSEY	GLGGKIAYDY	NNLFNKG	YIGSVVWMDKYETTLAAGISQPRN
g286	RGQTPQTRNRHPPRFGIR	FGRONRLRL	LQPLQRLY	RLGRLGYGQIR	NHACRRHQ	PAAQL
	310	320	330	340	350	360

a286.seq

1	ATGCACGACA	CCCGTACCAT	GATGATTAAA	CCGACC GCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTTCCG
101	AAAACAGGTA	GGCGGGTTTC	GCATTGTTCA	AAAACAAAG	CCCCGACACC
151	GAATCAGTTC	AATATAAAC	CAATTTCCCC	GTCGCGCAT	ACACGCAGGA
201	TAGTGAATTC	AAAGATATGG	TCAAGAACA	CTCGCGCTC	ATTACGCAG
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA
301	GCACCGGACA	ACGTTAAAA	AATGCTCCGC	AGCAAAGGCT	ATTTACAGAG
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGAGC	TTATACGGTA	CACATCACAC
401	CGGGCCCGCG	CACCAAATTC	GCGCAAGCTC	GCCTGCCAT	CTCTGGCGAC
451	ATCCTTTTCT	ACGGCAACCT	CGCCGAATAC	TACCGCAACG	CGCTGGAATA
501	CTGGCAGCAG	CCGGTAGGCA	GTGATTTCGA	TCAGGACAGT	TGGGAAAACA
551	GCAAACCTTC	CGCTCTCGGC	GCGGTAACGC	GCAAAGCCTA	CCCGCTTGCC
601	AAGCTGGGCA	ACATCCGGGC	GCGCGTCAAC	CCCGATACCG	CCACCGCGGA
651	TTTGAACGTC	GTCGTGGACA	GCGGCCGCCC	CATCGCCTTC	GCGACTTTTG
701	AAATTACCGG	CACGCAGCGT	TACCCCGAAC	AAATCGTCTC	CGGCTTTGGC
751	CGCTTCCAAC	CGGGCAGCCG	CTACGACCTC	GACCTGCTGC	TGCACTTCCA
801	ACAGGCGCTC	GAACAAAACG	GGCATTTATC	CGGCGCGTCC	GTACAAAGCC
851	ACTTCGACCG	GCTCCAAGGC	GACGCGCTCC	CGGTCAAAGT	CAGCGTAAAC
901	GAGGTCAAAC	GCCACAAGCT	CGAAACCGGC	ATCCGCCTCG	ATTTCGGAAT
951	CGGTTTGGGC	GGCAAATATC	CCTACGACTA	TTACAACCTC	TTCAACAAG
1001	GCTATATCGG	TTCCGTCGTC	TGGGAATATG	ACAAATACGA	AACCAAGCTT
1051	GCGCGCGGCA	TTCAGCAGCC	GGGCAACTAT	CGGGGCAACT	ACTGGACAAG
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCAAT
1151	TCTCCGGCGG	CATCTGGTAT	GTGCGCGACC	GCGCGGGCAT	CGATGCCAGG
1201	CTGGGGGGCG	AGTTTCTCGC	AGAAGGCGGT	AAAATCCCCG	GCTCGGATAT
1251	CGATTTTGGC	AACAGCCACG	CCACGATGCT	GACCGCTCTT	TGGAAACCGC
1301	AGCTGCTCAA	CACCGCTGTG	CTACCCGAAA	ACGGCCATTA	CCTCGACGGG

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1351 AAAATCGGTA CGACTTTGGG CGCATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAAACTCG
1451 GCACGTTTAT CATAACGGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCCGA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGACGCCGC
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTCGGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCTT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
  1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
  51 ESVKLPKPKFP VRIDTQDSEI KDMVEEHLPL ITQQEEVLD KEQTGF LAEE
101 APDNVKTMLR SKGYFSSKVS LTKDGAITV HITPGPRTKI ANVGVAI LGD
151 ILS DGNLA EY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLG NTRAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQA L EQNGHYS GAS VQADFDR LQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAIDYDYNL FNKG YIGSVV WMDMDKYETTL
351 AAGISQPRNY RGN YWTSNVS YNRSTQNL E KRAFSGGIWY VRDRAGIDAR
401 LGAEFLA EGR KIPGSDIDL G NSHATMLTAS WKRLN LNV L HPENGHYLDG
451 KIGTTLGAF L SSTALIRTS A RAGYFFTPEN KKLGT FFIIRG QAGYTVARDN
501 ANVP SGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTL SGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSP LA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

m286/a286 98.7% identity in 615 aa overlap

      10      20      30      40      50      60
m286.pep MHDTRTMMIKPTALLLPALFFFP HAYAPAADLSENKAAGFALFKNKSPDTESVKLPKPKFP
|||||
a286      MHDTRTMMIKPTALLLPALFFFP HAYAPAADLSENKAAGFALFKNKSPDTESVKLPKPKFP
      10      20      30      40      50      60

      70      80      90      100     110     120
m286.pep VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGF LAEEAPDNVKTMLRSKGYFSSKVS
| |||||
a286      VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGF LAEEAPDNVKTMLRSKGYFSSKVS
      70      80      90      100     110     120

      130     140     150     160     170     180
m286.pep LTKDGAITVHITPGPRTKIANVGVAILGDILSDGNLA EYRNALENWQQPVGSDFDQDS
|||||
a286      LTKDGAITVHITPGPRTKIANVGVAILGDILSDGNLA EYRNALENWQQPVGSDFDQDS
      130     140     150     160     170     180

      190     200     210     220     230     240
m286.pep WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPD TATADLNVVDSGRPIAFGDFEITGTQR
|||||
a286      WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPD TATADLNVVDSGRPIAFGDFEITGTQR
      190     200     210     220     230     240

      250     260     270     280     290     300
m286.pep YPEQIVSGLARFQPGMPYDL DLLLDFQQA L EQNGHYS GASVQADFDR LQGDRVPVKVSVT
|||||
a286      YPEQIVSGLARFQPGTPYDL DLLLDFQQA L EQNGHYS GASVQADFDR LQGDRVPVKVSVT
      250     260     270     280     290     300

      310     320     330     340     350     360
m286.pep EVKRHKLETGIRLDSEYGLGKIAIDYDYNL FNKG YIGSVVWMDMDKYETTLAAGISQPRNY
|||||
a286      EVKRHKLETGIRLDSEYGLGKIAIDYDYNL FNKG YIGSVVWMDMDKYETTLAAGISQPRNY
      310     320     330     340     350     360

      370     380     390     400     410     420

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670

m286.pep	RGNYWTSNVSYNRSTTQNLKRAFSGGVWYVRDRAGIDARLGAEFLEAGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLKRAFSGGIWYVRDRAGIDARLGAEFLEAGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFTIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286	KKLGTFTIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSFDIAYGH
a286	LVGSLLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTRFX
a286	SDKKIRWHISLGTRFX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

```

1  atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51  ctgtgggggc ggcggtggcg gatcgccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggccgcccc gttgttgctg aaaatgccg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgtag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgccga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaaataaac
501 gttgaccac tgtaaaggcg attcttgtaa tggtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaaagcat ataaaaaaga cgagcaacgg gagaattttg tcggttttgt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatatc atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttcgggcc
751 gagattccgc tgattcccgt caatcaggcc gatacgctga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcgatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttggttg
951 cacggccgtg tacaacggcg aagtgtgca tttccatatg gaaaacggcc
1001 gtccgtacct gtccggaggc aggtttgccc caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaatcc aaagccgcca tcgatgaaa cggttttaag gggacttgga
1151 cggaaaatgg cggcggggat gttccggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccc gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

```

1  MFKRSVIAMA CIFLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV
51  LPKEKKDEEA AGGAPQADTQ DATAGEGSQD MAAVSAENTG NGGAATTDNP
101 KNEDAGAQNQ MPQNAAESAN QTGNNQFAGS SDSAPASNPA PANGGSDFGR

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671

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151  TNVNGSVVID  GPSQNITLTH  CKGDSCNGDN  LLDEEAPSKS  EFEKLSDEEK
201  IKRYKKDEQR  ENFVGLVADR  VKKDGTKNYI  IFYTDKPPTR  SARSRRSLPA
251  EIPLIPVNQA  DTLIVDGEAV  SLTGHSGNIF  APEGNYRYLT  YGAEKLPFGS
301  YALRVQGEPA  KGEMLVGTAV  YNGEVLHFHM  ENGRPYPSGG  RFAAKVDFGS
351  KSVGIIIDSG  DDLHMGTKKF  KAAIDGNGFK  GTWTENGGGD  VSGRFYGPAG
401  EEVAGKYSYR  PTDAEKGGFG  VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1  ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTGT  CCCTTTCAGC
51  CTGCGGGGGC  GGCGGTGGCG  GATCGCCCGA  TGTCAGTCG  GCGGACACGC
101  TGTCAAAACC  TGCCGCCCTT  GTTGTTCCTG  AAAAAGAGAC  AGAGGCCAAG
151  GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201  AGGCAGTCAA  GATATGGCGG  CGGTTCGGGA  AGAAAATACA  GGCAATGGCG
251  GTGCGGTAAC  AGCGGATAAT  CCCAAAATG  AAGACGAGGT  GGCACAAAAT
301  GATATGCCGC  AAAATGCCGC  CGGTACAGAT  AGTTCGACAC  CGAATCACAC
351  CCCGGATCCG  AATATGCTTG  CCGGAAATAT  GGAAAATCAA  GCAACGGATG
401  CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451  GACGGAATGC  AGGGGGACGA  TCCGTCGGCA  GCGGGGCAAA  ATGCCGGCAA
501  TACGGCTGCC  CAAGGTGCAA  ATCAAGCCGG  AAACAATCAA  GCCGCCGGTT
551  CTTTCAGATCC  CATCCCCCGG  TCAAACCTTG  CACCTGCGAA  TGGCGGTAGC
601  AATTTTGGAA  GGGTTGATTT  GGCTAATGGC  GTTTTGATTG  ACGGGCCGTC
651  GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGGCAATA
701  ATTTCCTTGA  TGAAGAAGTA  CAGCTAAAT  CAGAATTTGA  AAAATTAAGT
751  GATGCAGACA  AAATAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAATT
801  TGTTCGGTTT  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851  TTATCTTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901  GCACGGTCGA  GGCGGTGCGT  TCCGGCCGAG  ATGCCGCTGA  TTCCCGTCAA
951  TCAGGCGGAT  ACGCTGATTG  TCGATGGGGA  AGCGGTCAGC  CTGACGGGGC
1001  ATTCGGGCAA  TATCTTCGCG  CCCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051  GGGGCGGAAA  AATTGCCCGG  CGGATCGTAT  GCCCTTCGTG  TTCAAGGCGA
1101  ACCGGCAAAA  GCGGAAATGC  TTGCGGGCGC  GGCCGTGTAC  AACGGCGAAG
1151  TACTGCATTT  CCATACGGAA  AACGCCCGTC  CGTACCCGAC  CAGGGGCAGG
1201  TTTGCCGCAA  AAGTCGATTT  CGGCAGCAAA  TCTGTGGACG  GCATTATCGA
1251  CAGCGGCGAA  GATTGCGATA  TGGGTACGCA  AAAATTCAAA  GCCGCCATCG
1301  ATGGAAACGG  CTTTAAGGGG  ACTTGGACGG  AAAATGGCAG  CGGGGATGTT
1351  TCCGGAAGT  TTTACGGCCC  GGCCGGCGAG  GAAGTGGCGG  GAAAATACAG
1401  CTATCGCCCG  ACAGATGCGG  AAAAGGGCGG  ATTCGGCGTG  TTTGCCGGCA
1451  AAAAAGAGCA  GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1  MFKRSVIAMA  CIFALSACGG  GGGGSPDVKS  ADTLSKPAAP  VVSEKETEAK
51  EDAPQAGSQ  QGAPSAQGSQ  DMAAVSEENT  GNNGAVTADN  PKNEDEVAQN
101  DMPQNAAGTD  SSTPNHTPDP  NMLAGNMENQ  ATDAGESSQP  ANQPDMANAA
151  DGMQGGDDPSA  GGQNAAGTAA  QGANQAGNNQ  AAGSSDPIPA  SNPAPANGGS
201  NFGRVDLANG  VLIDGPSQNI  TLTHCKGDSC  SGNNFLDEEV  QLKSEFEKLS
251  DADKISNYKK  DGKNDKFVGL  VADSVQMKGI  NQYIIFYKPK  PTSFARFERS
301  ARSRRSLPAE  MPLIPVNQAD  TLIVDGEAVS  LTGHSGNIFA  PEGNYRYLTY
351  GAEKLPGGSY  ALRVQGEPAK  GEMLAGAAVY  NGEVLHFHTE  NGRPYPTRGR
401  FAAKVDFGSK  SVDGIIDSGD  DLHMGTKQFK  AADGNGFKG  TWTENGSGDV
451  SGKEYGPAGE  EVAGKYSYRP  TDAEKGGFGV  FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep  MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETEAK
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287       MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA
          10      20      30      40      50      60

```

seq ID 6

672

	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQQGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDQNDMPQNAAGT						
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQNNDMPQNAA--						
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDFNMLAGNMENQATDAGESSQPANQPDMANAADGMQDDPSAGGQNAGNTA						
g287	-----						
	170	180	190	200	210	220	229
m287.pep	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNITLTHCKGDS						
g287	-ESANQTGNNQFAGSSDSAPASNPAPANGGSDFGRTNVGNVSVIDGPSQNITLTHCKGDS						
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP						
g287	CNGDNLLDEEAPSKSEFEKLSDEEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD						
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFAFRFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT						
g287	KPPT-----RSARSRRSLPAEIPVNPQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT						
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGS						
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYR						
g287	KSVDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSGRKYGPAGEEVAGKYSYR						
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKGFGVFAGKKEQDX						
g287	PTDAEKGFGVFAGKKDRDX						
	420	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1203>:

```

a287.seq
1  ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
51  CTGTGGGGGC GCGGTGGCG GATCGCCCGA TGTTAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTTACTG AAGATGTCGG GGAAGAGGTG
151 CTGCCGAAAG AAAAGAAAGA TGAGGAGGCG GTGAGTGGTG CGCCGCAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CCGTCAAGAT ATGGCGGCAG
251 TTTCGGCAGA AAATACAGGC AATGGCGGTG CCGCAACAAC GGATAATCCC
301 GAAAATAAAG ACGAGGGACC GCAAAATGAT ATGCCGCAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGGAAATCGG ACAACCGGCA
451 AACCAACCGG ATATGGCAAA TGCGGCGGAC GGAATGCAGG GGGACGATCC
501 GTCGGCAGGG GAAAATGCCG GCAATACGGC AGATCAAGCT GCAAATCAAG
551 CTGAAAACAA TCAAGTCGGC GGCTCTCAA ATCCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTTGACAGCG GTTCGGAAAA TGTAACGTTG ACACATTGTA
701 AAGACAAAGT ATGCGATAGA GATTTCCTAG ATGAAGAAGC ACCACCAAAA
751 TCAGAATTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA

```


a287.pep

m287/a287 77.2% identity in 501 aa overlap

	10	20	30	40	49
m287.pep	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTL SKPAAPVVSE-----				KETEA
a287	MFKRSVIAMACIVAL SACGGGGGGSPDVKSADTL SKPAAPVVTE				LDVGEEVLPKEKKDEEA
	10	20	30	40	50
	60	70	80	90	100
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN				DMPQNAAGT
a287	VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATT				DNPENKDEGPONDMPQNAADT
	70	80	90	100	110
	110	120	130	140	150
m287.pep	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDPS				SAGGQNAGNTA
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGGDPS				SAG--ENAGNTA
	120	130	140	150	160
	170	180	190	200	210
m287.pep	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDIANGVLIDGPSQNI				TITLTHCKGDS
a287	DQAANQAENNQVGGSQNPASSTNPNATNGGSDFGRI				NAVANGIKLDSGSENVTLTHCKDKV
	180	190	200	210	220
	230	240	250	260	270
m287.pep	CSGNNFLDEEVQLKSEFEKLSADADKISNYKKDGKNDKVFGLVADSVQMK				GINQYIIFYKP
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRV				KEKNGTKNYVIYKD
	240	250	260	270	280
	290	300	310	320	330
m287.pep	KP--TSFARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIF				FAPEGNYRY
a287	KSASSSSARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIF				FAPEGNYRY
	300	310	320	330	340
	350				

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	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVSDGIIDSGDDLHMGTOQFKAAIDGNGFKGTWTENGSGDVSQKFGYPAGEEVAGKYS					
a287	GSKSVSDGIIDSGDDLHMGTOQFKAVIDGNGFKGTWTENGSGDVSQKFGYPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGFGVVFAGKKEQDX					
a287	YRPTDAEKGFGVVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1  atgcacaccg gacaggcggt aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgctcaag caacctaccc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcggtg cgcccttacc gcaccttttc
201 acccttgect gtgctgcaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccggcgg ttaaccggca ttctaccctg
301 cggagcccg gactttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgctg cgcggtattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacagggt tcagacggca tacagcctaa actacacacc
451 ctggttcagg ctggcttcga tgaagccgtc caagtcgccc tccaatacgg
501 ctttggtggt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCPLV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCggTTTTG CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCGG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCPLV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFEVACTQVF					
g288	PCAARIITRNKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFEVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATGCGTTC TGTGTTGCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTC CTTTCTGTTC
251 CACTTTCCTG CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCCGC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFEVACTQVF					


```

g290.seq
  1  atggcaaaaa  tgatgaaatg  ggcgcgtggt  ggcgcggtcg  cgcgcgcgacg
51  gttttggggc  ggatggtctt  atctgaagcg  cgaaccgcag  gctgcttata
101 taccggaagc  ggtcaggcg  ggcgatatca  gccgcagcgt  tccgcgcgacg
151 ggcgagattt  gccgctccaa  cctggtatcg  tgcgcgcgcg  aggcttcggg
201 gcagattaaa  aagctttatg  tcaaactcgc  gcaacacggtc  aaaaagggcg
251 atttgattgc  ggaatcaat  tcgaccacgc  agaccaacac  gatcgatatg
301 gaaaaatcca  aattggaaac  gtatcaggcg  aagctggtgt  gcgcagagat
351 tgcatgtggc  agtcgcgaaa  aaaaatataa  gcgctcaggcg  gcgttgttga
401 aggatgatgc  gacctctaaa  gaagatttgg  aaagcgcgca  ggatgcgctt
451 gccgcgcgca  aagccaatgt  tgccgagttg  aagcgtttaa  tcagacagag
501 caaaatttcc  atcaataccg  ccgagtcgga  tttgggctac  acgcgcatta
551 ccgcgacatc  gcaggcgacg  tgggtggcga  tttccgtgga  agagggcgacg
601 actgtgaacg  cggcgcagtc  tacgccgacg  attgtccaat  tggcgaaatc
651 ggatattgat  ttgaacaaaa  tgcgatttgc  cgagggcgat  attaccaagg
701 tgaaggcggg  cgaggatatt  tcggtttacg  ttttgtccga  accggatacg
751 ccgattaagg  cgaagctcga  cagcgtcgac  cccgcggtga  ccacgatgtc
801 gtcgggcggc  tacaacagca  gtacggatac  ggcttccaat  gcggtctatt
851 attatgcccg  ttcgtttgtg  ccgaatcccg  acgcgcaaact  cgccacgggg
901 atgacgacgc  agaatacgtg  tgaatacgac  ggtgtgaaaa  atgttgttgt
951 tattccgtcg  tcgacctga  aaaaatcgcg  cgcaaggcg  ttcgtacgcg
1001 tgttgggtgc  ggacggcaag  gcagtggaac  gcgaaatccg  gaccggtatg
1051 aaagacagta  tgaataacga  agtgaaaagc  gggttgaaag  agggggacaa
1101 agtggtcata  tccgaaataa  ccgcgcgcga  gcagcaggaa  agcggcgaa
1151 gcqccetaqg  ccqccqccq  ccqccqataa

```

g290.pep

1	<u>MAKMMKWA</u> AV	<u>AAVAAA</u> AVWG	GWSYLKPEPQ	AAYITEAVRR	GDISRTVSAT
51	GEISPSNLVS	VGAQSGAQIK	KLYVKLGQQV	KKGDLIAEIN	STTQTNTIDM
101	EKSKLETYQA	KLVSQAIALG	SAEKYKQRQA	ALWKDDATSK	EDLESQAQDL
151	AAAKANVAEL	KALIRQSKIS	INTAESDLGY	TRITATMDGT	VVAIPVEEGQ
201	TVNAAQSTPT	IVQLANLDM	LNKMQIAEGD	ITKVKAGQDI	SFTILSEPDT
251	PIKAKLDSVD	PGLTMTSSGG	YNSSTDASN	AVYYYARSFV	PNPDGKLATG
301	MTTQNTVEID	GVKNVLLIPS	LTVKNRGGKA	FVRVLGADGK	AVEREIRTM
351	KDSMNTVEKS	GLKEGDKVVI	SEITAAEOOE	SGERALGGPP	RR*

```
m290.seq (partial)
1  ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51  ACTCGGGCAA CAGGTTAAAA AGGCGGATT GATTGCGGAA ATCAATTCTGA
101 CCTCCGAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GGAACACGTA
151 CAGGCGAAGT TGGTGTCCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGCGCT TATGGAAGGA AAACGCGACT TCCAAAAGAG
251 ATTTGGAAAG CGCGCAGGAT GCGTTTGCCG CGCCAAAGCA CATGTTGCC
301 GAGCTGAAGG CTTTAATCAG ACAGAGCAAA ATTTCCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACGCG AACGATGCAC GGCACGGTGG
401 TCGCGATTCT CGTGGGAAGC GGGCAGACTG TGAACGCGCG GCAGTCTACG
451 CCGCAGCATG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
501 GATTGCCGAG GCGGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTCTG
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGGTGA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GCGCGTTTACA ACACGAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTCT TTGTGCGCGA
```


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```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAAAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TGCGCGTGTT GGGTGGCGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

m290.pep (partial)

```

1  ..VSVGAAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
51  QAKLVSAQIA LGSAAEKKYR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSTD TA SNAVYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLI PSLTVKNRGG KAFVRVLGAD GKAAREIRT GMRDSMNTEV
301 KSLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

                                10      20      30
m290.pep                      VSVGAAQASGQIKILYVKLGQVKKGDLIAE
                                |||||
g290      PQAAAYITEAVRRGDISRTVSATGEISPSNLVSVGAAQASGQIKILYVKLGQVKKGDLIAE
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m290.pep      INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAAEKKYRQAALWKENATSKEDLESAQD
                                |||:||||:|
g290      INSTTQNTIDMEKSKLETYQAKLVSAQIALGSAAEKKYRQAALWKDDATSKEDLESAQD
                                90      100     110     120     130     140

                                100     110     120     130     140     150
m290.pep      AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
                                |:|||||
g290      ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAILPVEEGQTVNAAQST
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m290.pep      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
                                |||||
g290      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
                                210     220     230     240     250     260

                                220     230     240     250     260     270
m290.pep      GGYNSSTDASNAVYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
                                |||||
g290      GGYNSSTDASNAVYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
                                270     280     290     300     310     320

                                280     290     300     310     320     330
m290.pep      KAFVRVLGADGKAAREIRTGMRDSMNTEVKSLKEGDKVISEITAAEQQESGERALGG
                                |||||
g290      KAFVRVLGADGKAAREIRTGMKDSMNTEVKSLKEGDKVISEITAAEQQESGERALGG
                                330     340     350     360     370     380

m290.pep      PPRRX
                                ||||
g290      PPRRX
                                390

```


678

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GCGGGCTGTT GCGGCGGTCG CGGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTGAGGCGC GCGGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTTATG TCAAACCTCG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCCTAAA GAAGATTGG AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATT
551 CCGCAACGAT GGACGGCACG GTGGTGGCGA TTCTCGTGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGCGCGC TACAACAGCA GTACGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATCGAC GGTGTGAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTGGGTGTC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWAAV AAVAAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VGAQASGQIK KLYVKLGQV KKGDLIAEIN STSQTNTLNT
101 ESKLETYQA KLVSAQIALG SAEKKYKROA ALWKDDATAK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSSG YNSSTDASN AVYYARSFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTEVKS GLKEGDKVVI SEITAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

```

                                10      20      30
m290.pep                      VSVGAQASGQIKLYVKLGQVKKGDLIAE
                                |||
a290                          PQAAAYITETVRRGDISRTVSATGEISPSNLVSVGAQASGQIKLYVKLGQVKKGDLIAE
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m290.pep                      INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKROAALWKENATSKEDLESAQD
                                |||
a290                          INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKROAALWKDDATAKEDLESAQD
                                90      100     110     120     130     140

                                100     110     120     130     140     150
m290.pep                      AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
                                |:
a290                          ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m290.pep                      PTIVQLANLDMMLNKMQUIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPLTTMSS
                                |||
a290                          PTIVQLANLDMMLNKMQUIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPLTTMSS
                                210     220     230     240     250     260

                                220     230     240     250     260     270
```


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```

m290.pep  GGYNSSTDASNAYYYYARSFVNPDPGKLATGTTQNTVEIDGVKNVLIIPSLTVKNRGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a290      GGYNSSTDASNAYYYYARSFVNPDPGKLATGTTQNTVEIDGVKNVLIIPSLTVKNRGG
          270      280      290      300      310      320

          280      290      300      310      320      330
m290.pep  KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISITAAEQQESGERALGG
          :||||||||||||||||||||||||||||||||||||||||||||||||||||
a290      RAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISITAAEQQESGERALGG
          330      340      350      360      370      380

m290.pep  PPRRX
          ||||
a290      PPRRX
          390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccgga ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaag gcaaatcccc ggtcggcggc agcatctgcg acaatcccg
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacg cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLIAC GQTPVSNANA ESAVKAESAG KVAASLKAR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGEIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRNGNKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHPOKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCGCGCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAGAAA CCTATTCCGC CCAAGATTG AAAGTGTGTA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCGGA TTGTCCGTT
451 TGCAACCGCT TGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCTGCA CCCCAGATGCC GCGCGCAAGG
551 CGCAATCTT ATGGTGTGAG CCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAATTTCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACCGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC

```


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751 CAACTGGAGG AAATCATCCG CAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR
 51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTYSEFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILT	PFTVLPLLAC	GQTPVSNANA	EPAVKAESAG	KSVAAASLKAR	LEKTYSAQDL
g292	MKTKLIKILT	PFTVLPLLAC	GQTPVSNANA	ESAVKAESAG	KSVAAASLKAR	LEKTYSAQDL
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPV	KGIYEVVVSQ	RQIIYTDAEG	GYMFVGELIN	IDTRKNLTEE	RAADLNKIDF
g292	KVLVSSETPV	KGIYEVVVSQ	RQIIYTDAEG	GYMFVGELIN	IDTRKNLTEE	RAADLNKIDF
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIK	EVRGNGKLKV	AVFSDPDCPF	CKRLEHEFEK	MTDVTYSEFM	MPIAGLHPDA
g292	ASLPLDKAIK	EVRGNGKLKV	AVFSDPDCPF	CKRLEHEFEK	MTDVTYSEFM	MPIAGLHPDA
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQ	PDRAKAWTDW	MRKGKFPVGG	SICDNPVAET	TSLGEQFGFN	GTPTLVFPNG
g292	ARKAQILWCQ	PDRAKAWTDW	MRKGKFPVGG	SICDNPVAET	TSLGEQFGFN	GTPTLRLPQR
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMP	QLEEIIRKNQ				
g292	AHPKRLQPD	APGGNHPOK	PAVNPQX			
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATCCGCG CCAAGATTGT AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGCTCTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCTGCA CCCCAGTGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCGGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTTCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC
751 CAACTGGAGG AAATCATCCG CAAAATCAA TAA

```


This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLKR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPAET TSLGEQFGFN GTPTLVFPNG RSQSGYSMP
251  QLEEIIRKNQ *

m292/a292  100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep    MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLKR LEKTYSAQDL
              |||||
a292         MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLKR LEKTYSAQDL
              10      20      30      40      50      60

              70      80      90     100     110     120
m292.pep    KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
              |||||
a292         KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
              70      80      90     100     110     120

              130     140     150     160     170     180
m292.pep    ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
              |||||
a292         ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep    ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPAET TSLGEQFGFN GTPTLVFPNG
              |||||
a292         ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPAET TSLGEQFGFN GTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep    RSQSGYSMP QLEEIIRKNQX
              |||||
a292         RSQSGYSMP QLEEIIRKNQX
              250     260
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggct
 51  gggttcgggt gtcagaacat catcgaaccg ctttcctcgc gcgttacgac
101  gatattcgcc ttttcgacct acaatttttc cgaagcctgc cggcaccgct
151  tggcatcggg tgcggcggtt caagtcgaat cggcggagcg gtggcggtgaa
201  gccgttgaaa aaaccttata tggcgagggg ggcggaatgc agatgcaggc
251  gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgagggcgt gcgggaagcg gtatgcggac atcgggggcg atagtgtatc
351  aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgccg
401  tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcggtg
451  ttttttgaa gctgtggttt gtccgtcctg catacgggac ggggtgtcgcg
501  cgaggcggcg cgcgaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcggtcgga ctgctgttcg ccagggggaa tctagagtgc
601  actgcagcag catgccctc...
  
```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAVSVRA VRTSSNREPA ALRRYSAPRP TIFPKPAGTP
 51  WHRVRFRFSN RRTRGVKPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
101  PRRCGKRYAD IGGDSDTIRI RVERLEHRMS IYAVAHIIHL YCATAFVGGV
151  FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPPFAVG LLFARGTLES
201  TAAACP....
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

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m294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTTCGGGT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCGAC
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
 151 TGGCATCGGG TCGGCGGGT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCCTTGT CGGCGGCGTG
 451 TTTTGAAG TGCTGGTTT GTCCGTCCTG CATACGGGAC GGGTGTCTGG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
 701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC GGTCCGTTGG
 751 TCGAATACA TACAGCCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFFA AFRRYSAFQP TIFPKPADTP
 51 WHRVRRFKSN RMRGGKPLK KPYRPRGGC RCRRRAWTALS HNIAERARES
 101 PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFPFVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVCW
 251 SKYIHAVVET HMLLIVFLAK AMFYISW*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSAAVWSVRAVRTSSNRFFAALRRYSAFRPTIFPKPAGTPWHRVRRFKSN					
m294	MRITCAPMSLLSAAVWSIRVVRTSSNRFFAALRRYSAFRPTIFPKPADTPWHRVRRFKSN					
	10	20	30	40	50	60
g294.pep	70	80	90	100	110	120
m294	RRTRGVKPLKKPYLARGAECRCRRRAWTALSHNIAERARESPRRCGKRYADIGGDSDTIRI					
	70	80	90	100	110	120
g294.pep	130	140	150	160	170	180
m294	RVFRLEHRMSIYAVAHIIHLYCATAFVGGVFFEVLLVLSVLHTGRVSREARREVEKAMSYR					
	130	140	150	160	170	180
g294.pep	190	200				
m294	AVRVMFPFVGLLFARGTLESTAAACP					
	190	200	210	220	230	240
g294.pep	AVRVMFPFVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTTCGGGT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCGAC
 101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
 151 TGGCATCGGG TCGGCGGGT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
 201 GCCGTTGAAA AAACTTATC GTCCGAGGAG GGGCGAATGC AGATGCAGGC
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GGTGGAGTA CCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTGT CGGCGGCGTG
 451 TTTTGAAG TGCTGGTTT GTCCGTCCTG CATACGGGAC GGGTGTCTGG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

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701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAFRP TIFPKPAGTP
 51 WHRVRFRFSN RRTRGGKPLK KTYRPRRAEC RCRRTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMS YRVRMPFVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFMTL TLKILLAFSV LAHFAIAVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRV	VRTSSNRFPAAFRYSAF	OPTIFPKPADT	PWHRVRFRFSN		
a294	MRITCAPMSLLSAAVWSIRV	VRTSSNRFPAAFRYSAF	REPTIFPKPAGT	PWHRVRFRFSN		
	10	20	30	40	50	60
m294.pep	RRMRGGKPLKPYRPRGG	CCRRAWTALSHNIAER	ARESPRRCGKRYAD	IGDDSDTIRI		
a294	RRTRGGKPLKTYRPRRAE	CCRRTALSHNIAER	ARESPRRYGKRYAD	IGDDSDTIRI		
	70	80	90	100	110	120
m294.pep	RVFRLEHRMSIYAVAHIV	HLHYCAIAFVGGVFF	FEVLVLSVLHTGRVS	REARREVEKAMS	YSYR	
a294	RVFRLEYRMSIYAVAHIV	HLHYCAIAFVGGVFF	FEVLVLSVLHTGRVS	CEARREVEKAMS	YSYR	
	130	140	150	160	170	180
m294.pep	AVRVMFVVGGLLFASGIV	MAANRYLSILGEPFAT	SFMTLTLKILLAFSV	LAHFAIAVVK		
a294	AVRVMFVVGGLLFASGIV	MAANRYLSILGEPFAT	SFMTLTLKILLAFSV	LAHFAIAVVK		
	190	200	210	220	230	240
m294.pep	MARSTLTVGWSKYIHAV	VFTHMLLIVFLAKAM	FYISWX			
a294	MARSTLTVGWSKYIHTV	VFTHMLLIVFLAKAM	FYISWX			
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt
 51 gttgccacgc cgccagcagt tttccgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccgca cactgcacg gatgccgcgc ccaatttcgc caaccgcgcc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
 301 acggatcagg cggcggactt tcagataacc gttcagcgat tttccgaca
 351 gccgcgcatt cgccaaaaac agcggcacac ccgtctgcgc gcattccttc
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcgggcg
 451 gtgttcgcgc aaaaactgcc gtaccacgt tttttgtca tacggaagat
 501 agcggcattg cgcacgggga aacagaactt gcgcgggttc ccgtcccgtc
 551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaac gccgcggcaa
 601 ctccggtatc aagggtggg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcgccggtg acgggattcg gatcgggtt gccgaaacgc
 701 tcgtccctat gcgccgggta tgccggggca cttccggagc gtttgtccaa
 751 ataacgcgt atccatatcg gcgcaagcag ccacaatca tcataaagcc
 801 attggaacat cttctattt cctgcaaac aaatgccgtc cgaacgggtc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

684

g295.pep

```

1  MLGMARHDDQ QGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK
51  LPRQRFHVFH RHQVVFGIAA HLHGCRAQFR QPRRIRLRLR QTARQSGCG
101 TDQAAADFQIT VQFFRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIRPLEH LSISCKTNAV RTVRTAFRQR NQIS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

```

1  ATGTCGGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTC TCTGTTCGCA CGGTATGATG TCGTATTGCG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA
351 GCCCGCGATT CGCCAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC
401 ATCAGGTTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTGCGCG AAAAAGTACC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG CGCATCGGGA AACAGAACTT CGCGGTTTC CCGCCCGGTC
551 GGGGTCATCT GCGTCATCAG CAGCGCGGCA TCGGAAAAC GCCCGCGCAA
601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGCTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT GCGCCCGATA TGCCGGGGCA CTTCGGGAGC GTTTGTCCAA
751 ATAACGCGCT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATT CTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGGCAACGG AATCAAATAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep

```

1  MLGMARHDDQ QRIAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK
51  LPRQRFHLFR RYDVVFGIAA HLHGCRAQFR QPRRIRLCLR QTPRQSGGR
101 TDQAAADFQIT VQFFRQPRI RQKQRHTRAP AFPHQVGPDP GFHQNAEHRA
151 VFAQKLPYPR FVIRKIAAL RIGKQNLRGF PPRRGLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRLRL AETLVPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIRPLEH LSISCKTNAV XTQTAFRQR NQIS*

```

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQ	QRIAAILLPR	RQOFFRLVFT	PINARAAAHG	NRPASDAFFK	LPRQRFHLFR
g295	MLGMARHDDQ	QGIAAILLPR	RQOFFRLVFA	PINARAAAHG	NRPASDAFFK	LPRQRFHVFH
	70	80	90	100	110	120
m295.pep	RYDVVFGIAA	HLHGCRAQFR	QPRRIRLCLR	QTPRQSGGRT	TDQAAADFQIT	VQFFRQPRI
g295	RHQVVFGIAA	HLHGCRAQFR	QPRRIRLRLR	QTARQSGCGT	TDQAAADFQIT	VQFFRQPRI
	130	140	150	160	170	180
m295.pep	RQKQRHTRAP	AFPHQVGPDP	GFHQNAEHRA	VFAQKLPYPR	FVIRKIAAL	RIGKQNLRGF
g295	RQKQRHTRSP	AFLHQIGPDF	GFHQNAEHRA	VFAQKLPYPR	FVIRKIAAL	RIGKQNLRGF
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRLRL	AETLVPMRPI
g295	PSRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRMRL	AETLVPMRPV
	250	260	270	280	290	
m295.pep	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIRPLEH	LSISCKTNAV	XTQTAFRQR	NQISX
g295	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIRPLEH	LSISCKTNAV	RTVRTAFRQR	NQIS

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTC TCTGTCCGA CGGCATCAGG TCGTATTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGCGGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTGCGCCG GCATTCTTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTGCGCG AAAAACTGCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGTCATCT GCGTCATCAG CAGCGCGCA TCGGGAAC GCTGCCGCAA
601 CTCGCGTATC AAAGTTGGG CGGCACGCGT TTCCCGAC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCCGAGC GTTTGTCCAA
751 ATAACGCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDO QGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLFR RHQVVFEGIAA HLHGCRAQFR QPERRIRLRLC QTARQSRGGR
101 TDQAADFQIT V*RFFRQPRI RQQRHTRAP AFLHQIGPDF GFHQAETHRA
151 VFAQKLPYPR FFVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLFQ
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
a295	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
a295	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
a295	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
a295	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
a295	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
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51  GCTTGCCGTT TCGATTATTC TGGTGTcgcG GGCATACATT Gcttcgacag
101 agggggaccga gcgcgtcaga ccgcAGCGCG TggaacaaaA ACTGCCGCCG
151 CTGTCTTGGG gcggcaacgy CGTtcagacy gcaTATTGGG TGCAGGAGGC
201 GGTGCagcgy ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgy CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTGG TCGGCGGCCA
351 CGGCAGTGC CGCGAAGTGC AGTTTTttaC CGACGAAGAC GCGGAGCGCA
401 aTctGGTTCG TTTGGAaaaa AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GATGCCGATA TGAAGGTTTT GCCGACACTG CGTTCGGTGC TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701 CAACCCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGCGCGCTT
801 CAACATCGaG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGAGGCA
1051 CAAGGCAATG TCGCGGCGCG CGAGGTCATC GGTTTTGTCC GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GCGCGGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGAGGCG
1201 GACAAGGCGC CGTTTGCCGC GCAGAAACAG AAGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

```

g297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PORVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGSA REVQFFDDED GERNLVALEK KGGIWRRSAS
151 DADMVLPPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHGQOVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYDEDEGRV LQEKGGFNIE PLVYTRISSP FGYYRMPILH TWRLHTGIDY
301 AAPQGTFPVR SADGVITFKG RKGGYGNAMV IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVSGTGRST GPHLHYEARI NGQPVNPNVSV ALPTPELTQA
401 DKAFAFAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

```

m297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTCCGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGAACAAAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGCACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCAGCGAAA AATATGCGCG CGAAGCCGAT
301 TTGCGGCATT TCGGTGCCGA CCAGTCGGTT CATGTTTGG TCGGCGGCCA
351 CGCGCGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GCGGAGCGCA
401 ATCTGGTTCG TTTGGAaaaA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTGC TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGCGCGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGAGGCG
1051 GAAGGCAATG TCGCGGCGCG CGAGGTCATC GGTTTTGTCC GTTCGACCGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GCGCGGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGAGGCG
1201 GACAAGGCGC CGTTTGCCGC GCAGAAACAG AAGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

```

m297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV PORVEQNLP
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGA REVQFFDDED GERNLVALEK KGGIWRRSAS
151 EADMVLPPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

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201 EGDVRLMYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
 251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTTPVRA SADGVITFKG RGGYGNVAVM IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSII	ILVSAAYIASTERT	VRPQ	RVNQ	LPPLSWGGSGVQT	
g297	MAVFPLSAKHKYALRALAVSII	ILVSAAYIASTEGT	VRPQ	RVNQ	LPPLSWGGNGVQT	
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEA	VPQDGLADVLARSGMARDEI	ARITEKYGGEADLRHLRADQSVHVLVGGDGGA			
g297	AYWVQEA	VPQDGLADVLARSGMARDEI	ARITEKYGGEADLRHLRADQSVHVLVGGDGSA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTDE	DGERNLVALEKKGGIWRRSASEADM	KVLP	TLRSVVVKTSARGSLARA	EVFPV	
g297	REVQFFTDE	DGERNLVALEKKGGIWRRSASDADM	KVLP	TLRSVVVKTSARGSLARA	EVFPV	
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIF	AGRFSLDGLKEGDAVRLMYDSLYFHGQQA	AGDILAAEVVKGGTRHQAFY			
g297	EIRESLSGIF	AGRFSLDGLKEGDAVRLLYDSLYFHGQQA	AGDILAAEVVKGGTTHQAFY			
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGNYDE	DGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY				
g297	YRSDKEGGGGNYDE	DGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY				
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRA	SADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI				
g297	AAPQGTTPVRA	SADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAQGNVRGGEVI				
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPVSV	ALPTPELTQADKAFAAQKQKADALLARLR				
g297	GFVGSTGRSTGPHLHYEARINGQPVNPVSV	ALPTPELTQADKAFAAQKQKADALLARLR				
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1	ATGGCTGTCT	TCCCACTTTC	GGCAAAACAT	CGGAAATACG	CGCTGCGCGC
51	GCTTGCCGTT	TCGATTATTT	TGGTGTCCGC	GGCATAACAT	GCTTCGACAG
101	AGAGGACGGA	GCGCGTCAGA	CCGACGCGCG	TGGAACAAAA	ACTGCCGCCG
151	CTGTCTTGGG	GCGGCAGCGG	TGTTCAAGCG	GCATATTGGG	TGCAGGAGGC
201	GGTGCAGCCA	GGCGACTCGC	TGGCGGACGT	GCTGGCGCGT	TCGGGTATGG
251	CGCGGGACGA	AATTGCCCGA	ATAACGGAAA	AATATGGCGG	CGAAGCCGAT
301	TTGCGGCATT	TGCGTGCCGA	CCAGTCGGTT	CATGTTTTGG	TCGGCGGCGA
351	CGCGCGCGCG	CGCGAAGTGC	AGTTTTTTAC	CGACGAAGAC	GGCGAGCGCA
401	ATCTGGTCCG	TTTGGAAAAA	AAAGGCGGCA	TATGGCGGCG	GTCGGCTTCT
451	GAGGCGGATA	TGAAGGTTTT	GCCGACGCTG	CGTTCGGTCG	TGGTCAAAAC
501	GTCGGCGCGC	GTTTCGCTGG	CGCGGGCGGA	AGTGCCCGTC	GAAATTCGCG

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551 AATCCTTAAG CGGGATTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGCGGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTACGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TCGCGGCGCG CGAGGTCATC GGTTTGTGCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GGC GCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCGAATT GACGCAGGCG
1201 GACAAGCGCG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

a297.pep

```

1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV RQRVEQKLPP
51 LSWGGSGVQT AYWVQEA VQP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGD GGA REVQFFTD ED GERNLVALEK KGGIWRRSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEV PV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQ QVA AGDILAAEV V KGGTRHQAFY YRSDKEGGGG
251 GNYDEDEGRV LQEKGGFN IE PLVYTRISS P FG YRMHPILH TWRLHTGIDY
301 AAPQGT PVRASADGVIT FKG RGGYGNVAV M IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGR ST GPHLHYEAR I NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKH RKYALRALAVSIILVSAAYIASTERTERV RQRVEQNL PPLSWGGSGVQT					
a297	MAVFPLSAKH RKYALRALAVSIILVSAAYIASTERTERV RQRVEQKL PPLSWGGSGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEA VQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGD GGA					
a297	AYWVQEA VQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGD GGA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTD EDGERNLVALEK KGGIWRRSASEADMKVLP TLRSVVVKTSARGSLARAEV PV					
a297	REVQFFTD EDGERNLVALEK KGGIWRRSASEADMKVLP TLRSVVVKTSARGSLARAEV PV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSL YFHGQQAAGDILAAEVVKGGTRHQAFY					
a297	EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSL YFHGQQAAGDILAAEVVKGGTRHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGGNYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
a297	YRSDKEGGGGGNYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGT PVRASADGVIT FKG RGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
a297	AAPQGT PVRASADGVIT FKG RGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m297. pep	GFVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297. pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298. seq

1	ATGAAAACT	TTCTTCCCT	TTTCGCCTCC	ATACTGATGT	CTGCCCTGAT
51	TGCCGTGTGG	TTCAGCCAAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT
101	ACCACCGCAA	CAGCCCGCTC	GAACCGCTTG	CCGCCTACGG	ATGGTGGCGG
151	AGCGGAGCGG	CGTTGCAAGA	AAACGCCTAC	GCCCTTTCAG	ACGGCATCAA
201	AACCTTCTTG	TCCGGCGAAA	cgccccccac	ggCTCAAGAC	GGCGGTTCCG
251	CAGATATGCC	GCCTGAAGCC	GCCGCATCCG	AAGCCGCCCC	GCCGGCCGGC
301	GGAAACAGAT	GGAAACAAGG	CACCGAAGCC	GCCGCCGTCC	GCAGCGGCGA
351	CAAGTCTTTT	TTCCGCGGAG	ATTCGCTGAT	GCAGGCGGTT	GCGCCTTTCG
401	TGCAAAAAAG	CCTGAAACAG	CAATACGGCA	TGGAATCCGC	CAACCTCAGC
451	AAACAAAGCA	CGGGGCTTTC	CTATCCCTCA	TTCTTCGACT	GGCCGAAAAC
501	GATTGAAGAA	ACCTTGAAAA	AACATCCCGA	AATCAGCGTA	CTCGCCGTCT
551	TCCTCGGCC	GAAACGACCG	TGGGATTTCC	CCGTGCGCAA	ACGCTACCTC
601	AAATTCGCTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GCGTCGACCG
651	CATCCTTGAA	GCCGCACACA	CGCACCGCGT	CCAAGTCGTC	TGGCTCGGCA
701	TCCCCTACAT	GAAAAAAGTC	AAGCTCGACG	GTCAGATGCG	CTACCTCGAC
751	AAACTGCTTT	CGGAACACTT	GAAAGGCAAA	ATCATCCTGA	TTCCACCCG
801	GCAACACTG	AGCGGCGGGA	AAGgccGCTA	CACCGATTCC	GTCAACGTCA
851	ACGGCAAAAC	CGTCCGCTAC	CGCAGTAAGG	ACGGCATACA	CTTTACCGCC
901	GAAGGACAAA	AACTGCTGGC	GGAAAAATA	ATGGAATAAA	TCGTTTTTGA
951	ACCGAGTACG	CAACCATCAA	GTACACAGCC	ATGA	

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298. pep

1	MKNFLSLFAS	ILMSALIAVW	FSQNPINAYW	QQTYHRNSPL	EPLAAYGWWR
51	SGAALQENAY	ALSDGIKTFL	SGETPPTAQD	GGSDMPPPEA	AASEAAPPAG
101	GTEWKQTEA	AAVRSGDKVP	FAGDSLMOGV	APFVQKSLKQ	QYGI SANLS
151	KQSTGLSYPS	FFDWPKTIEE	TLKKHPEISV	LAVFLGPNDP	WDFPVGKRYL
201	KFASDEWAQE	YLKRVDRILE	AAHTRVQVW	WLGIPYMKKV	KLDGQMRYLD
251	KLLSEHLKKG	IILIPTAQL	SGGKGRYDTS	VNVNGKPVRY	RSKDGIFHTA
301	EGQKLLAEKI	MEKIVFEPST	QPSSTQP*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298. seq

1	ATGAAAACT	TTCTTCCCT	TTTCTCCTCC	ATACTGATGT	CTGCCCTGAT
51	TGCCGTGTGG	TTCAGCCAAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT
101	ACCACCGCAA	CAGCCCGCTC	GAACCGCTTG	CCGCCTACGG	ATGGTGGCGG
151	AGCGGTGCGG	CGTTGCAAGA	AAACGCCTAC	GCCCTTTCAG	ACGGCATCAA
201	AGCCTTCTTG	TCCGGCGAAA	CGCCGCCGAC	GGCTCAAGAC	GGCGGTTCCG
251	CAGATATGCC	GTCTGAAGCC	GCCGCATCCG	AAGCCGTCCC	TCAAAACCGGT
301	GAAACAGAT	GGAAACAAGA	CACCGAAGCC	GCCGCCGTCC	GCAGCGGCGA
351	CAAGTCTTTT	TTTGTGCGCG	ACTCGCTGAT	GCAGGCGGTT	GCCCCCTTCG
401	TGCAAAAAAG	CCTGAAACAG	CAATACGGCA	TGGAATCCGT	CAACCTCAGC
451	AAACAAAGCA	CGGGGCTGTC	CTACCCCTCA	TTCTTCGACT	GGCCGAAAAC
501	GATTGAAGAA	ACCCTGCAAA	AACATCCCGA	AATCAGCGTA	CTCGCCGTCT
551	TCCTCGGACC	GAAACGACCG	TGGGATTTCC	CCGTGCGCAA	ACTCTATCTC
601	AAATTCGCTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GTGTCGACCG
651	CATCCTTGAA	GCCGCACACA	CGCACCGCGT	CCAAGTCGTC	TGGCTCGGCA
701	TCCCCTACAT	GAAAAAAGCC	AAGCTCGACG	GACAGATGCG	CTACCTAGAC
751	AAACTGCTTT	CGGAACATTT	GAAAGGCAAA	ATCATCCTGA	TTCCACCCAC
801	GCACACCTG	AGCGGCGGGA	AAGACCGCTA	CACCGACTCC	GTCAACGTCA
851	ACGGCAAAAC	CGTCCGCTAC	CGCAGCAAGG	ACGGCATACA	CTTTACCGCC
901	GAAGGACAAA	AACTGCTGGC	GGCAAAAATA	ATGGAATAAA	TCGTTTTTGA
951	ACCAAGTACG	CAACCATCAA	GTACACAGCC	ATGA	

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep

```

1 MKNFLSLFSS ILMSALIAVW FSONPINAYW QQTYHRNSPL EPLAAYGWWR
51 SGAALQENAY ALSDGIKAPL SGETPPTAQD GGSADMPSEA AASEAVPQTG
101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS PFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
201 KFASDEWAQE YLKRVDRIE AAHTRVQVV WLGIPLYMKA KLDGQMRYLD
251 KLLSEHLKGK IILIPTHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
m298.pep	ALSDGIKAPLSGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKIFLSGETPPTAQDGGSDMPPEAAASEAAPAGGTEWKQGTAAAVRSGDKVF					
	70	80	90	100	110	120
m298.pep	FVGDSLMOGVAPFVQKSLKQYQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQYQYIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
m298.pep	LAVFLGPNDFWDFPVGKLYLKFADEWAQEYLKRVDRILEAAHTRVQVVWLGIPLYMKA					
g298	LAVFLGPNDFWDFPVGKRYLKFADEWAQEYLKRVDRILEAAHTRVQVVWLGIPLYMKV					
	190	200	210	220	230	240
m298.pep	KLDGQMRYLDKLLSEHLKGKIILIPTHTLSSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
g298	KLDGQMRYLDKLLSEHLKGKIILIPTAQTLSSGGKGRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq

```

1 ATGAAAAACT TTCTTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGTCAAGAC GCGGTTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAAGTGGC
301 GAAACAGAAT GGAAACAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
351 CAAAGTCTTT TTCGCCGCG ACTCGCTGAT GCAGGGCGTT GCACCCCTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGAAAA AACATCCGA AATCAGCGTG CTCGCCGTCT
551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTGAA GCGCACACA CGCACTACG CCAAGTCGT TGGCTCGGCA
701 TCCCCTACAT GAAAAAGCC AAGCTCGAC GACAGATGCG CTACCTAGAC

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751  AAACTGCTTT CGGAATATTT GAAAGGCAAA ATCATCTCTGA TTCCCACCGC
801  GCACACCCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851  ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901  GAAGGACAAA AACTGCTGGC GGCAAAATA ATGGAAAAA TCGTTTTTGA
951  ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
  1  MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
 51  SGAALQENAY ALSDGIKAEF SGETPPTAQD GGSADMPSEA AAPETAPQTG
101  ETEWKQNTAE AAVRTGDKVF FAGDSLMQGV APFVQKSLKQ QYGIESVNLS
151  KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201  KFASDEWAE YLKRVDRIE AAHTHYQVV WLGIPLYMKA KLDGQMYLD
251  KLLSEYLGK IILPTAHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
301  EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAEFLSGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAEFLSGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTAEAAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMQGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMQGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWDFPVGKLYLKFADEWAEYLRVDRILEAAHTRVQVVWLGIPLYMKA					
a298	LAVFLGPNDPWDFPVGKRYLKFADEWAEYLRVDRILEAAHTHYQVVWLGIPLYMKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMYLDKLLSEHLKGKIIILPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
a298	KLDGQMYLDKLLSEYLGKIIILPTAHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
  1  ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CCGCCACGCA
 51  GGCAGAAGCC CTGCCCCTCG CCTCCGTCAG CCCCGACACC GTTACCGTTT
101  CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151  AACGCCGCG CCTCGCCTTG GATGAAAAA CTCCGATCCG TCGCACAAGG
201  CAGCGGCGAG GCCTTCCGCA TCCTGCAAAT CGGCGACTCG CATACGCGC
251  GCGACTTCTT TACCGACGCC CTGCGCAAAC GCCTGCAAAA AACATGGGGC
301  GACGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351  GCGCGCGGTC CGTCACAGCG GCAACTGGCA AAGCTTCACC AGCAGGAACA
401  ATACCGGAGA TTTCCCGCTC GCGCGCATCC TCGCCCAAAC CGGCAGCGGC
451  GCGCGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

```


g299.pep

m299.seq

m299.pep

m299/g299 95.5% identity in 397 aa overlap

m299.pep MNPKHLIAFSALFAATQAEALPVASVSLDTVTVPSPAPYTDITNGLLTYGNASASPWMKK
| | | : | | | | | | | | | | | | | | | | | | | | | | : |

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g299	MNPKHFIAFSALFAATQAEALPVASVSPDVTVTSPSAPYTTDNGLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299.pep	LQSV AQSGSETFRILQIGDSHTAGDFFTD SLRKRLQKTWGDGGIGWVYPANVKGQRM AAV
	70 80 90 100 110 120
g299	LRSAVQSGSEAFRILQIGDSHTAGDFFTDALRKRLQKTWGDGGIGWVYPANVKGQRM AAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNTGDFPLGGI LAHTGSGGSMILTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFSTRNTGDFPLGGI LAQTGSGGSMILTASDGTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAALPLTITHEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGWQVLDTGAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDLSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDLSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNYTLGVCGTRFPVRLTEVQQMORRVARQGQTMFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKNYTLGVCGTRPVLLTEVQQMORRVARQGQTMFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVHFSAGYRRAEMLADSL EELVRSAAIRQX
	370 380 390
g299	GWAAKDGVHFSAGYRRAEMLADSL EELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

```

a299.seq
1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCC CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAA CTCCAATCCG TCGCACAAAG
201 CAGCGGCGAG ACCTTCGTA TCCTGCAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GCGCGCCGTC CGGCACAACG GTAAC TGGA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTGCTC GCGGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGCGGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGCGGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC
1051 GTTTCGAGCA TGAAAACTG GCTCAACCAC GGATGGGCCG CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCC
1151 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

```


This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101  DGGIGWVYPA NVKGQRM AAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151  GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG
351  VCSMKNWLNH GWAAKDGVHF SAKGYQRS AE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

```

      10      20      30      40      50      60
m299.pep  MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a299      MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
          10      20      30      40      50      60

      70      80      90     100     110     120
m299.pep  LQSV AQSGE TFRILQIGDSHTAGDFFTDSLRRKRLQKTWGDGGIGWVYPANVKQRM AAV
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a299      LQSV AQSGE TFRILQIGDSHTAGDFFTDSLRRKRLQKTWGDGGIGWVYPANVKQRM AAV
          70      80      90     100     110     120

      130     140     150     160     170     180
m299.pep  RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a299      RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
          130     140     150     160     170     180

      190     200     210     220     230     240
m299.pep  TVNGNTVSANGGGWQVLDTG AALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a299      TVNGNTVSANGGGWQVLDTG AALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
          190     200     210     220     230     240

      250     260     270     280     290     300
m299.pep  QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
          ||||||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||
a299      QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIDIADTEQKWLDTVRQIRDSLPAAGI
          250     260     270     280     290     300

      310     320     330     340     350     360
m299.pep  LIIGAPESLKNTLGVCGRPVRLETVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
          ||||||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||
a299      LIIGAPESLKNTLGVCGRPVRLETVQQMQRRIARQGQTMFWSWQNAMGGVCSMKNWLNH
          310     320     330     340     350     360

      370     380     390
m299.pep  GWAAKDGVHFS AKGYRRAAEMLADSLEELVRSAAIRQX
          |||||||||||||||:|||||:|||||:|||||
a299      GWAAKDGVHFS AKGYQRS AEMLADSLEELVRSAAIRQX
          370     380     390
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGTTGGGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCGTGT GGAACGGTG TTGTTTCTT TATTGGGCGT
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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCGGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGGCATFCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTTC CCGTTTAA AATCGATTGT TGTTTTATT TTCTTGTTGT
1001 TTGCGCTGCC GGGCATTGTT TATGGCCGGA TAACCCGAAG TTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTGGTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGCGCGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTAA TTTAAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGCGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTCTCTCT TAATTGCATG GATCGCCTTA TTCTGCATTT GGGTATTGTG
1551 TTTGGGTCG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1  MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTG LVSLLVGIA EKSGLISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPOLGPYQ SDLSQEBKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGAFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAO WAVTAPIFVP MMLAGYAPQ
451 VIQAAYRIGD SVTNIITPM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 APFLIAWIAL FCIWVFLGL PVGPGTPTFY PVP*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATATTTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTGTTGTCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCGGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCTG
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGT ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAAATCAGC CTTTGGGAAT ATAAAGGATT AATTGGGGCT GCGGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGGG GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGTT TCCGGTTCGC CGTTTATAAA
951 ATCGATTGTT GTTTTATTTT TCTGTTGTT TGCATGyCG GGCmTTGTTT
1001 ATGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

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1051 ATGGCCGAAT CGATGAGTAC TCTGGGCTT TmTTTGswCA kcATCTTTTT
 1101 TGCCGCACAG TTTGTGCGAT TTTTAAATTG GACGAATATT GGGCAATATA
 1151 TTGCCGTTAA AGGGGCGACG TTCTTAAAG AAGTCGGCTT GGGCGGCAGC
 1201 GTGTTGTTTA TCGGTTTTAT TTTAATTTGT GCTTTTATCA ATCTGATGAT
 1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TGCGCCGATT TCGTCCCTA
 1301 TGCTGATGTT GGCCGGCTAC GCGCCGAAG TCATTCAAGC CGCTTACCGC
 1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTCGG
 1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GCGGTGGGTA
 1451 CGCTGATTTT TATGATGTTG CCGTATTCG CTTTCTCTT GATTGCGTGG
 1501 ATTGCCTTAT TCTGCATTG GGTATTTGTT TTGGGCCTGC CCGTCGGTCC
 1551 CCGCGCGCCC ACATTCTATC CCGCACCTTA A

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

1 MHSIYFFKEK QMSQTDQTD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
 51 ASAVGAYFGL SVPDRPVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
 101 FTGFAPLGTV LVSLLGVGIA EKSLGISALM RLLLTSPRK LTTFMVFTG
 151 ILSNTASELG YVVLPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
 201 STIDPLLACI THQAAVVGPE ANWFFMFAST FVIALIGYFV TEKIVEPQLG
 251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVFVALSAL LAWSIVPADG
 301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
 351 MABSMSTLXL XLXXIFFAAQ FVAFNWTNI GQYIAVKGAT FLKEVGLGGS
 401 VLFIGFILIC AFINLMIGSA SAQWAVTAPI FVPMMLAGY APEVIQAAYR
 451 IGDVSTNIIT PMMSYFGLIM ATVIKYKKDA GVGTLISMML PYSAFFLIAW
 501 IALFCIWVVFV LGLPVGPGAP TFYPAP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from *N. gonorrhoeae*:

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
	:::					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDRPVGA KGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
	:::					
g302	SVPDRPVGA KGRADDGLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSLGISALMRLLLTSPRKLTTFMVVFTGILSNTASELGYVVLPLSAIIFHSLGRHPL					
	:::					
g302	EKSLGISALMRLLLTSPRKLTTFMVVFTGILSNTASELGYVVLPLSAVIFHSLGRHPL					
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMFASTFVI					
	:::					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFMAASTFVI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVALSALLAW					
g302	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

m302.pep
SIVPADGILRHPETGLVSGSPFLKSIVVFIFFLLFALGXVYGRVTRSLRGEQEVVNAMAE
|||:|||||:|||||:|||||
g302
SIVPADGILRHPETGLVAGSPFLKSIVVFIFFLLFALPGVYGRITRSLRGEREVVNAMAE
310 320 330 340 350 360

m302.pep
360 370 380 390 400 410
SMSTLXLXLXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGILICAFI
|||||:|||||:|||||:|||||
g302
SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAFLKEVGLGGSVLFIFIGILICAFI
370 380 390 400 410 420

m302.pep
420 430 440 450 460 470
NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
|||||:|||||:|||||:|||||
g302
NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIQAAYRIGDSVTNIITPMMSYFGLIMATV
430 440 450 460 470 480

m302.pep
480 490 500 510 520
IKYKKGAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFFYPAPX
|||||:|||||:|||||:|||||
g302
IKYKKGAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGTPTFFYPVPX
490 500 510 520 530

a302.seq

1	ATGCACTCAA	TATATTTTTT	TAAGGAGAAG	CAGATGAGTC	AAACCGATAC
51	GCAACGGGAC	GGACGATTTT	TACGCACAGT	CGAATGGCTG	GGCAATATGT
101	TGCCCGCACCC	GGTACGCTT	TTTATTATTT	TCATTGTGTT	ATTGCTGATT
151	GCCTCTGCCG	CGGTCGCTA	TTTCGGACTA	TCCGTCCCCG	ATCCGCGCCC
201	TGTTGGTGCG	AAAGGACGTG	CCGATGACGG	TTTGATTACG	GTGTGCAGCC
251	TGCTCGATGC	TGACGGTTTG	ATCAAAATCC	TGACGCATAC	CGTTAAAAAT
301	TTCAACGGTT	TCGCGCGGTT	GGGAACGGTG	TTGGTTTCTT	TATTGGGCGT
351	GGGAGTTGCG	GAAAAATCGG	GCTTGATTTC	CGCATTAATG	CGCTTATTGC
401	TCACAAAATC	TCCACGCAAA	CTCACTACTT	TTATGTTGTG	TTTACAGAGG
451	ATTTTATCTA	ATACCGCTTC	TGAATTGGGC	TATGTCGTCC	TAATCCCTTT
501	GTCCGGCCAT	ATCTTTTCAT	CCCTCGGCCG	CCATCGGCTT	GCCGGTCTGG
551	CTGCGGCTTT	CGCCGGCGTT	TCGGGCGGTT	ATTCCGCCAA	TCTGTTCTTA
601	GGCAACATCG	ATCCGCTCTT	GGCAGGCATC	ACCCAACAGG	CGCGCGAAAT
651	CATCCATCCC	GACTACGTCG	TAGGCCCTGA	AGCCAACCTG	TTTTTTATGG
701	TAGCCAGTAC	GTTTGTGATT	GCTTTGATCG	GTTATTTTGT	TACTGAAAAA
751	ATCGTCGAAC	CGCAATTGGG	CCCTTATCAA	TCAGATTTGT	CACAAGAAGA
801	AAAAGACATT	CGACATTCCA	ATGAATACAC	GCCTTTGGAA	TATAAAGGAT
851	TAATTTGGGC	TGGCGTGGTG	TTTGTGTGCT	TATCCGCCCT	ATTGGCTTGG
901	AGCATCGTCC	CTGCCGACGG	TATTTTGCGT	CATCCTGAAA	CAGGATTTGT
951	TTCCGGTTTC	CGGTTTTTAA	AATCAATTGT	TGTTTTTTAT	TTCTTGTGTT
1001	TTGCATCGCC	CGGCATTGTT	TATGGCCGGG	TAACCCGAAG	TTTGCGCGCG
1051	GAACAGGAAG	TCGTTAATGC	GATGGCCGAA	TCGATGAGTA	CTCTGGGGCT
1101	TTATTTGGTC	ATCATCTTTT	TTGCCGCACA	GTTTGTGCGA	TTTTTTAATT
1151	GGACGAATAT	TGGGCAATAT	ATTGCGCTTA	AAGGGCGCGAC	GTTCTTAAAA
1201	GAAGTCGGCT	TGGGGCGCAG	CGTGTGTGTT	ATCGGTTTTA	TTTTAATTGT
1251	TGCTTTTATC	AATCTGATGA	TAGGCTCCGC	CTCCGCGCAA	TGGGCGGTAA
1301	CTGCGCGCAT	TTTCGTCCCT	ATGCTGATGT	TGGCCGGCTA	CGCGCCCGAA
1351	GTCATTCAAG	CCGCTTACCG	CATCGGTGAT	TCCGTTACCA	ATATTATTAC
1401	GCCGATTGATG	AGTTATTTCG	GCTGTATTAT	GGCAGCGGTG	ATCAAATACA
1451	AAAAAGATGC	GGGCGTGGGT	ACGCTGATTT	CTATGATGTT	GCCGTATTCC
1501	GCTTTCTTCT	TGATTGCGTG	GATTGCCTTA	TTCTGCATTT	GGGTATTGTT
1551	TTTGGGCGCT	CCCGTCGGTC	CCGGTCGGCC	CACATTCTAT	CCCGACCTTT
1601	AA				

a302.pep

1 MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGLV LVSLLGVGIA EKSGLISALM RLLTTSKPRK LTTEMVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MMLAGYAPE
451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

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m302/a302 96.1% identity in 533 aa overlap

m302.pep	10	20	30	40	50	60
	MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNNMLPHPVTLFIIIFIVLLLIASAVGAYFGL					
a302	MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNNMLPHPVTLFIIIFIVLLLIASAAGAYFGL					
	10	20	30	40	50	60
m302.pep	70	80	90	100	110	120
	SVPDPRPVGAKGRADDGLIYVSLNADGFIKILTHTVKNFTGFAPLGTVLVSLGVGIA					
a302	SVPDPRPVGAKGRADDGLIHVVSLDADGLIKILTHTVKNFTGFAPLGTVLVSLGVGIA					
	70	80	90	100	110	120
m302.pep	130	140	150	160	170	180
	EKSGLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL					
a302	EKSGLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL					
	130	140	150	160	170	180
m302.pep	190	200	210	220	230	
	AGLAAAFAGVSGGYSANLFLSTIDPLLAGITQQAQIIHPDYVVGPEANWFFMVASTFVI					
a302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAQIIHPDYVVGPEANWFFMVASTFVI					
	190	200	210	220	230	240
m302.pep	240	250	260	270	280	290
	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFFVALSALLAW					
a302	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFFVALSALLAW					
	250	260	270	280	290	300
m302.pep	300	310	320	330	340	350
	SIVPADGILRHPETGLVSGSPFLKSIVVFIFFLLFALXGXVYGRVTRSLRGEQEVVNAMAE					
a302	SIVPADGILRHPETGLVSGSPFLKSIVVFIFFLLFALPGIVYGRVTRSLRGEQEVVNAMAE					
	310	320	330	340	350	360
m302.pep	360	370	380	390	400	410
	SMSTLXLXLIFFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI					
a302	SMSTLGLYLVIIFFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI					
	370	380	390	400	410	420
m302.pep	420	430	440	450	460	470
	NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV					
a302	NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV					
	430	440	450	460	470	480
m302.pep	480	490	500	510	520	
	IKYKKGAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX					
a302	IKYKKGAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

699

g305.seq
 1 ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
 101 GCAATCTGAT TGGTTTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
 151 CAGCTCGGTG CGGTTTTTGGC GGTAGTGTGTT GAATACCGGC AGCGTTTCAG
 201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
 251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTTC
 301 GACAAACAAA TCAAAGAGTA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
 351 GCTGGTTTTG GCGGTTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
 451 TTGATGATCG GTGTTGCCCA AGTGTGTTGCA CTGGTTCGG GTACGTCCCG
 501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
 551 CGGCAACGGA GTTTTCATTT TTCTTGCCG TTCCGATGAT GGTTCAGCA
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
 651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTGTTTCC GGTTCGTAG
 701 CGGTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT
 751 GCCTATTACC GCATTGTTT CGGCATTGTC ATCATAATAT TGTGGTTGTC
 801 GGGCTGGATA AGTTGGGAAT GA

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
 51 QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLAIAP IPAAVMGLLF
 101 DKQIKIYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
 151 LMIGVAQVFA LVPGTSRSGS TVMGMLWGI ERKTATEFSF FLAVPMMVAA
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
 251 AYYRIVFGIV IILWLSGWI SWE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)
 1 AtGGATT TTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
 101 GCAATCTGAT TGGTTTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
 151 CAGCTCGGTG CAGTTTTTGGC GGTAGTGTGTT GAATACCGGC AACGTTTCAG
 201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
 251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTTC
 301 GGCAWACAAA TCAAAGAGyA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
 351 GCTGGTtyTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
 451 TTGATGATCG GCGTTGCCCA AGTGTGTTGCA CTGGTTCGG GTACGTCCCG
 501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCAGT GAACGGAAAA
 551 CTGCGACAGA ATTCTCGTTT TTCTTGCTG TGCCGATGAT GGTTCGCCGA
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
 651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTGTTTCA GGCTTGGTAG
 701 CCGTAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
 51 QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLAIAP IPAAVMGLLF
 101 GXQIKEXLFN PLSVAVMLVL XGFILWVEK RQSRAPKIA DVDALRPIDA
 151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60

700

	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
m305	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKRSRAEPKIADVDPIDALMIGVAQVFALVPGTSRSGSTVMGMLWGI					
m305	XGFXILWVEKRSRAEPKIADVDPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFPLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
m305	ERKTATEFSFPLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1  ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCC
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CCGTTTGGC GGTAGTGTTC GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCAAACAAA TCAAAGAGTA TCTGTTTAA CCGTTGAGTG TGCAGTCAT
351 GCTGGTTTTG GGCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTTGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCCA AGTGTTCGCA CTGGTTCCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGGCCG TTCCGATGAT GGTTCGAGCA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTTCA GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAI AFIPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFFTLHDVGLI LIGFVAAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHNKVFIEIAIQLGAVLAVVF					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHNKVFIEITIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
a305	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGQIKEYLFNPLSVAVMLVL					

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	70	80	90	100	110	120
m305.pep	130	140	150	160	170	180
	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
a305	130	140	150	160	170	180
	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
m305.pep	190	200	210	220	230	240
	ERKTATEFSFFLAVPMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	190	200	210	220	230	240
	ERKTATEFSFFLAVPMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
m305.pep	FVSG					
a305	250	260	270			
	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

g306.seq

```

1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCCGTTTG  ATACTGGCAA  CGGTCAATAT  TGCCGGTATT  TTGCTTTATC
101  TGAACCAAGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151  CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201  CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251  AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301  GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351  AGAGCCGAC  GGACAGGCAG  TCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401  AACAAACCGT  CAGGGAAGAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451  AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAGA
501  AGAGAAAAAG  GCGGCGAAAG  AAAAAAGTGC  ACCCAAACCG  ACCCGGAAC
551  AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601  GAAGTGCGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651  CTGCAATGG  GCGCGTATGC  CGAACCCCG  AGCGCGGAAG  GGCAGCGTGC
701  CAAACTGGCA  ATCTTGGGCA  TATCTCCGA  AGTGGTCGGC  TATCAGGCGG
751  GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801  GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

g306.pep

```

1  MFMNKFQSG  KGLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101  ADKADEVBE  AGEPEBEPD  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151  KKA VKPSKET  EKKASKEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201  EVQKMNFG  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251  DIKRFTACK  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

m306.seq (partial)

```

1  ..GGTTGTCT  TCGGTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAATC  CCGGCTTCGT
101  CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGmAwAA  CCAGCyTAAG
151  GAAGACATCC  AACCTGAWCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201  TGCTGCGACA  GAGGCGAGC  AGTCGGATGC  GGAAAAGCT  GCCGACAAGC
251  AGCCCGTTGC  CGATAAGGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301  GAACGGGAAG  AGCCGACGG  ACAGGCAGTG  CGTAAGAAAG  CGTGACGGA
351  AGAGCGTGAA  CAAACCGTCA  GGGAAAAGC  GCAGAAGAAA  GATGCCGAAA
401  CGGTAAAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451  TCAAAAGAAG  AGAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501  CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAGCG  CGCAGTGCCG
551  CCGCAAAGA  AGTGAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

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601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
 651 CGTGCCAAAC TGGCAATCTT GGCATATCT TCCAAGGTGG TCGGTTATCA
 701 GCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)
 1 ..GLFFGLILAT VIIAGILFYLNQSGQNAFKI PASSKQPAET EILKPXNQXK
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
 101 EREEPDQAV RKKALTEERE QTVREKAQKK DAETVKKQAV KPSKETEKKA
 151 SKEEKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVOK MKTPTRRKQR
 201 IICKWARMPT VRARKGSPVN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
 251 MR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

m306.pep	10	20	30	40
	GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX			
g306	MF MNKFSQSGKLSGFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLK			
	10	20	30	40
	50	60	70	80
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
g306	NQPKEDIQPEPADQNALSEPDAVAKEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKKQAVKPSKETEKKASKEEKKAAKEKVAPKP			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKQAVKPSKETEKKASKEEKKAAKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSPVNWQSWA			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGGGSQRIICKWARMPTNPGARKGSPVNWQSWA			
	190	200	210	220
	230	240	250	
m306.pep	YLPKWSVIRRDIKRFTGCKAAICLPMRX			
g306	YLPKWSAIRRDIKRFTACKAAICLPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq
 1 ATGTTTATGA ACAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT
 51 CTTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTATC
 101 TGAACCAGAG CGGTCAAAAT GCGTTCAAAA TCCCGGTTCC GTCGAAGCAG
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCTA AGGAAGACAT
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
 251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA
 351 AAAGTCGGAC GGACAGGCAG TCGCAAGAA AGCACTGACG GAAGAGCGTG
 401 AACAAACCGT CCGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
 451 AAACAAGCGG TAAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAGA
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCGGAAC
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

703

601 GAAGTGCAGA AAATGAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
 651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
 701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTGCGTTAT CAGGCGGGAC
 751 ATAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
 801 A

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

a306.pep
 1 MFMNKFSQSG KGLSGFFFGL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
 51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
 101 ADKADEVEEK ADEPEREKSD GQAVRKKALT EEREQTVGEK AQKKDAETVK
 151 KQAVKPSKET EKKASKEEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
 201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
 251 IKRFTGCKAA ICLPMR*

m306/a306 93.7% identity in 252 aa overlap

	10	20	30	40		
m306.pep	GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPK					
a306	MFMNKFSQSGKGLSGFFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK					
	10	20	30	40	50	60
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEKAADKQPVADKADEVEEKAGEPEREEDP					
a306	NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD					
	70	80	90	100	110	120
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETTEKKASKEEKKAAKEKVAPKP					
a306	GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETTEKKASKEEKKAEKEKVAPKP					
	130	140	150	160	170	180
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY					
a306	TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY					
	190	200	210	220	230	240
m306.pep	LPRWSVIRRDIKRTGCKAAICLPMRX					
a306	LPRWSVIRRDIKRTGCKAAICLPMRX					
	230	240	250			
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

g307.seq
 1 atgaaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
 51 cgcagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgccgccc
 101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
 151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
 201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
 251 gcccgaaatc ggcatcgagg gagggcgagt tggacatcaa cgtcttccaa
 301 cacaaaacct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
 351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccgggcaaac
 401 tgaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccac
 451 gaccctgcc acttcgcacg cgccttggtg atgctgaacg aactgggttg
 501 gatcaaacct aaagacggca tcaatccgct gaccgcatcc aaagccgaca
 551 tcgcggaaaa cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
 601 ctgccgcgca gccgcgcgca cgtggatttt gccgtcgta acggcaacta
 651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

q307.pep

1	MKTFFKTLST	ASLALILAAC	GGQKDSAPAA	SAAAPSDNG	AAKKEIVFGT
51	TVGDFGDMVK	EQIQAELEKK	GYTVKLVFEF	DYVRPNLALA	EGELDINVFO
101	HKPYLDFFKK	EHNLIDITEAF	QVPTAPLGLY	PGKLKSLEEV	KDGSTVSAPN
151	DPSNFARALV	MLNELGWIKL	KGGINPLTAS	KADIAENLKN	IKIVELEAAQ
201	LPRSRADVDF	AVVNGNYAIS	SGMKLTEALF	QEPSFAYVNW	SAVKTADKDS
251	QWLKDVTEAY	NSDAFKAYAH	KRFEGYKYPA	AWNEGAAK*	

m307.seq (partial)

1 ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCCTGCC GCATGGAATG
101 AAGGCGCAGC CAAATAA

m307.pep (partial)

1 ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA AWNEGAAK*

Homology with a predicted ORF from *N. gonorrhoeae*

m307/q307

m307.pep 10 20 30
 QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
 |||||
 g307 SGMKLTEALFQEPSFAYVNWSAVKTADKDSOWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
 230 240 250 260 270 280
 39
 m307.pep AWNEGAARKX
 |||||
 g307 AWNEGAARKX

a307.seq

1	ATGAAAACCT	TCTTCAAAAC	CCTTTCGCC	GCCGCACTCG	CGCTCATCCT
51	CGCCGCCTGC	GGCGGTCAAA	AAGATAGCGC	GCCCGCCGCA	TCCGCTTCTG
101	CCGCGCCCGA	CAACGGCGCG	GCGAAAAAAG	NAATCGTCTT	CGGCACGACC
151	TCGCGCGAT	TCGCGGATAT	GGTCAAGAA	CAAAATCCAA	CCGAGCTGGA
201	GAAAAAAGC	TACACGCTCA	AACTGGTCTGA	GTTTACCAGC	TATGTGCGCC
251	CGAATCTGGC	ATTGGCTGAG	GGCGAGTNGG	ACATCAACGT	CTTCCAACAC
301	AAACCCCTATC	TTGACGACTT	CAAAAAAGAA	CACAATCTGG	ACATCACC GA
351	AGTCTTCCAA	GTGCCGACCG	CGCCTTTGGG	ACTGTATCCG	GGCAAGCTGA
401	ATACCTTGGA	AGAAGTCAAA	GACGCGACGA	CCGATATCCG	GCCCACCGAC
451	CCGTCCAAC	TCGCCCCGCT	CTTGCTGATG	CTCGACGAA	TGGCTTGGAT
501	CAAAC'TCAA	GANGGCATCA	ATCCGCTGAC	CGCATCCAA	GCGGACATTG
551	CCGAAAACCT	GAAAAACATC	AAAATCGTCT	AGCTTGAAGC	CGCGCAACTG
601	CCGCGTAGCC	CGCCCGACGT	GGATT'TGNC	GTCTGTAACG	GCAANTACGC
651	CATAAGCAGC	GGCATGAAGC	TACCGGAAGC	CTGT'TCCAA	GAACCGAGCT
701	TTCCTATATG	CAACTGGTCT	GCCGTCAAAA	CCGCCGACAA	AGACAGCCAA
751	TGGCTTAAAG	ACGT'AACCGA	GGCTATAAC	TCCGACGCGT	TCAAAGCCTA
801	CGCGCACAAA	CGCTTCGAGG	GCTACAAATC	CCCTGCCGCA	TGGAATGAAG
851	GCGGACGCAA	ATAA			

a307.pcp

1 MKTFFKTLSA AALALILAAC GGQKDSAPAA SASAAADNGA AKKXIVFGTT

705

```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFQH
101 KPYLDDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLKNI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

          39
m307.pep      AWNEGAAKX
          |||||
a307          AWNEGAAKX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCTT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGAACT
201 TTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTCGGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 CCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCG  CGATGTACCG  CAAGCCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTGCTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVYRIL  GVADNLYPCL  SDFCFETIIA  GLPLQAVLWE  RMMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPLE  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPK
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTCTT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGAACT
201 TTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGATATC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGcT  GACGCGtTGG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GwAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGCTt  TGTGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

706

1 MLNRVFYRIL GVADNLYPRL SDFCFFTTIIA GLPLQAVLWE RRMVRRLLII
 51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
 101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLDNMKR XTEMGGVVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFLGID TPDSA EWQGM A..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFQDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308	KTDGMLVAPCSMRTLASVAHGFQDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKPOADDIVAHSAHALSFLGIDTPDSA EWQGMA					
g308	VTEMGGVVFPVPAMYRKPOADDIVAHSAHTLSLFGIDTPDLA EWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTGCCG ACAATTTGTA
 51 TCCGTATTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
 101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
 151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGANCT
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
 301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
 351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCCGA
 401 CGCTTGCCCTC GGTCGTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
 451 GCGGATGTGG TTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
 501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
 551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCTG CGATGTACCG CAAACCGCAG
 601 ACGGCGGACG ACATAGTGGC GCACAGTGTT GCACACGCTT TGTCGCTGTT
 651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTA

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTTIIA GLPLQAVLWE RRMVRRLLII
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVVH GFGDNLLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLDNMXR VTEMGGVVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFLGID TPDSA EWQGM AD*

707

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRV	FYRILGVADNLYPRLSDFCFF	TI	IAGLPLQAVLWERRMMVRR	LI	IGISGASGFQY
a308	MLNRIF	YRILGVADNLYPYLSDFCFF	TI	IAGLPLQAVLWERRMMVRR	LI	IGISGASGFQY
	10	20	30	40	50	60
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALAD	FVHPIGNIGACIASGTF			
a308	GVKALXLLRAQDIETHLVVSKGAEMARASE	TXYARDXVYALAD	XVHPIGNIGACIASGTF			
	70	80	90	100	110	120
m308.pep	KTDGMLVAPCSMRTLASVAHGF	GDNLLTRAADVVLKERRRLVLMVRETPL	NLAHL	DNM	KR	
a308	KTDGMLVAPCSMRTLASVHGF	GDNLLTRAADVVLKERRRLVLMVRETPL	NLAHL	DNM	KR	
	130	140	150	160	170	180
m308.pep	XTEMGGVVFPPVPAMYRK	PQTADDIVAH	SVHAHLSLFGID	TPD	SAEWQ	GMA
a308	VTEMGGVVFPPVPAMYRK	PQTADDIVAH	SVHAHLSLFGID	TPD	SAEWQ	GMA
	190	200	210	220	230	
m308.pep	XTEMGGVVFPPVPAMYRK	PQTADDIVAH	SVHAHLSLFGID	TPD	SAEWQ	GMA
a308	VTEMGGVVFPPVPAMYRK	PQTADDIVAH	SVHAHLSLFGID	TPD	SAEWQ	GMA
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAACT
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATCGCGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGC CGCA
501 AACGCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAGCCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACGCGT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRV FYRIL GVADNLYPCL SDFCFFIIA GLPLQAVLWE RRMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMCR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHST AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAACT
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTCGCG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGATG GGATGCTGGT CGCCCTGT TCGATCGCGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGC CGCA
501 AACGCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAGCCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRV FYRIL GVADNLYPRL SDFCFFIIA GLPLQAVLWE RRMVRRLLI

```


708

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
 101 LADFXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLNMMKR VTEMGGVVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFLGID TPDSAEWQGM AD*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRVYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308-1	MLNRVYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVS KGAEMARASE TAYARDEVYALADFXVHPIGNIGACIASGTF					
g308-1	GVKALELLRAQDVETHLVVS KGAEMARASE TDYTKDEVYALADFXVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNMMKR					
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNMMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308-1.pep	VTEMGGVVFPVPAMYRKPO TADDIVAHSAHALSFLGIDTPDSAEWQGMADX					
g308-1	VTEMGGVVFPVPAMYRKPO TADDIVAHSAHALSFLGIDTPDLAEWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
 51 TCCGTATTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTGTTGCCG
 101 TGCAGCGCGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
 151 GGCATCAGTG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGGANCT
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
 251 AGATGCGCGC CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
 301 TTGGCGGACT TNGTGATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
 351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
 401 CGCTTGCCCT GGTCTGTCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
 451 GCGGATGTGG TTTGAAGGA AAGCGGCGCG CTGGTGCTGA TGGTCCGCGA
 501 AACGCGCGTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
 551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAACCGCAG
 601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT
 651 CGGAATCGAT ACGCCGGATT CGCGGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTTIA GLPLQAVLWE RRMVRRLLI
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
 101 LADFXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVVH GFGDNLLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLNMMKR VTEMGGVVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFLGID TPDSAEWQGM AD*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIFYRILGVADNLYPYLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
m308-1	MLNRVYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVS KGAEMARASE TXYARDXVYALADFXVHPIGNIGACIASGTF					
m308-1	GVKALELLRAQDVETHLVVS KGAEMARASE TAYARDEVYALADFXVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVVHGFNDLLTRAADVVLKERRRLVLMVRETPLNLAHLNMMKR					


```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLHLNDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPVPAMYRKQTADDIVAHSVAHALSLFGIDTPDSEWQGMADX
              |||||
m308-1      VTEMGGVVFPVPAMYRKQTADDIVAHSVAHALSLFGIDTPDSEWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

g311.seq

```

1  atgttcagtt  tcggtggttc  gtttgaccgc  ccgcagtatg  agttgggttc
51  gctgtcgctt  gttgctggac  ttgctgccc  gcgcgctttg  ggggtgttgg
101 gtttggaac  gcaaatcaag  tggccaaacg  atttggctgt  cggacgcgac
151 aaattgggct  gcattctgat  tgaacagtc  agggcggttc  gtaaacgggt
201 tgcgtggtc  ggtatcgcca  tcaatttcgt  gctgcccagg  gaagtggaaa
251 acgctgcttc  cgtgcagtcg  ctgtttcaga  cggcatcgcg  gcggggcaat
301 gccgatgccc  ccgtattgct  ggaacattg  cttgcggaac  tggcgcggtt
351 gttggaacaa  tatgcggaag  aagggttcgc  gccattttta  aatgagtatg
401 aaacggccaa  ccgcgaccac  ggcaaggcgg  tattgctgtt  gcgcgacggc
451 gaaaccgtgt  gcgaaggcac  ggtaaaaggc  gtggacggac  gaggcgcttc
501 gcacttgtaa  acggcagaag  gcgaacagac  ggtcgtcagc  ggcgaatatc
551 gcctgctggc  cgacaacagg  tcggtttccg  tgcgaagcgc  gccggattcg
601 gaacgttttt  tgcgtgttga  agcggggaac  agccggctca  agtggcgctg
651 ggtggaaaac  ggacgcttcg  caaccgtggg  cagcgcgccg  taccgcgatt
701 tgcgcctttt  gggcgcggtg  tggcgggaaa  agcgggatgg  aaatgtccgc
751 atcgtcggtt  gcgcgctgtg  cggagaatcc  aaaaaggcac  aagtgaagga
801 acagctcgcc  cgaaaaatcg  agtggctgcc  gtcttcgcga  caggctttgg
851 gcatacgcaa  ccactaccgc  caccctgaag  aacacggttc  cgaccgttgg
901 ttcaacgcct  tgggcagccg  ccgcttcagc  cgcaacgcct  gcgtcgctgt
951 cagttgcggc  acggcggtta  cgttgacgc  gctcaccgat  gacggacatt
1001 atctcggttc  aaccatcatg  cccggcttcc  acctgatgaa  agaatcgctc
1051 gccgtccgaa  ccgccaacct  caaccgcccc  gccggcaaac  gttacccttt
1101 cccgaccaca  acgggcaacg  ccgtcgcaag  cggcatgatg  gacgcggttt
1151 gcggctcgat  aatgatgatg  cacggccgtt  tgaagaaaaa  aaacggcgcg
1201 ggcaagcctg  tcgatgtcat  cattaccggc  ggcgcgcgcg  cgaaagtcgc
1251 cgaagccctg  ccgcctgcat  ttttgccgga  aaataccgtg  cgcgtggcgg
1301 acaacctcgt  catccacggg  ctgctgaacc  tgattgccgc  cgaaggcggg
1351 gaatcggaac  acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

g311.pep

```

1  MFSFGWAFDR  PQYELGSLSP  VAALACRRAL  GCLGLETQIK  WPNDLVVGRD
51  KLGILLETIV  RAGGKTIVAV  GIGINFLPK  EVENAASVQS  LFQTASRRGN
101 ADAAVLLETL  LAELGAVLEQ  YAEFGFAPFL  NEYETANRDH  GKAVLLLRDG
151 ETVCEGTVKG  VDGRGVLHLE  TAEGEQTVVS  GEISLRPDNR  SVSVPKRPS
201 ERFLLEGGN  SRLKWAVVEN  GTFATVGSAP  YRDLSPLGAE  WAEKADGNVR
251 IVGCAVCGES  KKAQVKEQLA  RKIEWLPSSA  QALGIRNHYR  HPEEHGSDRW
301 FNALGSRFRS  RNACVVVSCG  TAVTVDALTD  DGHYLGGTIM  PGFHLMKESL
351 AVRTANLNRP  AGKRYPFPTT  TGNASVSGMM  DAVCGSIMMM  HGRLEKKNKA
401 GKPVDVIITG  GGAAKVAEAL  PPAFLAENTV  RVADNLVIHG  LLNLIAEAGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

m311.seq (partial)

```

1  ATGTTTCAGTT  TTGGCTGGGT  GTTTGACCGG  CCGCAGTATG  AGTTGGGTTC
51  GCTGTGCGCT  GTTGCAGCAG  TGGCGTGTCT  GCGCGCCTTG  TCGCGTTTAG
101 GTTTGGATGT  GCAATTAAG  TGGCCCAATG  ATTTGGTTGT  CGGACGCGAC
151 AAATTGGGCG  GCATTCTGAT  TGAACGGTTC  AGGACGGGCG  GCAAAACGGT
201 TGCCGTGGTC  GGTATCGGCA  TCAATTTTGT  CTGCCCCAAN  GAAGTAGAAA
251 ATGCCGCTTC  CGTGCAATCG  CTGTTTCAGA  CCGCATCGCG  GCGGGGCAAT
301 GCCGATGCCG  CCGTGCTGCT  nnnnnnnnnn  nnnnnnnnnn  nnnnGGAAAT
351 CAGCCTGCCG  TCCGACNACA  GGCCGGTTTC  CGTGnCGAAG  CCGCGGGATT

```


710

```

401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAA ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTGCGCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCCG TTGCGCTGTG TCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCCGACC
701 GCTGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGCG GGTAAACGGT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrGGAACCA TCATGCCCGG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTTGCGGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGC CGGGCAA GCCTGTCGAT GTCATCATT CCGCGCGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCTGCCGCC TGCATTTTGT GCGGAAAATA CCGTGC GCGT
1101 GCGGACAAC CTGTCATTT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGGAATA TGAACAT....

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
51 KLGGILIEIV RTGGKTAVV GIGINFLPX EVENAASVQS LFTASRRGN
101 ADAAVLLXXX XXXXEISLR SDXRPVSVXK RRDSEFLLL DGGNSRLKWA
151 WVNGTFATV GSAPYRDLSP LGAEWAEEKAD GNVRIVGCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFTTTGNAV ASGMDAVCG SVMMHGRLK EKTGAGKPD VIITGGGAAG
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

m311/g311

```

              10      20      30      40      50      60
m311.pep      MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIEIV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311           MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRDKLGGILIEIV
              10      20      30      40      50      60

              70      80      90      100     110
m311.pep      RTGGKTAVVVGIGINFLPXKEVENAASVQSLFQTASRRGNADAALLXXX-----
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311           RAGGKTAVVVGIGINFLPXKEVENAASVQSLFQTASRRGNADAALLLETLAELGAVLEQ
              70      80      90      100     110     120

m311.pep      -----XXXXXXXXX
g311           YAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDGRGVLHLETAEGEQTVVS
              130     140     150     160     170     180

              120     130     140     150     160     170
m311.pep      XEISLRSDXRPVSVXKRRDSEFLLLDDGGNSRLKWA WVNGTFATVGSAPYRDLSP LGAE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311           GEISLRPDNRSVSVKRPDSEFLLLLEGGNSRLKWA WVNGTFATVGSAPYRDLSP LGAE
              190     200     210     220     230     240

              180     190     200     210     220     230
m311.pep      WAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311           WAEKADGNVRIVGCAVCGESKKAQVQEQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
              250     260     270     280     290

```


711

	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYFPFPTTGNASGMMDAVCGSVMMHGRLEKKTGAGKPVVDVIITGGGAAKVAEA					
g311	PAGKRYFPFPTTGNASGMMDAVCGSIMMHGRLEKKTGAGKPVVDVIITGGGAAKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1  ATGTTCAAGT  TTGGCTGGGT  GTTTGACCGG  CCGCAGTATG  AGTTGGGTTT
51  GCTGTCGCTT  GTTGCAGGCG  TGGCGTGCCT  GCGCGCCTTG  TCGCGTTTGG
101 GTTTGAAACG  GCAATCAAG  TGGCCAAACG  ATTTGGTCTG  CGGACGCGAC
151 AAATTGGGCG  GCATTCTGAT  TGAAACGGTC  AGGACGGGCG  GCAAAACGGT
201 TGCCGTGGTC  GGTATCGGCA  TCAATTTCTG  GCTGCCCAAG  GAAGTGGAAA
251 ACGCCGCTTC  CGTGCAATCG  CTGTTTCAGA  CCGCATCGCG  GCGGGGAAAT
301 GCCGATGCCG  CCGTGTGTCT  GGAAACGCTG  TTGGCGGAAC  TTGATGCGGT
351 GTTGTGCAA  TATGCGCGGG  ACGGATTTCG  GCCTTTTGTG  GCGGAATATC
401 AGGCTGCCAA  CCGCGACCAC  GGCAAGGCGG  TATTGCTGTT  GCGCGACGGC
451 GAAACCGTGT  TCGAAGGCAC  GGTAAAGGC  GTGGACGGAC  AAGGCGTTCT
501 GCACTTGGA  ACGGCAGAGG  GCAAACAGAC  GGTCGTCAGC  GCGGAAATCA
551 GCCTGCGGTC  CGACGACAGG  CCGGTTTCCG  TGCCGAAGCG  GCGGGATTCT
601 GAACGTTTTC  TGCTGTTGGA  CGGCGGCAAC  AGCCGGCTCA  AGTGGGCGTG
651 GGTGGAAAC  GGCACGTTCG  CAACCGTCGG  TAGCGCGCCG  TACCGCGATT
701 TGTCGCCTTT  GGGCGCGGAG  TGGCGGAAA  AGGTGGATGG  AAATGTCCGC
751 ATCGTCGGTT  GCGCCGTGTG  CGGAGATTTC  AAAAAGGCAC  AAGTGCAGGA
801 ACAGCTCGCC  CGAAAAATCG  AGTGGCTGCC  GTCTTCCGCA  CAGGCTTTGG
851 GCATACGCAA  CCACTACCGC  CACCCGAAG  AACACGGTTC  CGACCGCTGG
901 TTCAACGCCT  TGGGCAGCCG  CCGCTTCAGC  CGCAACGCCT  GCGTCGTCGT
951 CAGTTGCGGC  ACGGCGGTAA  CGGTTGACGC  GCTCACCGAT  GACGGACATT
1001 ATCTCGGGGG  AACCATCATG  CCCGTTTCC  ACCTGATGAA  AGAATCGCTC
1051 GCGGTCGGA  CCGCCAACCT  CAACCGGCAC  GCGGTAAGC  GTTATCCTTT
1101 CCCGACCACA  ACGGGCAATG  CCGTCGCCAG  CCGCATGATG  GATGCGGTTT
1151 GCGGCTCGGT  TATGATGATG  CACGGGCGTT  TGAAAGAAAA  AACCGGGGCG
1201 GGCAAGCCTG  TCGATGTCAT  CATTACCGGC  GCGGGCGCGG  CAAAAGTTGC
1251 CGAAGCCCTG  CCGCCTGCAT  TTTTGGCGGA  AAATACCGTG  CCGTGCGCGG
1301 ACAACCTCGT  CATTACGGG  CTGCTGAACC  TGATTGCCGC  CGAAGGCGGG
1351 GAATCGGAAC  ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1  MFSFGWVFD  R POYELGSL  SP VAAVACRR  AL SRLGLKTQ  IK WPNDLVV  GRD
51  KLGGLIET  V RTGGKTVA  VV GIGINFLP  K EVENAASV  QS LFQTASR  RGN
101 ADAAVLE  TL LAELDAVL  LQ YARDGFAP  FV AEYQAANR  DH GKAVLL  LRDG
151 ETVFEGT  VKG VDGQGV  LHLE TAEGKQTV  VS GEISLRSD  DR PVSVPK  RRD
201 ERFLLLD  GGN SRLKWA  WVEN GTFATVGS  AP YRDLSP  LGAE WAEKVD  GNV
251 IVGCAVC  GEF KKAQVQ  EQLA RKIEWLP  SSA QALGIRN  HYR HPEEHG  SDR
301 FNALGS  RRF RNACVV  VSCG TAVTVDA  LTD DGHYLG  GTIM PGFHL  MKESL
351 AVRTAN  LNRH AGKRY  PFTT TGNASG  MM DAVCGS  VMM HGRLE  KKTGA
401 GKPV  DVIITG GAAKVA  EAL PPAFLA  ENT RVADNL  VIH LLNLIA  AEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILITV					
a311	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILITV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAVVGIGINFLPXEVENAASVQSLFQTASRRGNADA AVLXXXXXXXX-----					
a311	RTGGKTVAVVGIGINFLPXEVENAASVQSLFQTASRRGNADA AVLLETLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVDDGQGVHLHLETAEGKQTVVS					
	130	140	150	160	170	180
m311.pep	-EISLRSDXRPSVXKRRDSEFLLLDGGSRLKWAWVNGTFATVGSAPYRDLSPLGAE					
a311	GEISLRSDXRPSVXKRRDSEFLLLDGGSRLKWAWVNGTFATVGSAPYRDLSPLGAE					
	190	200	210	220	230	240
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHP EEHGSDR					
a311	WAEKVDGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHP EEHGSDR					
	250	260	270	280	290	
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTV DALTDDGHYLG GTIMPGFHLMKESLAVRTANLNR					
a311	WFNALGSRRFSRNACVVVSCGTAVTV DALTDDGHYLG GTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTGNASGMMDAVCGSVMMHGR LKEKTGAGKPVDV IITGGGAAKVAEA					
a311	HAGKRYPFPTTGNASGMMDAVCGSVMMHGR LKEKTGAGKPVDV IITGGGAAKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNMI AEGREYEH					
a311	LPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGCCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGCCGTT
201 TTTGATGCC GAAGGTTTGC GCGATCTGGG GGAAGGTCG GGTTCAGCA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCTT GATGTTAGT TTCGGCTGGG CGTTTGACCG GCCCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA CTTGCGTGCC GGCGCGCTTT
501 GGGTGTTTGG GGTGGAAGAA CGCAAATCAA GTGGCCAAAC GATTGTTGTC
551 TCGACGCGCA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGCGGGGC
601 GGTAAACCGG TTGCCGTGGT CCGTATCGGC ATCAATTTGC TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGCGAA TGCCGATGCC GCCGTATTGC TGGAACATT GCTTGGCGAA
751 CTGGCGCGCG TGTGGAACA ATATGCGGAA GAAGGGTTCG CGCCATTTT

```



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801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGGACGG CGAAACCGTG TCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACCTGGA AACGGCAGaa ggCGAACAGa cgtcGtcag
951 cggcGaaATC AGcctGCGGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGTgtttg aaggcgggaa cagccggctc
1051 aAGTGGcgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGcCC
1101 gtaCCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGCGCGATG
1151 GAAATGTCCG CATCGTCGGT TCGCGCGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTcAG CCGCAACGCC
1351 TCGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCTTT TCCCGACCAC AACGGGCAAC GCCGTCGCA GCGGCATGAT
1551 GGACGCGGTT TCGCGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTLVKPSHWR VLAELADGLP QHVSQALAREA DMKPOQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGDRDKLG GILLETVRAG
201 GKTVAVVIGI INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVRGVDG
301 RGVHLLETAE GEQTVVSGEI SLRPNDRSVS VPKRPDSERF LLEGGNSRL
351 KWAVVENGTF ATVGSAPYRD LSPGLAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHPE EHGSDRWfNA LGSRRFSRNA
451 CUVVSCGTAV TVDALTDG YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYPFPTTTGN AVASGMMDAV CGSIMMHGR LKEKNGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGCGCGA CATACCGGGG
151 CTGTTGCCGC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTTGGCGT
201 TTTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTGC GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 CGCGCGATTG CGCCGGACAA GCGCGACAAA ACCATATCGG TGACCCACCT
351 GCAAGTAAG GGCAGGGGCG GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA GTGGCGTGTC GCGCGCCCTT
501 GTGCGGTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTTGGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAACCGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGCT CGGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTGCTGC TGGAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTTGTTGCA ATATGCGCGG GACGGATTTG CGCCTTTTGT
801 GCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTC TGCACCTGGA AACGGCAGAG GGCAAAACAG CGGTCGTCAG
951 CGGCGAANTC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGGGGATTC GGAACGTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGCGGT GGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TCGCTGTGT GCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTcAG CCGCAACGCC
1351 TCGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCA GCGGCATGAT
1551 GGATGCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTGAAC ATGATTGCCG

```


1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFOTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDPRQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGDRKLG GILLETVRTG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVGDG
301 QGVLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWA EADGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAL GIRNHYRHPE EHGSDFWFNA LGSRRFSRNA
451 CVVSCGTAV TVDALTDDGH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYPFPTTTGN AVASGMDAV CGSVMHMRGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

	10	20	30	40	50	60
m311-1.pep	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m311-1.pep	LVRPLAVFDAEGLRELGERSGFQOTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQOTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m311-1.pep	GRGRQGRKWSHRLGECLMFSFGWVFDPRQYELGSLSPVAACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m311-1.pep	DLVVGDRKLGILLETVRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGDRKLGILLETVRTAGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m311-1.pep	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
g311-1	AVLLETLLAELGAVLEQYAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m311-1.pep	QGVLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLLDGGNSRLKWAUVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRSVSVPKRPDSERFLLLEGGNSRLKWAUVENGTF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m311-1.pep	ATVGSAPYRDLSPGLAEWA EADGNVRIVGCAVCGEFKKAQVQEQALARKIEWLPSSAQAL					
g311-1	ATVGSAPYRDLSPGLAEWA EADGNVRIVGCAVCGESKKAQVKEQALARKIEWLPSSAQAL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m311-1.pep	GIRNHYRHPEEHGSDFWFNALGSRFRFSRNACVVVSCGTAVTVDALTDDGHYLGGTIMPGF					
g311-1	GIRNHYRHPEEHGSDFWFNALGSRFRFSRNACVVVSCGTAVTVDALTDDGHYLGGTIMPGF					
	430	440	450	460	470	480
	490	500	510	520	530	540
m311-1.pep	HLMKESLAVRTANLNRHAGKRYFPFPTTTGNAVASGMDAVCGSVMHMRGLKEKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYFPFPTTTGNAVASGMDAVCGSVMHMRGLKEKTGAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	


```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMAAEGREYEHIX
              |||||||||||||||||||||||||||||||||||||||||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNIAAEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTTGGCGGT
201 TTTTCGATGC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTCACAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 CGGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGGGCA GTGGCGTGCC GCGCGCCTT
501 GTCGCGTTTG GGTTTGAAAA CGCAATCAA GTGGCCAAAC GATTGTTGTCG
551 TCGGACGCCA CAAATTTGGC GCATTTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGTGGT CGGTATCGGC ATCAATTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCTAG ACGGCATCGC
701 GCGCGGGAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTTGATGCGG TGTGTTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGCGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGCGG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTC TGCACCTTGA AACGGCAGAG GGCAACAGA CGGTCTGTAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GCGCGGATTC GGAACGTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCCG
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TGCTCTCGTG TCAGTTGCGG CACGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTT CACCTGATGA
1451 AAGATCGCTC CGCGGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTGCGCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGCGCT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGGCGCGC
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGCG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTVLKPSHWR VLAELADGLP QHVSQARMAD DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDRPQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGDRKLG GILIVRTTG
201 GKTVAVVIGI INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLE
251 LDVAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEGTVKGVDF
301 QGVHLHLETA EKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAFYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAL GIRNHYRHEP EHGSDRWANA LGSRRFSRNA
451 CUVVSCGTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

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a311-1/m311-1 98.5% identity in 591 aa overlap

```

              10      20      30      40      50      60
a311-1.pep  MTVLKPSHWRVLAELADGLPOHVSQARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              |||||
m311-1      MTVLKLSHWRVLAELADGLPOHVSQARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              10      20      30      40      50      60

              70      80      90      100     110     120
a311-1.pep  LVRPLAVFDAEGLRELTERSFGFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              |||||
m311-1      LVRPLAVFDAEGLRELTERSFGFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              70      80      90      100     110     120

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716

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECIMFSFGWVFD	RPQYELGSLSPVA	AAVACRRALSRLGLKTQIKWPN			
m311-1	GRGRQGRKWSHRLGECIMFSFGWVFD	RPQYELGSLSPVA	AAVACRRALSRLGLDVIKQWPN			
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILIE	TVRTGGKTVAVVGIGIN	FVLPKEVENAASVQSLFQTASRRGNADA			
m311-1	DLVVGRDKLGGILIE	TVRTGGKTVAVVGIGIN	FVLPKEVENAASVQSLFQTASRRGNADA			
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQ	AAANRDHGKAVLLLRDGETVFE	GTVKGVDG			
m311-1	AVLLETLLVELDAVLLQYARDGFAPFVAEYQ	AAANRDHGKAVLLLRDGETVFE	GTVKGVDG			
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVS	GEISLRSDDRPVSVPKRRD	SERFLLLDGGNSRLKWAVVENGTF			
m311-1	QGVHLHLETAEGKQTVVS	GEISLRSDDRPVSVPKRRD	SERFLLLDGGNSRLKWAVVENGTF			
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPLGAEWA	EKV DGNVRI	VGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL			
m311-1	ATVGSAPYRDLSPLGAEWA	EKADGNVRI	VGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL			
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPPEEHGSDRWF	NALGSRFRSRNACVVV	SCGTAVTVDALTD	DGHYLG	GGTIMPGF	
m311-1	GIRNHYRHPPEEHGSDRWF	NALGSRFRSRNACVVV	SCGTAVTVDALTD	DGHYLG	GGTIMPGF	
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAG	KRYPFPTTGN	AVASGMMDAVCGSVMMH	GRLEKKTGAGKP		
m311-1	HLMKESLAVRTANLNRHAG	KRYPFPTTGN	AVASGMMDAVCGSVMMH	GRLEKKTGAGKP		
a311-1.pep	550	560	570	580	590	
	VDVIITGGGA	AKVAEALPPAFLA	ENTVRVADNLVIHGLLN	LIAAEGGESEHTX		
m311-1	VDVIITGGGA	AKVAEALPPAFLA	ENTVRVADNLVIYGLLN	MIAAEGREYEHIX		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTaccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACAttta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTtccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgAGact
301 tTGGACAAGG CAGCCAAAGC CATCGCGGTG TCCTTTATCG GcggCTTTTC
351 CGCGTGGTG CAAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCCGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CCAAATCGT CGTGTCTGTC AACCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAAATCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTTGT CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC

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717

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCGAAGA CGAAGGTATG ATTGCCGCCG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCC GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCAGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQIRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKTKAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGGMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTIVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCCTACG GCAAAATATC TGCTGCGCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACCTCAGCGT GGCGCAAAC
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTGCGCTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCGG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACCGTC AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAAAATTGT CGTGTCTGCG AACCGGGTGG AAGACAACCC GTTTWTGGCG
601 GCGCGGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTGCG GCGTATCCGG
651 CCCAGGTGTC GTAAAGCCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAACCTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCCTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTGCGCGA CCCGCCCCGT CGGCGACTCA GTGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAT GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CACGGTCGAG TTCGGCGGCT TGTGGGCTA
1251 CGCGCCTGTG ATGCCGCTCA AAGAAGGTTC GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQIRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNPFXA
201 GAFHGSDDAV INVGVSGPGV VKAALENS DA TLTTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGLLGYAPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

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718

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

m312.pep	10	20	30	40	50	60
	MSIQSGEILETVKMVADQNFVDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT					
g312	MSIQSGEILETVKMVADRNFDVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT					
	10	20	30	40	50	60
m312.pep	70	80	90	100	110	120
	AKYLSAKYGVPIVNQRI SVTPIAQIAAATHADSYVSVQAQTLDKAAKAIGVSFIGGFSALV					
g312	AKHLSAKYGVPIVNQRI SVTPIAQIAAATKADSYVSVQAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
m312.pep	130	140	150	160	170	180
	QKGMSPSDEVLRISPEAMKTTDIVCX SINIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	QKGMSPSDEVLRISVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	130	140	150	160	170	180
m312.pep	190	200	210	220	230	
	FGCAKIVVFCNAVEDNPFKAGAFHGSG--DAVINVGVS GPGVVKAALENS DATLTLEVAE					
g312	FGCAKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVS GPGVVKAALENS DAVSLTEVAE					
	190	200	210	220	230	240
m312.pep	240	250	260	270	280	290
	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
m312.pep	300	310	320	330	340	350
	GTTAALALLNDVAVKKGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	GTTAALALLNDVAVKKGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
m312.pep	360	370	380	390	400	410
	CSVGLDMI AVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKT VGDVTFEFGGLLG					
g312	CSVGLDMI AVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKT VGDVTFEFGGLLG					
	370	380	390	400	410	420
m312.pep	420	430	440			
	YAPVMPVKEGSCEVFVNRGGRI PAPVQSMKNX					
g312	YAPVMPAKEGSCEVFVNRGGRI PAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

```

1  ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTGCGCA
51  CCAGAATTTC GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAC CGACATCGAC GTGTTGAACC AAAATATTTA CAACAAAATT
151 ACCACGGTCG GCAAAGACTT GGTGGCGACA GCAAATATC TGTCTGCCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCTGTCACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAAT

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719

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301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTGCGCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGGCGCCGGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTTCTGC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGCCCG GGTGTCGTAA AAGCCGCGTT GGAAAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACGCGCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CGGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCGGTT TGTTCGGTCG CTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATTCGGT TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CTTGTTGGGC TACGCGCCTG TAATGCCGTT AAAAGAAGGC TCATGCGAAG
1301 TGTTCGTCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

a312.pep

```

1  MSIQSGEILE TVKMDVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGGMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GLIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMDVADQNF	DVRTITIGID	LHDCISSDINVLN	QNIYNKITT	TVGKDLVTT	
a312	MSIQSGEILETVKMDVADQNF	DVRTITIGID	LHDCISTDIDVLN	QNIYNKITT	TVGKDLVAT	
	10	20	30	40	50	60
m312.pep	AKYLSAKYGVPIVNQRISVT	PIAQIAAATHADS	YVSVAQTL	DKAAKAIGVS	SFIGGFSALV	
a312	AKYLSAKYGVPIVNQRISVT	PIAQIAAATHADS	YVSVAQTL	DKAAKAIGVS	SFIGGFSALV	
	70	80	90	100	110	120
m312.pep	QKGMSPSDEV	LIRSIPEAMKTT	DIVCX	SINIGSTRAGINM	DAVKLAGETV	KRTAEITPEG
a312	QKGMSPSDEV	LIRSIPEAMKTT	DIVCSSINIG	STRAGINMDAV	RLAGETIKR	TAEITLEG
	130	140	150	160	170	180
m312.pep	FGCAKIVVFC	NAVEDNPF	XAGAFHGS	GDVAVINV	GVSGPGVV	KAALENSDATTLTEVAE
a312	FGCAKIVVFC	NAVEDNPF	MAGAFHGS	GEADAVINV	GVSGPGVV	KAALENSDATTLTEVAE
	190	200	210	220	230	240
m312.pep	VVKKTAFKIT	RVGELIGRE	ASKMLNIP	FGILDLS	PTPPVGDS	VARILEEMGLSVCGTH
a312	VVKKTAFKIT	RVGELIGRE	ASKMLNIP	FGILDLS	LAPTPAVGDS	VARILEEMGLSVCGTH

720

	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDAVKKGMMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDAVKKGMMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq

```

1  atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
51  tttaacgcagc ggcaaaaaaa aggcggccgc gctgacgctc ttggcgcatg
101 cgcgcaaagg tttggttgcc gttttgcttg cagcgtgct tcaagaaccg
151 ctcggtttat cgcacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggccggtgt ttttcggatt taagggcggc aaaggcgtgg
251 caacggcatt gggcggtgct ctggcactct ctcccgcaac tgccttggtc
301 tgcgcgttga tttggcttgt gatggcattc ggcttcaaag tatectccct
351 tgccgcgctg gtcgccacaa ccgccgcccc cettgcccga ctgtttttta
401 tgccgcatac ttcttggtt ttcgcaaccc tcgcaatcgc catattgggtg
451 ttgtccgccg ataagagcaa catcctcaac ctgattaaag gcaaagaaag
501 caaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMAP GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAIALV
151 LLRHKSNILN LIKGKESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGCTGT TTTTCGGATT TAAAGCGGCG AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCGCAAC TGCCTTGGTC
301 TGCgcgttga TTTGGCTTGT TATGGCATTC GGCTTCAAGG TGCTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTGCGCGCA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGCGGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMAP GFKVSSLAAL TATTAAPVAA SFFMPHVSIV WATVAIALLV
151 LFRHKSNIIVK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYSGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
g313	MDDPRTYSGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFGKGGKVATALGVLLALSPATALVCALIWLVMAFGFKVSSLAAL					
g313	VALAALVGHMWPVFFGFGKGGKVATALGVLLALSPATALVCALIWLVMAFGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIAALLVLRHKSNIIVKLLLEGRESKITGGSRX					
	: : : : : : : : : : : : : : :					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNIKKGESKIGEKRX					
	130	140	150	160	170	

a313.seq

1	ATGGACGACC	CGCGCACCTA	CGGATCGGGC	AATCCGGGGG	CAACCAATGT
51	TTTACGCAGC	GGCAAAAAAA	AGGCGGCCGC	GCTGACGCTC	TTGGGCGATG
101	CGGCCAAAGG	TTTGGTTGCC	GTTTTGCTTG	CACGCGTGCT	TCAAGAACCG
151	CTCGGTTTAT	CCGACAGCGC	AATCGCGGCC	GTCGCATTCG	CCGCGCTGGT
201	GGGGCATATG	TGGCCGGTGT	TTTTTCGGAT	TAAAGCGCGG	AAAGGCTGTG
251	CAACGCATG	GGGCGTGCTT	CTGGCACTCT	CTCCCAAC	TGCGTTGGTG
301	TGCGCGTTGA	TTTGGCTTGT	GATGGCATTG	GGCTTCAAGG	TGTCCTCCCT
351	TGCCGCGATTA	ACCGCCACAA	TGCGCGCCCC	CCTTGCCGCA	CTGTTTTTTA
401	TGCCGCATAC	TTCTTGGATT	TTTCGCAACCC	TCGCAATCGC	CATATTGGTG
451	TTGCTCCGCG	ATAAGAGCAA	CATCCTCAAC	CTGATTAAAG	GCAAAGAAAG
501	CAAAATCGCG	GAAAAACGCT	GA		

a313.pep

1 MDDPRTYGS G NPGATNVLR S GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51 LGLSDSAIAA VALAALVGHM WPVFVGFGKG KGVATALGVL LALSPTTALV
101 CALILVLMAF GFKVSSLAAL TATIAAPLAA LFEMPHTSWI FATLAIAILV
151 LLRHKSNIIL LIKGESKIG EKR*

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYSGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
a313	MDDPRTYSGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFVFGFKGKGKVATALGVLLALSPATALVCALIWLVMAFGFKVSSLAAL					
a313	VALAALVGHMWPVFVFGFKGKGKVATALGVLLALSPPTALVCALIWLVMAFGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFMPHVSWWVATVAIALLVLRHKSNIIVKLLLEGRESKIGGSRX					
a313	TATIAAPLAALFMPHTSWIFATLAIALVLLRHKSNIILNIKKGKESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
  1  atgaaattac aacaattggc tgaagaaaaa atcggcggtc tgattgtgtt
 51  cacgctgctt gtagtcagtg tccgtctgtt gattgaagtt gtgcccttgg
101  cctttaccaa ggcggcaaca cagccggcgc cggcggtgaa gccttacaat
151  gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201  ctgccactct caaatgattc gtccgttcgc tgcggaaacc gagcggtacg
251  gtcattactc tgttgccgga gagtcggttt acgaccatcc gttccaatgg
301  ggttccaaac gtaccggtcc tgatttggca cgtgtgggcg gccgctattc
351  cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401  agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451  gatgcaaccg ttgccaaacat gaaggctttg cgtaaagtag gtactcctta
501  cagtgatgag gaaattgcga aagcgcttga ggctttggca aacaaatccg
551  agctggatgc ttagtcgcc tatctgcaag gattgggtct ggctttgaaa
601  aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
  1  MKLQQLAEK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201  NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
  1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  ALCAGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GCGGCAACA CAGCCGGCGC CGGCGTGAA GCCTTACAAT
151  GCCCTGCAGG TTGCCGACG CGATATTAC ATCCGTGAGG GCTGTACAA
201  CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGAAACC GAGCGTTACG
251  GTCATTACTC TGTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401  AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCCAATCAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGCA AACAAATCCG
551  AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601  AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
  1  MKLQQLAEK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201  NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

m401/g401

	10	20	30	40	50	60
m401.pep	MKLQQLAEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
g401	MKLQQLAEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m401.pep	IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW					

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```

g401      |||||
          IREGCYNCHSQMIRPPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWLNARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
g401      HRIHLLNPRDVPESNMPAFWLNARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGCGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAA
151 GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGCGAAACC GAGCGTTACG
251 GTCATTACTC TGTGCGCGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTC CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAEK IGVLVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPPFRAET ERYGHYSVAG ESVDHPFQW
101 GSKRTGPDLA RVGGGRYSDEW HRIHLLNPRD VVPESNMPAF WLNARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

          10      20      30      40      50      60
m401.pep  MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
a401      MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
          10      20      30      40      50      60

          70      80      90      100     110     120
m401.pep  IREGCYNCHSQMIRPPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          |||||
a401      IREGCYNCHSQMIRPPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWLNARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
a401      HRIHLLNPRDVPESNMPAFWLNARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttccttacc ggattATTGA GCTTGGGtAt agaagtCtTg tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTTTC atttattctt
151 gcctGttttc tgACCGtat cgcgcgcgc gCgTATTTTG GCAAACGGAT
201 TTGCCGcAGC CGCTTTGTTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccgaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCTGtctgc
351 CGtcGTCAGG GGGTTGATTT TCCCCTTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTTCT GCTGctgtcc
551 cTTTGTttTg tacaCTGtTC CAAAAAGTC TCCGACTGAA TGcAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTCTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG GCCGTCCGA TAGGTTGATT GAAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTttATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGATTG AGTACAGGT CGTGGGCGCG CGTCTTGCTT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGacg agccgcAAAT CGCACCgCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCCTG TGAGTGGCGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgctTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTcctt AATAAAGAAC
1301 TGCTCaagca aCGCCTTTcc cgGTTGATTT GGCCGGAAAG CGGCAGgcac
1351 gtATTGACA GCAGACCCGT GGATGCTGCA GCACAAAAGG TTgtctctCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNP SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPQAFSFLI
51  ACFLTGIavg AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAWLLT
101 GFSGFVHHAG IPITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPRDLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRI FVVGL STGSWARVLS
301 AIPQMqSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI RMTEPSAGAE VITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCnTTC
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACCCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGcAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCGGT ATCTTCATTA CCCTGCTGCG
351 CGTCGTCAsa sGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCCG CamCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TWTGATTTCT GCTGCTGTCC
551 CTTTGTttTg TACACTGTTT CAAAAAGTC TCCGACTGAA TGcAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcYtAC TGCCGGATTC

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```

651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TCGGTTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAG
801 CCGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCGGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAAT CGCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGCTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCAGG ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTG GGCCGGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCCT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACCGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL
51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICKIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSGWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEPLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVVSRLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPAQAFSFTLACFLTGIAVG					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVPAQAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICKIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQQIYLLICLIS					
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICKIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQQIYLLICLIS					
	130	140	150	160	170	180
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDPDRLIENKHGIVAVY					
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDPDRLIENKHGIVAVY					
	190	200	210	220	230	240
m402.pep	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS					
g402	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS					
	250	260	270	280	290	300

726

```

g402      |||||:|||||
          HRDGDKVYGANVYDGAYNTDIFNSVNGIERAYLLPSLKSGIRRIFFVVGSLTGSWARVLS
          250      260      270      280      290      300

          310      320      330      340      350      360
m402.pep  AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRPDEKFDLILM
          |||||
g402      AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRPDEKFDLILM
          310      320      330      340      350      360

          370      380      390      400      410      420
m402.pep  NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          |||||
g402      NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          370      380      390      400      410      420

          430      440      450      460      470      480
m402.pep  VGSATPVVFPNKELLKQRLSRLIWPESGRHFVDSSTVDAQAQVVSRLIQMTEPSAGAE
          |||||
g402      VGSATPVVFPNKELLKQRLSRLIWPESGRHFVDSSTVDAQAQVVSRLIRMTEPSAGAE
          430      440      450      460      470      480

          490
m402.pep  VITDDNMIVEYKYGRGIX
          |||||
g402      VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1   ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT T ATATGCTTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTCCTCGT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC CGGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTCCTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTGAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTCCAATG TTTATTTGCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTTC CAAAAAAGTC TCCGACTGAA TGCAGTGTCTG
601 TGAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TCGCGTTTAC CATAGAGATG GTGATAAGGT TGTATTGCG
751 GCGAATGTAT ACGACGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGCTT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCAGG ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTG GGCCGGAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTCCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1   MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL

```


51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFWAGIADF LILGAAWLLT
 101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
 151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
 201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
 251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVVG STGSWARVLS
 301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
 351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
 401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
 451 VFDSSTVDAA AQKVVSRLMI QMTEPSAGAE VITDDNMIVE YKYGRGI*

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPOAFSFTLACFLTGIAVG					
a402	MDIVNTKPNTSLIYMLSFLSGLLSLGIEVLWVRMFSFAAQSVPOAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVVG STGSWARVLS					
a402	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVVG STGSWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402.pep	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
a402	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402.pep	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFSSTVDAAAQKVVSRLMIQMTEPSAGAE					
a402	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFSSTVDAAAQKVVSRLMIQMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402.pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGTACTCCA
251 TTGATGCACT GATTGCGGCG GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSGLTG LTSLSLTINA PALSRQSDG SGRSSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAPEA
251 AYKENYALWM GPYKVSKEIK PTEGLMVDFF DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGTACTCCA
251 TTGATGCACT GATTGCTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCAGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK

```



```

51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYETT AETTSGLTG LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRF AVEQELVAASARA AVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRF AVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDY TYPREYETTAETTSGLTG					
m406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDY TYPREYETTAETTSGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406.pep	LTSLSTLNAPALSRQSDGSGSRSS LGLNIGMGDYRNETLT TNPRDTAFLSHLVQTVF					
m406	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLT TNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGPX					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGTGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```


730

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501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAA
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACAGAAG GATTAATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
  1 MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
  51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
 101 DYTYPRIYET AETTSGLTGL TTSLSTLNA PALSRQSDG SGSKSSLGLN
 151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
 201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
 251 AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301 SHEGYGYSDE AVRRHRQGPQ *

m406/a406 98.8% identity in 320 aa overlap

      10      20      30      40      50      60
m406.pep MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKDMDLQALHGR
a406      MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKDMDLQALHGR
      10      20      30      40      50      60

      70      80      90     100     110     120
m406.pep KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRIYETTAETTSGLTGL
a406      KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRIYETTAETTSGLTGL
      70      80      90     100     110     120

      130     140     150     160     170     180
m406.pep LTTSLSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF
a406      LTTSLSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF
      130     140     150     160     170     180

      190     200     210     220     230     240
m406.pep FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
a406      FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
      190     200     210     220     230     240

      250     260     270     280     290     300
m406.pep IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTTEGLMVDFS DIRPYGNHTGNSAPSVEADN
a406      IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTTEGLMVDFS DIQPYGNHMGNSAPSVEADN
      250     260     270     280     290     300

      310     320
m406.pep SHEGYGYSDEVVRQHRQGPQX
a406      SHEGYGYSDEAVRRHRQGPQX
      310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
  1 atggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
 51 ggcaggcgga gatggcaaga tgcagcatca ctttgacggc aggttgctgc

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731

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101  tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgagggg
151  cagctgggtc atgtcgcttc agccgatgga gaagccgctg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggc cagaccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcgat cggttcgtat acgctgccgc
501  cgaccagggt ggcgatttcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcca caggggatgc gtaaccggcg atcgggcgga
651  taatttcgcg tttagtttcg tcgtcttggt tgtcaaatc caacaaggct
701  ttcgggtgga tgccgatttg cgggttgatg ataaattcca tacgcgcca
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  tgccgacggt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taattgttac gtccagcagg ccggcataga taaagccggg
901  atcgcccttc gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggctgcatt gccgcagccg acgacggcag gaataaccag ttcgcgcgcg
1001 atgatggcgg cgtggcagggt gcgtccgccc cggttggtca cgatggcgga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcgat tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgcacaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 ctctctggga tttagcgggt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgctcc ccattcgata tccatcgggc gcccgtagtg
1351 tttttcgatg gtcagcgcgt agtgtgcca ctcggtgatt tcttcgctcg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgcccg cttcggtctt gtcggtgaaa atcattttga tgtgttcga
1501 acccatggtc ttgcgcagga tggcgggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggatc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLADT DIFVLLAAGG DGKMQHHFDG RVAIVKRFPH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFGFVGVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVVKF QQGFRVDADL AVDDKFHTRQ
251 ADAFAQIGIE ABCEFGIADV HHDFDGCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHG
351 STFHFGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHLLTD FLTDGTTFAQ
401 DGFFAVDQVA AQVAAFFFLG FDGFGAGLQD VEFVAVQAVAS PFDIHRAAVV
451 FFDGQRVVQC LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGFEBI KFVRVDRALY DVFAQTVRGG NKDDLTVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggtcggac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgagggg
151 cagttgggtc atgtcgcttc agccgatgga gaagccgctg aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacgttggc caacccatt tcctcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagtgttcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcgat cggttcgtat acgttgccgc
501 cgaccagggt ggcgatttcg ttggatttga agtcggacat acggacgatg
551 gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601 ttatcgcacg tagaagtcca caggggacgc gtaaccggcg atacggcggg
651 taatttcgcg ttttaattcg tcgtcttggt tgtcaaatc caacaargct

```


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701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca gggtggcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact tttacaggtg ctttaggcatt attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttcg gcacaggata cggtaacttc ttgaccgttt ttcagcaatt
951 cgggtgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggc acggccgcgg cggttggtta cgatggcaga
1051 agcagctttc atcacgggtt cccaatccgg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaaagc gcgcaggttg cggttgccct
1251 cttcttgga ttttacgggt tcgggacggg cttgcaggat gtagagtgtt
1301 ccgtccaagc cgtcgctcc ccattcgata tccatcgggc ggccgtagt
1351 ttttctgatg gtcagtgcgt aatgcgcca ctcagtaatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgtttga
1501 acccatggtt ttacgcagga tggcgggcgt gccggytttg agcgtgggtt
1551 tgaacacatr aaattcgtcc gggttgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggagg aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
1  MVGXALTADA DIFVLLAAGG DGKVVQHHFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FFXVVLVVKF QXFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ PTRDDGGVAG TAAAVGNDGR
351 STFHHGFPIR IGHVGNFYVA GFDGIHLGSI FNQAHALTD FLTDGAAPAX
401 YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQCVMRQ LSNFFVNGE AVAVFLGDI VGYGTFGFCF VGKNHFDVFX
501 THGFTQDGG LARFERGFEX KFVRVDRTRY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

```

m501.pep      10      20      30      40      50      60
               MVGXALTADADIFVLLAAGGDGKVVQHHFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG
               ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501           10      20      30      40      50      60
               MVGRTLTAADTDIFVLLAAGGDGKMQHHFDGRFAFVKRFGHQAAVSVEAEGQLGHVVRADG

m501.pep      70      80      90     100     110     120
               EAVEVLQELFRQYRVARQLAHHNQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501           70      80      90     100     110     120
               EAVEVLQELFRQYRVARQLAHHNQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG

m501.pep     130     140     150     160     170     180
               QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFVGVGH
               |||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501          130     140     150     160     170     180
               QTHFVTNAFQGFQGETVFEALGNITRRTTEAQHRVFFMRVYVAADQVGVFGFVGVGH

m501.pep     190     200     210     220     230     240
               TDDGFTRINRCCQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLFVKFQQGFRVDADL
	190 200 210 220 230 240
	250 260 270 280 290 300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDI GNLYVQQTGIDKAG
	: : : : :
g501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFDGCFWHIVQDIGNLYVQQAQIDKAG
	250 260 270 280 290 300
	310 320 330 340 350 360
m501.pep	IAFGTGYGNFLTVFQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
	: : : : :
g501	IAFGTGYGNFLTVFQEFGRIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
	310 320 330 340 350 360
	370 380 390 400 410 420
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGA AFXYGFVA VDGEAAQVA VALFLG
	: : : : :
g501	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGTTFAQDGF FAVDGVAAQVA AVALFLG
	370 380 390 400 410 420
	430 440 450 460 470 480
m501.pep	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDQCVMRQLSNFFVGNGEAVAVFLGDID
	: : : : :
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDQQRVVCLGDFVGNGEAVAVFFGDFD
	430 440 450 460 470 480
	490 500 510 520 530 540
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGG LARFERGF EHXKFVRVDR TLYDVFAQT VRRG
	: : : : :
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGF EHIKFVRVDRALYDVFAQT VRRG
	490 500 510 520 530 540
	550
m501.pep	NKDDLIVXGFGVEGEHHT
	:
g501	NKDDLIVVAGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq	(partial)
1	ATGGTCCGAC GGGCCTTGAC CGCAGATGCC GACATATTTG TTCTGCTTGC
51	GGCAGGCGGA GATGGCAAGG TGCAGCATCA CTTTGACGGC AGGGTTGCGT
101	TCGTCAAACG ATTCCGATAC CAAGCCGCTG TCGCGGTCGA GACCGAGGCT
151	CAGTTGGGTC ATGTCGTTCT AGCCGATGGA GAAGCCGTCG AAGTATTGCA
201	GGAATTGTTT CGCCAATACC GCGTTGCTCG GCAGCTCGCA CATCATAATC
251	AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301	GACAACGGCT TCGGCTTCGC CCAAAGTGCG GACGAACGGA ATCATGATTT
351	CAACGTTGGT CAACCCCAT TCAATCGCGA CGCGTTTCAA GGCTTTGCAT
401	TCCAAGGCGA AACAGTCTTT GAAGTTGTCG GCGACATAAC GCGCCGACCC
451	ACGGAAGCCC AACATCGGGT TTTCTTCATG CGGTTCTGAT ACGTTGCCGC
501	CGACCAGGTT GCGGTATTCT TTGGATTGTA AGTCGGACAT ACGGACGATG
551	GTTTTACGCG GATAAACCGA TGCGGCCAAT GTCGCCACGC CTTCCGCGAT
601	TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACCGGCG ATACGGCGGG
651	TAATTTCCGC TTTTAATTCG TCGTCTTGTT TGTCAAATTC CAACAAGGCT
701	TTGGGGTGGA TACCGATTGT GCGGTTGATG ATAAATTCCA TACGCGCCAA
751	GCCGATGCCT TCGCTGGGCA GGTGCGGAA GCTGAATGCG AGTTCGGGAT
801	TGCCGACGTT CATCATGACT TTTACAGGTG CTTTAGGCAT GTTGTCACAA
851	GCAACATCGG TAATTTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901	ATCGCCTTCG GCACAGGATA CGGTAACCTT TTGACCGTTT TTCAGCAATT
951	CGGTTGCATT GCCGCAGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG

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1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGTT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTGCGACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT
1251 CTTCTGGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGCCT AATGCCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGTTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGAC GACGTTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGGTCGT AACCGGATTC
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```

1 MVGRALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVVKF QQGFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAAFAQ
401 DGFFAVDRKA AQVAAFFFLG FDGFGTGLQD VEFVQAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFVGNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTGTF
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

m501.pep	10	20	30	40	50	60
	MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRLTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
m501.pep	70	80	90	100	110	120
	EAVEVLQELFRQYRVARQLAHHNQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHHNQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
m501.pep	130	140	150	160	170	180
	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH					
m501.pep	190	200	210	220	230	240
	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQGFGVDTDL					
m501.pep	250	260	270	280	290	300
	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDNIGNLYVQQTGIDKAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVQSNIGNLYVQAGVDEAG					
m501.pep	310	320	330	340	350	360
	IAFGTGYGNFLTIVFQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFPIR					
a501	IAFGTGYGNFLTIVFQQFGCIAAADNGRNTQFARDDGGVAGTSAPVGHDDGGSFAFHHRFPIW					


```
g502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcgcggtt gtcctctgac
51  cgtcgcggtc gcttccgcac aggcggggcg ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca aaccgtccaa
151 agcaaaaaga aaacccaacg cgcgcacggc acgtttcaaaa tctctgcgcc
201 ggccctcttc aattgggaat acactttgcc ctacagacag actattgtcg
251 gcgacgggtc aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcggcggc agccccgcgc ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgcggg
451 ctaccaatac atccgcacatc gtttcaaagg cggcaacctc gccgccatgc
501 aqcttaa
```

g502.pep

1	<u>MMKPHNLFQF</u>	<u>LAVCSLTVAV</u>	<u>ASAQAGAVDA</u>	LKQFNNDADG	ISGSFTQTQV
51	SKKKTQTAHG	TFKILRPGLF	KWEYTLPYRQ	TIVGDCQTIV	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	RGNAQTQRR
151	LPIHPERLQR	ROPRRHAA*			

```
m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gctccctgac
51  cgtcgcgcgc gcttcgcgac aggcggggcg ggtagacgcg cttaaagcaat
101 tcaacaacga tgccgacggg atcagcggca gcttcaccca amccgtccaa
151 wgcaaaaaga aaacccaaa cgcgcagcgc acgttcaaaa tccctgcgacc
201 gggccttttc aatggggaat acaccaaact t.acaggcaa acctcgtgcg
251 gcgacgggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgcg ccatcctgtc
351 gaacaaarcc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgccggcta
451 ccaatacatc cgcatacggc tcaaaggcgg caacctcgcc gccatgcagc
501 ttaa
```

```
m502.pep
  1  MMKPHNLQFQ LAVCSLTVA ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XKKKKTQTAHG TFKILRPLGF KWETTKLYRQ TIVGDGQTWV LYVDVLAQVT
101 KISQDQAIGFV SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQRRRL
151 PPHPHRLORR OPRRHAAX
```


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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502 .pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 .pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLTPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 .pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502 .seq

```

1  ATGATGAAAC CGCACAACT GTTCCAATTC CTCGCGGTTT GCTCCCTGAC
51  CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT AACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG GGCAACGCC AAACGCAACA ACGCCGGCTA
451 CCAATACATC CGCATCGGCT TCAAAGGCGG CAACCTCGCC GCCATGCAGC
501 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502 .pep

```

1  MMKPHNLFQF LAVCSLTVSVA SAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51  SKKKTQTAHG TFKILRPGLF KWEYTSFYKQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV GNAQTQQRRL
151 PIHPHRLQRR QPRRHAA*

```

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502 .pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVAASQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 .pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSFYKQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 .pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```

1  ATGatGAAAc  cgcaCaacct  gttccaaATtC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTGGACGCG  CTCAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201 GGGCCTCTTC  AAATGGGAAT  ACACCTTGCC  CTACAGACAG  ACTATTGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGGTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAA
601 GCGGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKTQTAHG  TFKILRPGLF  KWEYTLPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIGG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  RATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSSIF  GGLTNPQLS  RGAFFKTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```

1  ATGATGAAAC  CGCACAACTT  GTTCCAATTC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTAGACGCG  CTTAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201 GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATAGGCGGC  AGCCCCGCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGCTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGGTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAA
601 GCGGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKTQTAHG  TFKILRPGLF  KWEYTKPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIGG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  LATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSSIF  GGLTNPQLS  RGAFFKTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG					
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG					
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAGYQYIRIGFKGNNLAAMQLKDSFGNQTSSIF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGNNLAAMQLKDSFGNQTSSIF					
	130	140	150	160	170	180


```

          190      200
m502-1.pep  GGLNTNPQLSRGAFKFTPPKGV DVL SNX
            |||
g502-1      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
          190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACTT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51  CGTCTCCGTC GCTTCCGCAC AGGCGGGGCG GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT AACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCG CCATCCTGTC
351 GAACAAACCC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGCG
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51  SKKKTQTAHG TFKILRPLGF KWEYTSPIKQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAI GG SPAAILSNKT ALESSYLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQT SIFS GGLNTNPQLS RGAFTFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

          10      20      30      40      50      60
a502-1.pep MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG
            |||
m502-1      MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG
          10      20      30      40      50      60

          70      80      90      100     110     120
a502-1.pep TFKILRPLGFKWEYTSPIKQ TIVGDGQTVWLYDVDLAQVTKSSQDQAI GGSPAAILSNKT
            |||
m502-1      TFKILRPLGFKWEYTKPYRQ TIVGDGQTVWLYDVDLAQVTKSSQDQAI GGSPAAILSNKT
          70      80      90      100     110     120

          130     140     150     160     170     180
a502-1.pep ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKG GNLAAMQLKDSFGNQT SIFS
            |||
m502-1      ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKG GNLAAMQLKDSFGNQT SIFS
          130     140     150     160     170     180

          190     200
a502-1.pep GGLNTNPQLSRGAFKFTPPKGV DVL SNX
            |||
m502-1      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgtcggcatc ggtaatcatt ttgttccatg ccgcttcgat
51  ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaatatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTSNF
51  ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

m503.pep
1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
51 ASAAEMRSLR PLCARNAR*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

```

      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLR
          |||||:|||||||||||||||||||||||||||||||||||||||:|
g503      MSAPSASVILFHAASISASSCSGKGVSKIHWRISLPTRASSETSSSTSNFARAAEMRSFR
          10      20      30      40      50      60

      69
m503.pep  PLCARNAR
          |||||
g503      PLCARNAR

```

```
a503.seq
1  ATGTC CGCGC CGCCGGC ATC GGC AACCAT TTTG TCCATG CCGCTTCGAT
51  TTCGCGCATCG AGCTG TTCGG GGAAGGGCGT GTCAA AATC CATTGGCGGA
101 TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
151 GCCAGTGGCG CGGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC
201 GCGGTAG
```

a503.pep
1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNE
51 ASAAEMRSLR PLCARNAR*

		10	20	30	40	50	60
m503.pep		MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLP TRASSATSSTSNFASAAEMRSLR					
a503		MSAPPASATILFHAASISASSCSGKGVSKIHWRI SLP TRASSATSSTSNFASAAEMRSLR					
		10	20	30	40	50	60
	69						
m503.pep		PLCARNARX					
a503		PLCARNARX					

g503-1.seq

```
1  ATGGCGCGGT  CGTTGTACAG  GGAGGCGAAA  ACGTGGCGCA  TCGCTTTTTT
51  AACGTTATCC  AAGCCATTGA  TATTACAGAA  GGTTTCCTGT  TGGCCGGCAA
101 ATGATGCGTC  GGGCAGGTCT  TCGGCGGTTC  CGGAAGAGCG  TACGGCAACG
151 GAAATGTCCG  CGCGCTCGGC  ATCGGAATAC  ATTTTGCTCC  ATGCCGCTTC
201 GATTTCCGGA  TCGAGCTGTT  CGGGAAAGGG  CGTGTCCTAA  ATCCATTGGC
251 GGATTTCTTT  GCCGACGCGT  GCCAGTTCGG  AAACGCTCTC  GACATCCAAT
301 TTTGCCAGAG  CGGCGGAAAT  GCGTTCGTTC  AGACCGTTGT  TGCGGAGAAA
351
```


The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1357>:

This corresponds to the amino acid sequence <SEO ID 1358; ORF 503-1>:

g503-1 / m503-1 89.9% identity in 119 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1359>:

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEEETATEMSAPPASAT					
m503-1	MARSLYREANTWCIASLTLSKPLMFKKVSCCPANDASGRSSAVAEEETATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRI	SLPTRASSATSSTSNFASAAEMRSLRPLCARNARX				
m503-1	ILFHAASISASSCSGKGVSKIHWRI	SLPTRASSATSSTSNFASAAEMRSLRPLCARNARX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

```

g504.seq
1  atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgcacccat ccgcgtgaac
151 catcctttga ccttgccacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccacgtgtga ccgcacccgt gatgcggcag ggcaggcgggt
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattatTTTT
551 ggctgaccgg cacgcgcagc ggcttgagc agcaataccg ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcaacaat tcatgctggc tgcggaaaac
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atccccgaa ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cgttacggct tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccctgt cgcggggtgc gcttttggtc tatctcggct cggatttggt
1101 ggttttgggt acagtattta tgttttatgt gccccaaaaa cgggcgtggg
1151 tattgttttc aaacdgcaca atccgttttg ctatgtcttc ggccgcgagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

```

g504.pep
1  MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKRS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPABI REQFMLAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQODKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLHLS MDAYTGLTEY PAPMLQLDQ FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

```

m504.seq.
1  atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgcacccat ccgcgtgaac
151 catcctttga ccttgccacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcgggt
501 cgaatataaa aactatatgc tgccggtttt gcaggaaacg gattatTTTT
551 ggattaccgg cacgcgcagc ggcttgagc agcaataccg ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaag gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcaacaat tcatgctggc tgcggaaaac
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atccccgaa ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggc tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgctc gggtttgcag

```


1051 atgacccggtt ccccggtgtc gcttttggtc tatctcggct cgggtgctgtt
 1101 ggtattgggtt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
 1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgcagc
 1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
 1251 gctcggcaag gacttgaatc atga

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..

1 ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN HPLTLHGITI					
	:					
g504	MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN HPLTLHGITI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGS DLTFKAWN LGDASREPVVLK ATSIHQFPLE IGKHKYRLEF DQFTSMNVED					
	:					
g504	YQASFADGGS DLTFKAWN LRDASREPVVLK ATSIHQFPLE IGKHKYRLEF DQFTSMNVED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKSLKSTLXDVRA VTQEGKKYTN IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ					
	:					
g504	MSEGAREKSLKSTLNDVRA VTQEGKKYTN IGPSIVYRIR DAAGQAVEYK NYMLPILQDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRSG LQQQYRWLR IPLDKQLKAD TFMALREFLK DGEGRKRLVADATKGAPAEI					
	:					
g504	DYFWLTGTRSG LQQQYRWLR IPLDKQLKAD TFMALREFLK DGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR					
	:					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKQQDKMQGYFYEMLYGVMNAALDETIR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
	:					
g504	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m504.pep	YLGSVLLVLGT VLMFYVREK RAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK					
	:					

743

g504 YLGSVLLVLGTVFMFYVPKKRAWLFSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq
 1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTGAAGA AATTCCATAT
 51 CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG
 101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC
 151 CATCCTTTGA CCTTGCACGG CATCACGATT TATCAGGCGA GTTTTGCCGA
 201 CGCGGTTTCG GATTTGACAT TCAAGGCGTG GAATTGGGT GATGCTTCGC
 251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAATT TCCGTTGGAA
 301 ATTGGCAAAC ACAAATATCG TCTTGAGTTC GATCAGTTTA CTCTATGAA
 351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAAGC CTGAAATCCA
 401 CGCTGAACGA TGTCCGCGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT
 451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATCGGCGAG GGCAGGCGGT
 501 CGAATATAAA AACTATATGC TGCCGGTTTT GCAGGAACAG GATTATTTTT
 551 GGATTACCGG CACGCGCAGC GGCTTGACAG AGCAATACCG CTGGCTGCGT
 601 ATCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTCGCTGA
 651 GTTTTTGAAA GATGGGGAAG GCGCAAACG TCTGTTGCC GACGCAACCA
 701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TGCGGAAAAC
 751 ACGCTGAACA TCTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
 801 TACGTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT
 851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGATGA AACCATACGC
 901 CGGTACGGCT TGCCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT
 951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA
 1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTTGCAG
 1051 ATGACCCGTT CCCCGGGTGC GCTTTTGGTC TATCTCGGCT CCGTGCTGTT
 1101 GGTATTGGGT ACGGTATTGA TGTTTATGT GCGCGAAAAA CCGGCGTGGG
 1151 TATTGTTTTT AGACGGCAAA ATCCGTTTTG CCATGTCTTC GGCCCGCAGC
 1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
 1251 GCTCGGCAAG GACTTGAATC ATGACTGA

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep
 1 ILVQDLPFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMALAE
 251 TLNIFAQKGY LGLDEFITSN IPKEQDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQOD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWLFSQDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPFEV	KLKKFHIDFY	NTGMPRDFAS	DIEVTDKATG	EKLERTIRVN	HPLTLHGITI
a504	ILVQDLPFEV	KLKKFHIDFY	NTGMPRDFAS	DIEVTDKATG	EKLERTIRVN	HPLTLHGITI
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGS	DLTFKAWNLG	DASREPVVLK	ATSIHQFPLE	IGKHKYRLEF	DQFTSMNVED
a504	YQASFADGGS	DLTFKAWNLG	DASREPVVLK	ATSIHQFPLE	IGKHKYRLEF	DQFTSMNVED
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKS	SLKSTLXDVR	AVTQEGKKYTN	IGPSIVYRIR	DAAGQAVEYK	NYMLPVLQEQ

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```

|||||
a504      MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEEQ
           130      140      150      160      170      180

           190      200      210      220      230      240
m504.pep  DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
           |||||||
a504      DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
           190      200      210      220      230      240

           250      260      270      280      290      300
m504.pep  REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
           |||||||
a504      REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
           250      260      270      280      290      300

           310      320      330      340      350      360
m504.pep  RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
           |||||||
a504      RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
           310      320      330      340      350      360

           370      380      390      400      410      420
m504.pep  YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
           |||||||
a504      YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
           370      380      390      400      410      420

m504.pep  DLNHDX
           |||||
a504      DLNHDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1  atgtttcggtt  tacaattcag  gctgtttccc  cctttgcgaa  ccgccatgca
51  catcctgttg  accgccctgc  tcaaatgcct  ctccctgctg  tcgctttcct
101 gtctgcacac  gctgggaaac  cggctcggac  atctggcggt  ttacctttta
151 aaggaagacc  gcgcgcgcat  cgctcgccaa  atgcggcagg  cgggtttgaa
201 ccccgacacg  cagacggtca  aagccgtttt  tgcggaaacg  gcaaaatgcg
251 gtttggaact  tgcccccgcg  tttttcaaaa  aaccggaaga  catcgaaaca
301 atgttcaaag  cggtagacgg  ctgggaacac  gtgcagcagg  ctttggacaa
351 gggcgaaagg  ctgctgttca  tcacgccgca  catcggcagc  tacgatttgg
401 ggggacgcta  catcagccag  cagcttcctg  tccacctgac  cgccatgtac
451 aagccgccga  aaatcaaagc  gatagacaaa  atcatgcagg  cgggcagggt
501 gcgcggcaaa  ggcaaaaccg  cgcccaccgg  catacaagg  gtcaaacaaa
551 tcatcaaggc  cctgcgcgcg  ggcgaggcaa  ccatcatcct  gcccgaccac
601 gtcccttctc  cgcaggaagg  cggcggcgtg  tgggcggatt  ttttcggcaa
651 acctgcatac  accatgacac  tggcggcgaa  attggcacac  gtcaaaggcg
701 tgaaaaccct  gtttttctgc  tgcgaaacgc  tgcccgcagg  acaaggcttc
751 gtgttgacac  tccgccccgt  ccaaggggaa  ttgaacggca  acaaagccca
801 cgatgccgcc  gtgttcaacc  gcaataccga  atattggata  cgccgttttc
851 cgacgcagta  tctgtttatg  tacaaccgct  ataaaacgcc  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1  MFRLQRLFP  PLRTAMHILL  TALLKCLSL  SLSCSLHT  LGN  RLGHAFYLL
51  KEDRARIVAN  MRQAGLNPD  QTVKAVFAE  AKCGLELAP  FFKKPEDIET
101 MFKAVHGW  VQALDKGEG  LLFITPHIG  YDLGGYISQ  QLPFHLTAMY
151 KPPKIKAI  D  IMQAGVRGK  GKTAPTGIQ  GKQIIKALR  GEATIILPDH
201 VPSPQEGGV  WADFFGKPA  Y  TMTLAAKLA  H  VKGVKTLFF  C  CERLPDQGQF
251 VLHIREVQGE  LNGNKAHDA  A  VFNRNTEY  WI  RRFPTQYLF  M  YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

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m505.seq (partial)

```

1  GGCGATGTTT GTTTACAATT CAGGCTGTTT CCCCCTTTGC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTTGCAGAA ACGGCAAAAG
251 GCGGTTTGGA ACTTGCCCCC GCGTTTTC AAAAAACCGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCAGGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTCCGCGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCCACC
601 ACGTCCCTC CCCTCAAGAA GCGGGGAAG GCGTATGGT GGATTTCTTC
651 GGCAACCTG CCTATACCAT GACGCTGGCG GCAATATTGG CACACGTCAA
701 AGGCGTGAAG ACCCTGTTTT TCTGCTGCGA ACGCTGCGCT GCGCGACAAG
751 GTTTCGATTT GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCGTGTT CAACGCAAT GCCGAATATT GGATACGCCG
851 TTTCCGACG CatATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSLL PLSCSLHTLGN RLGHILAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLELAPA FFRKPEDTET
101 MFKAVHGWEE VQALDKHEG LLFITPHIGS YDLGGYISQ QLPPPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAXLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRAEYW IRRFPETHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCSLHTLGNRLGHILAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLLSLSCSLHTLGNRLGHILAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEEHVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKCGLELAPAFFKKPEDTETMFKAVHGWEEHVQALDKGEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEEHVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKCGLELAPAFFKKPEDTETMFKAVHGWEEHVQALDKGEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFHLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQG					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFHLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQG					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIIILPDHVPSQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIIILPDHVPSQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTH					
g505	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTH					
	240	250	260	270	280	289
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTH					
g505	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTH					
	240	250	260	270	280	289

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

```
a505.seq
1   ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCGCGC TTTTTCAGAA AACCAGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGCG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GAAAAACCG CGCCTACCAG CATAAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGCG ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAGGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

```
a505.pep
1   MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
101 MFKAVHGWEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VVWDFFGKPA YMTLAAKLA HVKGVKTLFF CCELRPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*
```

m505/a505 99.0% identity in 287 aa overlap

m505.pep	10	20	30	40	50	60
	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	70	80	90	100	110	120
	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQALDKHEG					
	70	80	90	100	110	120
m505.pep	130	140	150	160	170	180
	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSIQG					
	130	140	150	160	170	180
m505.pep	190	200	210	220	230	240
	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
	190	200	210	220	230	240
m505.pep	250	260	270	280		
	CCELRPGGQGFDLHIRPVQGEELNGDKAHDAVFNRNAEYWIIRFPPTHI					
a505	CCELRPGGQGFDLHIRPVQGEELNGDKAHDAVFNRNAEYWIIRFPPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTGT ACCGCCCTGC TCAATGCTCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTGGGAC ATCTGGCGGT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CCGGTTTGAA
201 CCCCAGCCCC AAAACGGTCA AAGCCGTTTT TCGGGAACG GCAAAAGGCG
251 GTTTGGAAC TCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACGCGCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CCGGCAGGGT
501 TCGCGGCAAA GGA AAAACCG CGCCTACCAG CATACAAGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CAGCTCAAAG
701 GCGTGAAGAA CTGTTTTTC TGCTGCGAAC GCCTGCTGG CCGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHLPFYLL
51  KEDRARIVAN MRQAGLNPD PTKVAVFAET AKGGLLELAP FFRKPEDLET
101 MFKAHVHGEH VQALDKHEG LLFIPPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIKD IMQAGRVRGK GKTAPTSIQG VKQIKALRS GEATIVLPDH
201 VPSQEGGEG VVVDFFGKPA YMTLAAKLA HVKGVKTLFF CCELRPGGGG
251 FDLHIRPVQG ELNGDKAHDA AVFNRAEYW IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLPPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHLPFYLLKEDRARIVAN					
g505	MFRLQFRLPPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHLPFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPDPTKVAVFAETAKGGLLELAPFFRKPEDLETMPKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTKVAVFAETAKGGLLELAPFFRKPEDLETMPKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	MRQAGLNPDPTKVAVFAETAKGGLLELAPFFRKPEDLETMPKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTKVAVFAETAKGGLLELAPFFRKPEDLETMPKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	LLFIPPHIGSYDLGGYISQQLPFPLTAMYPKPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFIPPHIGSYDLGGYISQQLPFPLTAMYPKPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505-1.pep	LLFIPPHIGSYDLGGYISQQLPFPLTAMYPKPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFIPPHIGSYDLGGYISQQLPFPLTAMYPKPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505-1.pep	VKQIKALRSGEATIVLPDHVPSQEGGEGVVVDFFGKPAYMTLAAKLAHVKGVKTLFF					
g505	VKQIKALRSGEATIVLPDHVPSQEGGEGVVVDFFGKPAYMTLAAKLAHVKGVKTLFF					
	190	200	210	220	230	240
m505-1.pep	VKQIKALRSGEATIVLPDHVPSQEGGEGVVVDFFGKPAYMTLAAKLAHVKGVKTLFF					
g505	VKQIKALRSGEATIVLPDHVPSQEGGEGVVVDFFGKPAYMTLAAKLAHVKGVKTLFF					
	190	200	210	220	230	240
m505-1.pep	CCELRPGGGGFDLHIRPVQELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX					
g505	CCELRPGGGGFDLHIRPVQELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKTPX					
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLPPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHLPFYLLKEDRARIVAN					
a505	MFRLQFRLPPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHLPFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLPPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHLPFYLLKEDRARIVAN					
a505	MFRLQFRLPPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHLPFYLLKEDRARIVAN					
	70	80	90	100	110	120

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```

m505-1.pep  MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMPKAVHGWEHVQQALDKHEG
a505          MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMPKAVHGWEHVQQALDKHEG
              70      80      90      100     110     120

              130     140     150     160     170     180
m505-1.pep  LLFITPHIGSYDLGGRIYSQQLPFPFLTAMYKPPKIKAIIDKIMQAGRVRGKGKTAPTSTIQG
a505        LLFITPHIGSYDLGGRIYSQQLPFPFLTAMYKPPKIKAIIDKIMQAGRVRGKGKTAPTSTIQG
              130     140     150     160     170     180

              190     200     210     220     230     240
m505-1.pep  VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFGPKPAYTMTLAAKLAHVKGVKTLFF
a505        VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFGPKPAYTMTLAAKLAHVKGVKTLFF
              190     200     210     220     230     240

              250     260     270     280     290     299
m505-1.pep  CCEERLPGGGQFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
a505        CCEERLPGGGQFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAAACAA AGCCTGTTC TCGCGTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTT GCGCAAGTCG GGTGTGTGCT
201 GCCATGGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GGCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GCGGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGGC GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGAACCTCGC CGCGCTCGAT GGCTTCGTAC AGGTGCGGCT
651 GATGGCTTTC GCGGTCGTGC GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAATTTCA CCCAAAACG
751 TTCGCCGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGGG CTTGCGGCAG CAGCGTCCAG AAGTCCAGT TGTGTGTGCG
901 GGAACGCATA TTGGTGCAGG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCGGACC
1001 ACATCCCACT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG TGTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGCGCGC CGTTGTTTAT
1351 GGTACAGATG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCTTT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTTGAATCG
1501 ACATTTTATT TTCCTTTGCG AAAAATAATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

```

1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHVQ EQGARLAEVV VIVLAVVPVC
51  RVAVDQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRAT
101 RTIDGDLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRLDLVH

```


749

201 RPFRELAALD GFVOVALMAF AVVGDDFCFSF FVGQVFNPLL AAEMEFHPKT
 251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVC
 301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQRKTAD
 351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGQAVL IVGNGRAVVH
 451 GQMGYGAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFFFAKTM DAIIRQDFRY *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
 51 TGCCGAACAA TGCCTGTTTC TCGCGTCGT TCATCAGGTT GAACAGGGCG
 101 CGCGGTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
 151 CGCGTCGCGG TTGATTTTCA AAGGCGGTTC GGCGAATCG GGTGTGTGCT
 201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAAGCT GCCGyAGTTG
 251 CCGTCGCGCG GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
 301 CGGACGATTG ACGGGAATTT GGCGGAAGTT TACGCCCAA CGGTAGCGTT
 351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTTC ATCTsGGCTG
 401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGCGG ATTGTTCCAC
 451 ATCGGCGAAG AAGTTTTCGG GATTGCGGT CTCAAACGGA TGATAAGGTA
 501 CTTTTCCGC GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC
 551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
 601 GCGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC AGGTTTTTAA
 651 TGCCTTGTG GGTGCGGAAA TGGAATTCA CCCAAAACG CTGCGCTGCT
 701 TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
 751 GCCGCGGGG ATGCCGCGGT CGTTCATCAC GATGGTAACT TGGTGCAGTG
 801 CTTCCGGCAG CAGCGTCCAG AAGTCCAGT TGTGTTGGC AGAGCGCATA
 851 TTGGTGCAGG GGTGCGGTTT GACGGCTTTG TTCAGGTGCG GGAACCTACG
 901 CGGTCGCGC AGGAAGAACA CGGGCGTGT GTTGCCGACC ACATCCAGT
 951 TGCCCTTCTTC GGTATAAAAT TTCAAGGCAA AACC CGCGAT GTCGCGTCT
 1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
 1051 CTCTGGTTTT TTGCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC
 1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTC AGTCATCGCT
 1151 CTTGTTCTCT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC
 1201 GATTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
 1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT
 1301 ACGCCAAGAT TTTCGCTATT AA

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHVQ EQGARLAEIV VIVLAVVPVC
 51 RVAVDFFQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
 101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTGNE VARCEGGLFPH
 151 IGEVVFGLAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHLDLVH
 201 RPFRLAALD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
 251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFQ QRPEVPVVC
 301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQKKTAD
 351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVVH
 451 GQMGYRAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFFPVKTM DATIRQDFRY *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQVEQGARLAEIVVIVLAVVPVCRAVDFFQRRF					
	:: ::					
g506	MAVFDEVGRVIAHCGGGVVKQSLFLRVVHVQVEQGARLAEVVIVLAVVPVCRAVDFFQRRF					
	10	20	30	40	50	60

750

m506.pep	70	80	90	100	110	120
	GESGILLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAAXVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
m506.pep	130	140	150	160	170	180
	VIEQTRLQHFIXAGADTGVNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTRLQHFIRARADTGVNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	190	200	210	220	230	240
	VKRMIRYFFRVCFRHLDDVHRPFRKLAAFDGFXXVALMAFAVVGDFFGFFVGVQVFNALL					
g506	VKRMIRHFFGIGFRHLDDVHRPFRRELAALDGFVQVALMAFAVVGDFFCSFFVGVQVFNPLL					
	190	200	210	220	230	240
m506.pep	250	260	270	280	290	300
	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQGFQQRPEVPVVCG					
	250	260	270	280	290	300
m506.pep	310	320	330	340	350	360
	RAHIGARVAFDGFVQVQVGEFARVAQEEHGRVVADHIPVAFPGIKFQGTADVAFCIGCAAF					
g506	GTHIGARIAFDGFVQVQVGEFARVAQEEHGRVVADHIPVAFPGIEFQKTADVAFRIGCAAL					
	310	320	330	340	350	360
m506.pep	370	380	390	400	410	420
	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
m506.pep	430	440	450	460	470	480
	IQPQILRQRAARTGGQAVLIVGNRRRAVHVGQMGYRAFGGSHRSCSFSQVGMGGKRLTV					
g506	IQPQILRQGAARAGGQAVLIVGNRAVHVGQMGYGAFGGSHRSCSFSQVGMGGKRLTV					
	430	440	450	460	470	480
m506.pep	490	500	510	520		
	RFGGKRIRNRFLDCNKPLESTFYFPFVKTMDAIRQDFRY					
g506	RFGGKRIRNRFLDCNKPLESTFYFPFAKTMDAIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTCGC GCGGCGGTGT
51  TGCCGAACAA TGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGGCG
151 CGCGTCGCCG TTGATTTTCA AAGCGGTTTC GGCGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GTCCTTGTC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGGTTG ACAGGGATT TGGCGAAGTT CACGCCCAAG CGGTAGCGTT
351 CGCGTCGGC GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATACGGCA CTTTTTCCG ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGAAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT

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751

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651 GATGGCTTTC ACGGTCGTCG GCGATGATT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTG GGTGCGGAAA TGGAAATTTCA CCAAAAAACG
751 CTCGCCTGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCACTG CTTCGGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTG GTTGCCGACC
1001 ACATCCCACT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTGGG TGATGTCTGT CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTGCGCA ACAGGCGCGC CGTTGTTTAT
1351 GGTGAGATGG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

a506.pep

```

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVLRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEVFGIAV QLEFAHNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RPFRLAALD GEVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFQG QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYKRTERRAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVH
451 GOMGYRAFGG XHRSCFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVLRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAALDFGXXVALMAFAVVGDDFGGFFVGQVFNALL					
a506	VKRMIRHFFRIGFRHDLVHRPFRKLAALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC					
a506	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHIPVAFFGIKFGKTDVAFICGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHIPVAFFGIELQRKTADVAFICGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQORAARTGGQAVLIVGNRRRAVHVGQMGYRAFGGSHRSCSFSQVQMGKRLTV					
a506	IQPQILRQORAARTGGQAVLIVGNRRRAVHVGQMGYRAFGGXHRSFSQVQXGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTM DATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKTM DATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTTTCCTG CTTCAGACGG
101 CCTTTGCGCT CTTGCTGCTT GGCAACGGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCGCGCTTG AGCGTGGCTT GGACTTCTTC CAATTGCGGC
251 AGACGCTCTT CGTGTTCCGC AACCTGCATC GCCCATTCCG CCAATTCCGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTGC CCGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT
501 GACTGCTGCT CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNLFGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFFDLQLVF LKLHADLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTTAAGGCTT GGTTTTCCTG TTTCAGACGA
101 CCTTTGCGCT CTTGCTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCGGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTGCGGC
251 AGACGCTCCT CGTGTTCCGC AACCTGCATC GCCCATTCCG CCAGCTCCGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTA ACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTGC TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCAT
501 GCACTGCTGCT CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLQQGG CFLRGGGFGF VGQVXGLVFL FQTTFALEVL GNRLFGMGKL

```


51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLLVFG NLHRPFRQLG
101 LFFFDLQLVF FKLHADLLLL LMNALXLRRL CLLVAFDALV QVLLMADLEFF
151 OTGNLLAOHA ALVAOFMHCL LLRLFGSLQG VYFVV*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m507.pep		MLLLTLQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLF	GMGKLLLLLQ	RQF	AA		
		:	:	:	:	:	:
g507		MLLPALQGGGFLSGGGFGLVGQVQGLVFLLTAFALFVLGNLFG	MGKLLLLLQ	RQF	AA		
		10	20	30	40	50	60
		70	80	90	100	110	120
m507.pep		AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQ	LGLFF	FDLQ	L	VFKL	HADLLLL
		:	:	:	:	:	:
g507		AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQ	FGLLFF	DLQ	L	VFKL	HADLLLL
		70	80	90	100	110	120
		130	140	150	160	170	180
m507.pep		LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLA	QHAALVAQFM	HCILLRL	FGSLQ		
		:	:	:	:	:	:
g507		LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLA	QHAAFVAQFV	YCILLRL	FGSLQ		
		130	140	150	160	170	180
m507.pep		VYFV					
		:					
g507		VYFV					

1	ATGCTCTTGC	TGGCTTTGCA	ACAAGGCGGC	AGCTTCCTGC	GCGGCGGCGG
51	TTTCGGCTTC	GTCAGGCAGA	TTCAGGGCTT	GGTTTTCTTG	TTTCAGACGA
101	CCTTTGCGCT	CTTCGTGCTT	GGCAACGGTT	TGTTTCGGCAT	GGCAAGCTG
151	CTGCTGCTTC	AACGCCAGTT	CGCGGCGGAT	GCGGTTTGCC	TCGTCCTGCT
201	GGGTTTGGAA	GCGGCATTG	AGTGTGGCTT	GGGTTTCTTC	CAATTGCGGC
251	AGACGCTCTT	CGTGTTCGGC	AACCTGCAATC	GCCCATTCGC	CAATTCCGTT
301	TTGCTTTTCT	TCCGCCTGCA	ACTCGTTTTT	TTCAAGCTGC	ACGCGGATTT
351	GCTGCTGCTC	CTGATGGATG	CGCTGCATCT	GCGCCTGCGC	CGCCTGCTTG
401	TGCGGTTTCGA	TGCGTTTGGTG	CAGGTTTTGC	TGATGGCGGA	TTTGTTCTTC
451	CAAAACGGGCA	ATCTGTTTCG	GCAACACGCC	GCGTTTGTTG	CCCAATTTCGT
501	GCAACGGCCTG	CTGCTGCGAC	TGTTTCGGCAG	TCTGCAAGGC	GTGTACTTCG
551	TCGTTTTAA				

1 MLLLLALQQGG SFLRGGGGFG VRQIQGLVFL FQTTFALFVL GNGLFGMGKL
51 LLLQRQFAAD AVCLVLLGLE GGIECGLGFF QFGQTLFVFG NLRHPFRQFG
101 LLFFRLQLVF FKLHADLLLL LMDALHLRLR RLLVAFDALV QVLLMADLEFF
151 QTGNLFAQHA AFVAQFVHRL LLRLFGSLOG VYFVV*

	10	20	30	40	50	60
m507.pep	MLLLTLQGGGCF	LRGGGFGFVGQ	VXGLVFLFQTT	FALFVLGNRLF	FGMGKLLLLQ	RQFPAAD
	:		1:			
a507	MLLLALQGGG	SFLRGGGFGFV	RQIQGLVFLFQ	TTFALFVLGN	LFGMGKLLLLQ	RQFPAAD
	10	20	30	40	50	60
	70	80	90	100	110	120

g508.seq

1	ATGGTAGCGT	TTGCGCTTGA	TCAGGCCTC	CTGCTGCTGC	AACAGGGCGG
51	TTTGGGTGGC	GGCCTGAAGC	TGCGGCAGCT	TGGTTTGCAG	GGTTTGTACG
101	CGGGCGTATT	GCTCCCTGCC	CTGTTCTCTA	ATCTGCGCGA	GTTTTTCCTG
151	CACGGCGATG	TATTTCTTCG	CCAGCGTGTG	TACGGTTTCG	GTCAACTCGT
201	CGAGCTTGAT	GTGCTGCTCG	TCGTTTGTGA	ACTCGGTTTC	ATAGGCGGAG
251	GCAAGCTCTT	GCCGGCGTTC	CTGCCAGTCC	AGGGTTTGCT	GTTTCGAGCCG
301	GGCGATTTCG	TGCCGGTAGT	TTTGTTTTTG	CGGGTTGAGT	TTGTGGACGG
351	CGACTTCGGC	AAGCCCGTAT	TGGCGGTTGG	CTTCCAACAG	GGCAAGCTGC
401	GCCTGTTTCA	GACGGCCTTG	CTGCTCTTGG	CGGCTGTGCG	CGGTGTTTTC
451	CTGCTGGTGT	TCGAGTTTCG	CGGCGGCTTC	CTGCAAAGTA	GCGATGTCGT
501	CTGA				

g508 . pep

1 MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLRFFFL
51 HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEKLLPAF LPVQGLLFEP
101 GDLLPVVFL RVEFVDGDFG KPVLAVGFQQ GKLRLFOTAL LLLAAVRGGL
151 LLVFFEGGGF LOSSDVV

m508.seq

1	ATGGTAGCGT	TTGGCGTTGA	TCAGGGCTTC	CTGCTGCTGC	AACAAGGCGG
51	TTTGGGTGGC	GGCCTGAAGC	TGCGGCAGCT	TGGTTTGACAG	GGTTTGCACT
101	TTAGCGTATT	GCTCCCTGCC	CTGTTCTCTA	ATCTGCGCAG	GTTTCTCTTG
151	CACAACAATA	TATTCTTCGT	CCAAGGCTCG	TACGGCTTCG	CTTAATTCTT
201	CAAGCTTGAT	GTGCTGCTCG	TCGTTTTTGA	ACTCGGTTTC	ATAGGCGGAG
251	GCAAGCTCTT	GCTGGCGTTC	CTGCCAGTCG	AGGGTTTGCT	GTTCAAGCTG
301	GGCGATTTCG	TGCCGGTAGT	TTTGTTTTTG	CTGGTTGAGT	TTGTGGACGG
351	CGACTTCGGC	AAGCCCGTAT	TGGCGGTTGG	CTTCCAACAG	GGCAAGCTGC
401	GCCTGTTTCA	GACGGCCTTG	CTGCTCTTGG	CGGCTGTGCG	CGGTGGTTTG
451	CTGCTGGTGT	TCGAGTTCGG	CGGCGGCTTC	CTGCAAGGTA	ACGATGTGCT
501	CTGA				

m508.ppt

1 MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLREFLL
51 HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLAF LPVEGLLFKL
101 GDLLPVVFL LVEFVDGDFG KPVLA VG FQQ GKRLRFOTAL LLLAAVRGGL
151 LLVFEEGGGF LOGNDVV*

Homology with a predicted ORF from *N. gonorrhoeae*

m508/q508

	10	20	30	40	50	60
m508.pep	MVAFGVDQGLLLQQGGGLGGLKLRQLGLQGLHFSVLPLALFLNLREFLLHNINFFVQGL					
	: : : : :					
g508	MVAFGVDQGLLLLQQGGGLGGLKLRQLGLQGLYAGVLLPALFLNLREFFLHGDFVFQVRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAFFFKLDVLLVVLELGFIGEGKLLAFLPVEGLLPKLGDLLPVVLFLLVEFVDGDFG					
	: : : :					
g508	YGFGQLVELDVLLVVLELGFIGEGKLLPAFLPVQGGLLFEPGDLLPVVLFRLVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQQGLRRLFQTALLLLAAVRGGLLVFEFGGFLQGNDDV					
	: :					
g508	KPVLAVGFQQGLRRLFQTALLLLAAVRGGLLVFEFGGFLQSSDVG					
	130	140	150	160		

```
a508.seq
  1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGCAG GGTTTGTACG
101 CCGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTCGCGCA GTTTCCTCTG
151 TACGACAATA TATTCTTCGT CCAAACTCTG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT TGTGGCGTTC CTGCCAATCG AAGGTTTGGT GTTCAAGCTG
301 GGC AATTTCG TGTGCTAGT TTTGTTTTTG CTGTTTGAAG TGTGTGACGG
351 CGACTTCGGC AAGCCCGTAT TTGGCGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGGATTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA
```

```
a508.pep
  1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLREFLL
51  YDNIFFVQTL YGFAQLFELD VLLVVLELGF IGEGKLLILAF LPIEGLLFKL
101 GNLLLVVFL LVELVDGDFG KPVLAGVFQQ GKRLRFQTL LLLAAVRGGL
151 LLVFEFGGGF LONGDVV*
```

	10	20	30	40	50	60
m508.pep	MVAFGV	DQGFLLL	QGGGLGG	LKLRLQ	LGLOGL	HFSVLLPALFLNLREFLLHN
a508	MVAFGV	DQGFLLL	QGGGLGG	LKLRLQ	LGLOGL	YAGVLPFTLLNLREFLLYDN
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFA	FFKLDV	LLVVLE	LGFIGE	GKLLLA	FLPVEGLLF
		:				
a508	YGFA	QFLFEL	DVLLVV	LELGFIGE	GKLLLA	FLPIEGLLF
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVL	AVGFGQ	GKLR	LFQT	ALLLLA	AVRG
a508	KPVL	AVGFGQ	GKLR	LFQT	TLLLLA	AVRG
	130	140	150	160		

q509.seq

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```

1  atggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggtt tgtttttgct cttcggttcag gctgtgttag
101 tcttccaagc ctgctgtgtt gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttgggcccga gcataaggct cgagaaagcc gaatttgcag cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aagggttctt cgtgcggcg atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac ttgacgcgg cggatggaaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgtgcggta aaaacggaac
551 acggcatcgg cgtggcggtg gaaggcaaa cgcagggttt cgccagaaac
601 aaacggattg ccgtcgcggt cgcgcggat ccagccgcg attttaagga
651 tattcggaac gcggacatcg ggatagccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cacgccgttg ttgatttcgt cgttgacgct gattttgtgg cggcgcgttt
801 cgtggtctcg ccacaagccc agaagcacgg tgcgatttc gcggcgagc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttcg gcagcagcg
901 gcggatgcgg cgggtgaaat tcaaaacggt ttggcgttgc acttcggtcg
951 ggtgcgcggt caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgtgg atttggcggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg gccgaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtc ggaagtggac aagagtttga
1251 ccgtttcgac aaccaacggc gaggttctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgcggcc aaagccgcgt ctttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcatcgcg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagtga acgcgcggc acggcggcgt
1501 tacaatgccg cgcaactggt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgccgccctt gccctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GPKKAHREDG
251 HAVVDFVVD AEFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAFAALRQOR
301 ADAAVEIQNG LALHFGRVRG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCVVVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRADV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLRI
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPKCR LKLNAAARRR
501 YNRPLFFSE HHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLRRIGR RRPCISPPR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCCGCAA CAGGGCGGTT TGTTTTGTCT CTCGTTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CCGCGTGTTC
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTGTA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGCGGTT AGGGTTCTTC GGCGCGGGCG ATTTCTTCGT CCGGCGATTT
451 GTCGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCGCATA GAAGCGGAAC

```


m509.pep

1	MVAVCDKRAV	QRTLMAQFAQ	QGGFLFLFVQ	AVVVFQACVL	EKLGNHIGVF
51	ACVLAQVERH	HVKAEHGYGT	DEVQCATAFGK	QTAADVVDKGT	LQFFQIIQKL
101	LCSRIRLEKA	EFAAHTQTER	ARFAHSARHN	VGDDAAVGGF	GAGDFFVGRF
151	VGQRRYIAVD	FDAADGERQF	AVEFVEFAAI	EAEHGIGVAA	EGKAQGGFRN
201	KRIAVAVAAD	PAADFEDVRN	ADAGIGRLKV	VFHLAVELGQ	GFEKAHREDG
251	HAVVDVFVDA	EFVAARFAGL	PQAQGDSDVDF	AAQPCQVRGI	GAAPALRQQC
301	ADAAVEAXDG	LALHFGRVRG	QNGNGNRIVQ	LPLHRFAVGF	PRFEPADGFR
351	QAAFRAAASG	FFVDLAAAFV	VHVFGDVQNL	GEQAAGQGXI	VGLLFLVQLRQ
401	YFFNQCRAVV	GGSGQEPDCTD	NQRGFFVQVE	VEQGLFQKFR	VRQRSRVLWI
451	VQNMQLHDFS	LSSAVNIIVNV	QPMPCQQTV	HTLTARVPKC	RLKLNAARRQ
501	RYNRRLFFFS	EHHDHHDRTN	QRRCIPAAVQ	PPHPLGRNRH	RRAAETFRRA
551	YFGRRLRFGG	CRRTXTPLPL	RVSAR*		

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

m509/g509

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGHNHIGVFACVLAQVERH					
	: :					
g509	MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVFQACVLEKLGHNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAEHGYGTDEVCGTAFGQKTAADVVDKGTLLQFFQIIQKLLCRSIRLEKAEFAAHTQTER					
	: : : : : :					
g509	HVEAEHGHGTDEVCGTAFGKQAAADVVDKGTLLQFFQIIIEKFLGRSIRLEKAEFAAAHQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVGDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
	: :		: :		:	
g509	ARFAHSARHNVGNAAVRFFGAGDFFVRREGCQCHYVVVDFDAADGKRQFAVKFVEFAAV					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHFLAVELGQ					
	::: : : : : :					
g509	KTEHGIGVAAEGKAQGFARNKRIAVAVAADPAADFDIRNADIGIGRLKVVFHFLAVEFGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFPEKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAAFALRQQC					
	: : : : : :					
g509	GFKKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQKHGVDFAAQPCQRVGIGAAAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m509.pep	ADAAVEAXDGLALHFGRVRGQNGGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAAFRAAASG					
	: : : : :					
g509	ADAAVEIQNGLALHFGRVRGQNGGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAAFCCVVAG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m509.pep	FFVDLAAAFVHVFGDVQNLGEQAAGQXIVGLLFVQLRQYFFNQCRVVGSGQEFDCFD					
	: : : : : :					
g509	IFVDLAAAFVHVFGDIQNLGEQPAQKRQIVGLPFVQLRQYFFNQCRVVGSGQEFDRFD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m509.pep	NQRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV					
	: : : : :					
g509	NQRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFPLI-AVNTVNVNVPQMPHPCQTV					
	430	440	450	460	470	
	490	500	510	520	530	540
m509.pep	HTLTARVPKCRCLKLNAARRQRYNRPQLFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH					
	: : : : :					
g509	HTLTTHVPKCRCLKLNAARRRRYNRPQLFFSEHHHDHRTQRRRTPAAVQPPHPLGRNRH					
	480	490	500	510	520	530
	550	560	570			
m509.pep	RRAAETFRRAYFGRRRLRRFGCRRTCPTLPLRV SAR					
	: : : : :					
g509	RRAAEAFRRAYFGRRRLRRIGRRRCPISPFRGSAR					
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509.seq
1  ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGCGGGCT TGTTTTGCT CTTCGTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGT TG GAAAAGCTCG GCAACCACAT CGGCGTGT TT
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAACCGGC CTTCGGCAAG CAGGCGGGCTG
251 CCGTTGTCTGA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTTCTTC GCGCGGGCGG GTTCTTTCGT CGGGCGATT T
451 GTCGGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTGAGTTC CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGCGCGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCGCGGT CGCCGCGCGT CCAGCCGCGG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCGG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTTCG CTGTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTTC GCGCGCGAGC
851 CGTGCCAGCG CGTCGGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

```


This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

m509/a509 93.0% identity in 575 aa overlap

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFOACVLEKLGNHIGVFACVLAQVERH					
a509	: : : : : : : : : : : : : :					
	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVFOACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLOFFQIIQKLLCRSIRLEKAEFAAHTQTER					
a509	: : : : : : : : : : : : : : :					
	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGMLOFFQIIIEKFLCRSIRLEKAEFAAHTQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVGDGAAGVFFGAGDFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
a509	: : : : : : : : : : : : : :					
	ARFAHSARHNVGNATVGGFFGAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m509.pep	EAEHGIQVAAEGKAQGGFRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHFLAVELGQ					
a509	: : : : : : : : : : : : : : : :					
	KTEHGIQVAAEGKTQGGFRNERIAVAVAADPAADFEDVRNADIGIGRLKVVFHFLAVELGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFKAHREDGHAVVDFVVDAEFVAARFAGLPOAQQDSVDFAAQPCQRVGIGTAFALRQQC					
a509	: : : : : : : : : : : : : : :					
	GFKKAHRKDGHAVVDFVVDAEFVAARFAGLPOAQQDSVDFAAQPCQRVGIGTAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360


```

m509.pep      ADAAVEAXDGLALHFGRVRVQNGGNRIVQLPLHRFAVGFPFRFEPADGFRQAAAFRAAASG
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
a509          ADAAVEIQDGLALHFGRVRVQNGGNRIVQLPLHRFAVGFPFRFEPADGFRQAAAFRAAASG
                310          320          330          340          350          360

                370          380          390          400          410          420
m509.pep      FFVDLAAAEVVHVFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVSGSQEFD C F D
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
a509          FFVDLAAAEVVHVFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVSGSQEFD R F D
                370          380          390          400          410          420

                430          440          450          460          470          480
m509.pep      NQRRGFFVQEEVQGLFQKFRVRVRQSRVLWIVQNMQLHDFSLS SAVNIVNV PQMPHPCQTV
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
a509          NQRRGFFVQEEVQGLFQKFRVRVRQSRVLWIVQNMQLHDFS LI -AVNTVNV PQMPHPCQTV
                430          440          450          460          470

                490          500          510          520          530          540
m509.pep      HTLTARVPKCRLKLNAAARRQYRNRPQLFFSEHHHDH DRTQRRCIPAAVQPPHPLGRNRH
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
a509          HTLTARVPKCRLKLNAAARRQYRNRPQLFXSEHHHDH DRTQRRCIPAAVQPPHPLGRNWH
480          490          500          510          520          530

                550          560          570
m509.pep      RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
a509          RRAAETFRRAYFGRRLRRFGCRXPCFISPLPASARX
1540          1550          1560          1570

```

```
g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggttattcct gccccaagcg
51  ggatagtgcc ttttggcagg cgttgtccat atcgggtatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggagggttt caataggtcg
151 tggacgacgt tgagcgcgcc cataatgacg attttttcgc tgtccgcgac
201 gcggccgcct tcgcggatgg cttcggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tctctgcggc gcgtgttgac agtcagccgg
301 ggcgtgcata acttcgatgt agacttgttc gatgttcate ctttaatcct
351 ttttgcgcg tttctgcgcy ttgggggagg cgcgcgtcca gtgcgcgta
```

g510.pep
1 MPSRTPOGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51 WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFDVDLF DVHPLILIAA FPAVGGGALP VR*

```
m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTTATTCTT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGGCTATT TTACGCGCAA
101 AATCGCCGAT TCGCAATATC CCGCGGTTCA GGGAGGCTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTTTCG TGTCGGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTGCGCTTT GCCGTGAGC ATTCCGACTG
251 CCTGCAACAG TGTTCTTTT TCTTCTGCCG GCGTGTGAC GGTGACCGCG
301 GCGGTGCAwG ACTTCsAtGT GGACTTGTTC GATGTTCA TCCTTAATCCT
351 TATTGCTGCG TTTCTGCCA TTGGGGGAGG CGCGCTGCCA GTGCGCTGA
```

m510.pep

1	MPSRTPQGKR	GYSCAKRDSA	FWQALSISAI	LRAKSPIAKS	PPFREVFNRS
51	WTTLSAAIMT	IFLSLATRPP	SRMASALPLS	IPTACNSVSF	SSAGVLTVSR
101	GVXDFXVDLF	DVHPLILIAA	FPAIGGGALP	VR*	

Computer analysis of this amino acid sequence gave the following results:

761

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSAFWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSSAAIMT					
	:					
g510	MPSRTPQGKRGYSCPKRDSAFWQALSISVILRAKSPIAKSPPFREVFNRSWTTLSSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

```

1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTTATTCCT GCGCCAAGCG
51 GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCCGGCTTT GCCGTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 G.CGTGCATG ACTTCGATGT GGACTTGTTT GATGTTCATC CTTTAATCCT
351 TATTGCTGCG TTTCCTGCCG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

```

1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNR
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 XVHDFDVLDF DVHPLILILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSAFWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSSAAIMT					
a510	MPSRTPQGKRGYSCAKRDSAFWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

```

1  atgaaagtgc ttgttttagg tgcgggtggt gccggcgat cctccgtgtg

```


g512.pcp

m512.seq (partial)

m512.pep (partial)

m512/q512

```

m512.pep      10      20      30
               VLERYGVPYRRLKPEECAEFEPALARVTAK
               |||||
g512          TDMNFEGRKKGTLQIFRQTEEVEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK
               130      140      150      160      170      180

               40      50      60      70      80      90
m512.pep      IAGGLHLPADATGDWRLFTENLYKLQCEKGVRFHFNQISRIDHNGLRIKTVETKQGGLK
               |:|||||:|||||:|||||:|||||:|||||:|||||
g512          IVGGLHLPADATGDCRLFTENLYKLQCEKGVRFYFNQTISRIDHNGLRKAVETKQGGLK
               190      200      210      220      230      240

               100      110      120
m512.pep      QMPLSARSVASAGRFWRSWISICPFIPSKAIP
               |||||:|||||
g512          QMPLSARSAASAGLCWRSWISICPFIPSKAIP

```


763

250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
  1 ATGAAAGTGC TTGTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCGCCGTG
 51 GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAACCAAGT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GCGGTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTCGAGCC TCGCTGGCA CGCGTTACCG
551 CCAAATTCG CCGCGGCCTG CACCTGCCCG CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG
651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTGTGCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
  1 MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
 51 YTPPWAAPGI PTKALKWLFK SHPLLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMFR RFEAQTMNF EGRKKGTLOI FRQTKEVEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVVPYRRLKPEECAEFEPALARVTAK
a512                                |||||
TGMNFEGRKKGTLOIFRQTKEVEAAKQDIAVLERYGVVPYRRLKPEECAEFEPALARVTAK
      130      140      150      160      170      180

      40      50      60      70      80      90
m512.pep IAGGLHLPADATGDWRLEFENLYKLCQEKGVRFHFNQNISRIDHNLRIKTVETKQGGLK
a512      |||||
IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQTISRIDHNLRIKTVETKQGGLK
      190      200      210      220      230      240

      100      110      120
m512.pep QMPLSARSVASAGRFWRWSWISICPFIPSKAIPX
a512      |||||
QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
      250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
  1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
101 TTTGTCTTGG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTGCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTGGCGTG
351 GGTCTATTTC GGC GCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```


764

501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQOPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq
 1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGAAGGT ATGATTCAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTC GCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGCATCATG GCGTGGATCA ACCTCGTCGC CATCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQOPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQOPYG DLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQOPYG DLSGAALTQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILEM FAFSTVIGNY AYAESNVQFI KSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILEM FAFSTVIGNY AYAESNVQFI KSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMRLDYTAKLKMKG DPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMRLDYTAKLKMKG DPEFKLSEHP					
	130	140	150	160	170	180
	190					
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

765

```

1  ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51  CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACACGGGC TTTGTCCAAT TCCGCCGTGT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTTC TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTGGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGGCT GGGGAGAAA
451 TGGCTGGGCG TGTTGTTTCG CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTCG CGATACCGTC AAAGCGGCGT
551 GGGGTGGGA GCCTCATTAT GTCGCGCTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTAATCGGCG GTCTGATTTT
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTC CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTCT ATACCATCAT
951 CGTTTGTTCT TGCACCGCCT TCATCATCTT GATTACCAA CAGCCTTACG
1001 GCGATTAGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCCGTC ATCCTGTTTA TGTTTGCCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1  MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLFFTVTTG FVQFRLEGRS
51  IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGPGPA
101 VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGVFVEA VQNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPMI PDVFGQIFSG
251 AFKFDAAAGG LLGGLISQTM MMGIKRGLYS NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VFVDTIIVCS CTAFIILYQ QPYGDLGSA LTOAAIVSQV
351 GQWGAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||
a513
260 270 280 290 300 310
DAAAGLLGGLISQTM MMGIKRGLYS NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
m513.pep
TIIVCSTAFIILYQ QPYGDLGSAALTQAAIVSQVQWGAGFLAVILFMFAFSTVIGNY
|||||
a513
320 330 340 350 360 370
TIIVCSTAFIILYQ QPYGDLGSAALTQAAIVSQVQWGAGFLAVILFMFAFSTVIGNY

100 110 120 130 140 150
m513.pep
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANVPLVWDMADMAMGIMAWINLVAILL
|||||
a513
380 390 400 410 420 430
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANVPLVWDMADMAMGIMAWINLVAILL

160 170 180 190
m513.pep
LSPLAFMLLRDYAKL KMGKDPEFKLSEHPGLKRRIKSDVWX
|||||

```


a513 LSPLAFMLLRDYTA KLKMGKDPEFKLSEHPGLKRRIKSDVWX
 440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq
1 atggttcaaa tacaggttgt gcgcgcgcc gccgttgccc gtggtctgca
51 ttccgagttt gcgcgcgctg taactgccga ggaaatagcc ttcgacaatg
101 ccgttttgaa tcacgaagcg cggcgcggtg gcaacacctt ccgcatcaaa
151 atagctgctg cggaaagagc ggggatgtg cggttcttcg cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgctgatcag gaaactgctt
251 tggcggtaga gcgcgcgcc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccgaa acggtggtat cgaagaggac ggggtagctg cctgtcggga
351 tgctgcggct gccgagtcgg cgcaaatgac gccgggcggc ggtttgaccg
401 atggtttcgg ggctgtccat atccgatggc cggcaggcgg aatcgtaacca
451 gtagtcgcgc tgcattccgt ttctgtcggc gccgacgacg ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgggtgtcgg caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc
601 gatgcgggtg tccgtgtcca acgctgcctg ttcgcattgt ttgccaagc
651 cgacggcgcc ttccgtatcc aaatccatt cgtggttaaag gtccgggtcg
701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc
751 ttccgcgggtg tggcggcgga tgcgcgcggc gccgcgcgac gtgtcgcgca
801 gggcttggtc ggagaagtcg gcggtgccgg cgcggccttt gcgtttgccg
851 acgtaaacgg taatgtccag cgatttgtcc tgctggaact cgatttgttc
901 gatttcgccc aagcgacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggcttcggc ggcggtcgcg cccgctgctt ttgccaagtc gagcgtgcgg
1001 cggcagaggt cgaggagttc ggaagcgggt tggttgaaca gcataacaat
1051 ctttcttggt ggagcgttgt ggcattttaa

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep
1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNVAVLNHEA RRGNTFRIK
51 IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAEVEEF GSGVVEQHNN
351 LSWWSVVF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)
1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC
151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTGCGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGGCG CGGGCGGGCG TTTGACCGAT GGTTCGGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCGGTA AACGTATTGG
401 TAATGGCCGG TTGTCACCGC CGGCCTTCG GAGTTTTCGA TGCCTCATC
451 CTCGTTGAGG GCGGCTTGT CGCATTGTTT TGCCAAGCCG ACGGCGGCTK
501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGCG CAACCGTCTT CGGCGGTGTG
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTGACAG GCTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTCG GTTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTGTCTCTG CTGGAACCTG ATTTGTTsGA TTTsGCCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGGCGCG GCAGAGGTG
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

[illegible]

a515.seq~

1	ATGGTTCAAA	TAAAGGTTGT	GCGCGCGGCC	GCGGTTGCC	GTGGTCTGCA
51	TTCGAGTTT	GCGCGCGCTG	TAAGTCTGA	GGAAATAGCC	TTCGACAATG
101	CCGTTTTGAA	TCACGAAGCG	CGGTGCGGTG	GCAACGCCTT	CCGCATCAAA
151	ATAGTCTGCTG	CGGAAGAGC	GGGGGATGTG	CGGTTCTTCG	CGCAGGTTGA
201	GGAAATCGGG	CAGGACTTTT	TTGCCGATGC	TGTGCATCAG	GAAACTGCTT
251	TGGCGGTAGA	GCGCTCCGCC	GGAGAGTGC	CCGACGAGGT	GTCCGATTAAG
301	ACCGCCCGAA	ACGGTGGTAT	CGAAGAGGAC	GGGGTAGTTG	CCTGTCGGGA
351	TGCTGCGGCT	GCGGAGTCGG	CGCAAAAGTC	GGCGGCGCGC	GGTTTGACCG
401	ATGGTTTCCG	GGCTGTCCAT	ATCCGATATG	CGGCAGGCGG	AATCGTACCA
451	GTAGTCCGCG	TGCATGCGGT	TTTCTGCGC	GGCAACGACG	CTGCAGGAAA
501	TGCTGTGGTG	CGTGCTTTGC	CGGTGTGCGG	CAAAACCCTG	GGTGTTCGCC

a515.pep

m515/a515 92.1% identity in 304 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1423>:

g515-1.seq

1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA


```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCCT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCGCCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGGCGGCGCG GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCGTGCGG GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAACCCGTG GGTGTGCGG
551 TAAACGTATT GGTAGTGTCC GGTTTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGTGCCTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTGCGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTGCGGCA
801 GGGCTTGTTC GGAGAAGTCG CCGGTGCGCG CCGGCGCCTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTGTGCC TGCTGGAACG CGATTGTTC
901 GATTTCCGCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAGT
951 CGGCTTCGGC GCGGTCGCGC CCCGCTGCTT TTGCCAAGTC GAGCGTGGCG
1001 CCGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAA
1051 CTTTCTTGTT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RRGGNTFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADDEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFLVLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGTTGT GCGCGCGGCC GGCCTTGCCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CCGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCCT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGCGGCGG GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGG GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAACCCGTG GGTGTGCGG
551 TAAACGTATT GGTAAATGCC GGTTTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTGCGCGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGTCTTGCA
801 GGCCTTTTTC GGAGAAGTCG GCAGTACTGG CCGGCGCCTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCC TGCTGGAACG CGATTGTTC
901 GATTTGCGCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEEIA FDNAVLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADDEVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGG FALFCQADGG FRIQIPFVVK VGVADVFCQO TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGGF GEVSTGAAG AFADVNGNVQ RLVLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

	10	20	30	40	50	60
g515-1.pep	MVQIQVVRAAGVARGLHSEFARA	VTAEIEAFD	NAVLNHEARRGGNTFRIKIA	AAAERAGDV		
m515-1	MVQIQVVRAAGVARGLHTEFARA	VTAEIEAFD	NAVLNHEARCGGNAFRIKIA	AAAERAGDV		
	10	20	30	40	50	60

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	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGLTDGFGAVHIRMAAGGIVPVVALHAFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGADVLRHQ					
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGADVFCCHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLLLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGGGFDGVLQGFGEVGGSTGAFAFADVNGNVQRLVLLLELDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVFGGGRARCFQVERAAAEVEEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGTTGT GCGCGCCGCC GCGGTTGCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CCGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTTCTTCG CGCAGGTTGA
201 GGAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGGC CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCCG CGCAAAGTGC GCGGGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTCG CCGTGTGCGG CAAAACCGTA GGTGTTCGCG
551 TAAACGTATT GGTATGGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATC CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTGCGCGGC GCGCGGACG GTGTGCGGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCTTT GCCTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTGTCC TGCTGAAACT CGATTTGTTT
901 GATTCGCCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAGNAVVR RALPVCCKTV GVAVNVLMVA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNNGGIEEDGVVACRDAAA					

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```

m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70          80          90          100         110         120

a515-1.pep   130          140          150          160          170          180
AESAQSAAGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
|||||
m515-1      AESAQSAAGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130          140          150          160          170          180

a515-1.pep   190          200          210          220          230          240
GVAVNVLMAGLHRRAFGVFDALILVQGGLEFALFCQADGGFRIQIPFVVKVGADVLRHQ
|||||
m515-1      GVAVNVLMAGLHRRAFGVFDALILVQGGLEFALFCQADGGFRIQIPFVVKVGADVLRHQ
              190          200          210          220          230          240

a515-1.pep   250          260          270          280          290          300
LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
|||||
m515-1      TGIGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
              250          260          270          280          290          300

a515-1.pep   310
DFAQPHADALSQX
|||||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

```

g516.seq
1   atgttgttcc gtaaaacgac cgccgccgtt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgccggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacggt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgcccc atttgaaaag ggcagcctgg tgatgatggg
201 .cgggaaatac tggttcgccg tcaatcccg aagctgcacg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccg gtcaaattcg aagcgcccgg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaaa
451 ctcgacaatc ggaccattta cacgcgtgc gtatccgcca aaggcaaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaatg
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggcggccgcg gtgctggtct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

```

g516.pep
1   MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAA VLVLPALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

```

m516.seq
1   ATGTGTGTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGCGC CTTCCGTTGTG
151 GTTGCCGAAG ACAATGCCCC ATTGGAAGAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCCGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCTT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCCTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```


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501 CTACGCCACA CCGCAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
 551 TGCCTGCCGA TATTTATTAC ACGGTTACTG AAGAACATAC CGACAAATCC
 601 AAGCTGTTTG CAAATATCTT ATATACGCCC CCCTTTTGA TACTGGATGC
 651 GCGGGCGCG GTACTGGCCT TGCCTGCGGC GGCTCTGGGT GCGGTCGTGG
 701 ATGCCGCCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep

1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
 51 VAEDNAQLEK GSLVMMGGKY WFPVNPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSQN FSTEGCLRLY DTDKPADIAK LKQLGFEAVK
 151 LDNRTIYTTC VSAKGKYAT PQKLNADYHF EQSVPADIYY TVTEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK					
	: : : : :					
g516	MLFRKTTAAVLAATLILNGCTMLRGMNPNVSQTITRKHVDKDQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWFPVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN					
	: : : : :					
g516	GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m516.pep	FSTEGCLRLYDTDKPADIAKLKQLGFEAVKLDNRTIYTTCVSAKGKYATPQKLNADYHF					
	: : : : :					
g516	FSTGGLCLRLYDTGRPDDIAKLKQLGFEAVKLDNRTIYTTCVSAKGKYATPQKLNADYHF					
	130	140	150	160	170	180
	190	200	210	220	230	239
m516.pep	EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
	: : : : :					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAAVLVLPALIAAANSSDK					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq

1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
 51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAG GGCAGCCTGG TGATGATGGG
 201 CCGGAAATAC TGGTTCGTCG TCAATCCTGA AGATTCGGCG AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTTG CCTACCAAGC CFTGCGGGTC AAATCGAAT CGCCCGCCAG
 351 CCAGAATTTC AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTGAAGC GGTGGAACCTC
 451 GACAATCGGA CCATTACAC GCGCTGCGTC TCCGCCAAG GCAAATACTA
 501 CGCCACACCG CAAAACCTGA ACGCCGATTA TCATTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAA ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCGGT
 651 GGGCGCGGTG CTGCGCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

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```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WVVNPEDSA KLTGILKAGL DKQFQMVPEP
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDVAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

              10      20      30      40      50      60
m516.pep      MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60

              70      80      90      100     110     120
m516.pep      GSLVMMGGKYWVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSON
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           GSLVMMGGKYWVVNPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALPVKLESPASQN
              70      80      90      100     110

              130     140     150     160     170     180
m516.pep      FSTEGCLCLRYDTPKADIACLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           FSTEGCLCLRYDTPKADIACLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
              120     130     140     150     160     170

              190     200     210     220     230     239
m516.pep      EQSVADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDVAVGAVLALPVAALIAATNSSDKX
              180     190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatcgagg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51 cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 cgggtgaagg tatgaaata cagtcctgcc acgccgtgca gtttctcagc
151 tgcgtctttc aatcccgatt tgatgtttt gggcaggtcg atttggtcgg
201 tgtcgccggg aatgacggct ttcgcgccga agccgatgcg ggtcaggaac
251 attttcattt gttcgggctt ggtgttttgc gtttcgtcga ggatgatgta
301 tgcgccgttg agcgtcctgc cgcgcatata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSHAVQFLT
51 CVFQSRFDVF GQVDLAGVAG NDGFRAEADA QEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDFLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTACAGCGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGAC AACGTCTTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGTTGTGCA GTTCTCAGC
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTGCGCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAAGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GTTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCTGCG CGCGCATATA GGCAGCGGG GCGATTTCAG
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```


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451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
g517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : :					
g517	FNQLGYTVKAHQVIEGIIKRTKVGVDFLGQVSGQEAQFLTGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAG GATGCCGGAC AACGTCTTCG
101 CCGTAAAGG TGTGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCAGC
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTGAGGAAC
251 ATTTTCATTT GTTCGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGGCATATA GGCGAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTGGAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLQTF					

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	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1   atgacgtttt  cggcggcaaa  gctcaacatt  tcggcactga  tgttgtgtct
51  ttcggcagga  atgaccgttt  tactttccgc  ttttttactg  ctccgaccgg
101 aaggcagcat  cttattcaac  cattttttca  gcataaatat  tctgaccgga
151 agagcggcat  ctccacgggc  aaccgtgttc  agactgcata  aggcggtagc
201 attccacaag  atgccgaaaa  ccataagcaa  aatgcgtaga  aactacgccg
251 tccgaatcac  gccgcctcct  cggcgggcaa  cgcttcatta  taacagattg
301 ccccttaaaa  aatcagaccc  tgctttgtg  gcggagtctg  aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1   MTFSAAKLNI  SALMLCLSAG  MTVLLSAFLL  LRPEGSILFN  HFFSINILTR
51  RAASPRATVF  RLHQAVREFH  MPKTISKMR  NYAVRITPPP  RAATLHYNRL
101 PLKKSDFAFV  AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1   ATGACGTTTT  CGGCGGCAAA  GCTCAACATT  TCGGCACGGA  TGTGTGTCT
51  TTCGGCAGGA  ATGACCGTTT  TACTTTCCGC  TTTTCTACTG  CTCCGACCGG
101 AAGGCAGCAT  CTTATTCAAC  CATTTTTCA  GCATAAATAT  TCTGACCCGA
151 AGAGCGGCAT  CTCCACAGGC  AACCCTGTT  AGACGGCATC  AGGCGCGGTT
201 TGCAAGATGC  CGTACCATAA  ACAAAGGCG  TAGAAACTAC  GCCGTCCGAA
251 TCACGCCGCC  CTCGCG.GCG  GCAACGCGT  ATTATAACAG  ATTGCCCTCC
301 GCGGCAGGCT  TAGTGCGGCG  GGAGCGCCG  CGTTGCGCAG  TAATATTGTC
351 TAACGGGAGG  AAAAAATCAG  ACCCTGCTT  TGTGGCAGAG  TCTGAAATT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1   MTFSAAKLNI  SARMLCLSAG  MTVLLSAFLL  LRPEGSILFN  HFFSINILTR
51  RAASPOATVF  RRHQAREFAR  RTINKRRRNY  AVRITPPSXA  ATRHYNRLPS
101 AAGLVRRERR  RCAVILSNGR  KKSDFAFVAE  SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep      MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
g518           MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
                10      20      30      40      50      60

                70      80      90      100     110
m518.pep      RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSN
g518           RLHQAVRFHKMPKTISKMRNYAVRITPPPPRAATLHYNRLPL-----
                70      80      90      100

                120     130
m518.pep      GRKKSDFAFVAESEI
g518           --KKSDFAFVAESEI
                110

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTITACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTC A GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCACGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPRATVF					
a518	MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP SAAGLVRRERRRCAVILSNG					
a518	RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP -----					
	70	80	90	100		
	120	130				
m518.pep	RKSDPAFVAESEIX					
a518	-KKSDPAFVAESEIX					
	110					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgcccgtt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcccctg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcy tcgctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta ttccaagta accgatccca aactcgccctc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcccgg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgcc
551 gtattgccga atccgaaggc cgtaaaatcg acaaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgcaaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaaag
851 aagacaatac gcgattaag cccgccaagg ttgccgaaat cgggaaccct
901 aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGKSFV VIPQOEHVHV ERLGRFHRAL TAGLNILIPP
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```


m519.seq	(partial)					
1	..TCGTTATCG	GCGTATGGA	GTTGGACAAA	ACGTTTGAAG	AACGCGACGA	
51	AATCAACAGT	ACTGTTGTTG	CGGCTTTGGA	CGAGGCGGCC	GGGgCTTgGG	
101	GTTGTAAGGT	TTTGGCTTAT	GAGATTAAAG	ACTTGTTTCC	GCCGCAAGAA	
151	ATCCTTCGCT	CAATGCAGCG	GCAAATTACT	CCCGAACAACG	AAAAACCGCG	
201	CGTATCGCC	GAATCCGAAG	GTCGTAATAAT	CGAACAAATC	AACCTTGCcA	
251	GTTGTCAGCG	CGAAGCCGAA	ATCCAACAAT	CCGAAGGCGA	GGCTCAGGCT	
301	GCGGTCAAATG	CGTCAAATGC	CGAGAAATATC	GCCCGCATCA	ACCGCGCCAA	
351	AGGTGAAGCG	GAATCCTTGC	GCCTTGTTCG	CGAAGCCAAT	GCCGAAGCCA	
401	TCCGTCAAAT	TGCCGCGGCC	CTTCAAACCC	AAGGCGGTGC	GGATGCGGTC	
451	AATCTGAAGA	TTGCGGAACA	ATACGTCGCT	GCGTTCAACA	ATCTTGCACG	
501	AGAAAGCAAT	ACGCTGATTA	TGCCCGCCAA	TGTTGCCGCAC	ATCGGCGCAAC	
551	TGATTTCTGC	CGGTATGAAA	ATTATCGACA	GCAGCAAAAC	CGCCAAaTAA	

```
m519.pep      (partial)
  1  ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGSQREAE IQQSEGEAQA
101 AVNASAEQI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEAYVA AFNNLAKESN TLIPMANVAD IGLSISAGMK IDSSSKTAK*
```

[illegible]

```
a519.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATFCCTTTGT GTCATCCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCCTTTCCA TCGCGCCCTC AGCGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTTCGCTG AAAGAAATTC CTTTAGACCTT
```


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```

201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCAA GCGGGTGGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCCG GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

a519.pep

```

1  MEFFIILLAA VVVFGEKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 99.5% identity in 199 aa overlap

```

                                10      20      30
m519.pep                      SVIGRMELDKTFEERDEINSTVVAALDEAA
                                |||||
a519      YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
                                90      100     110     120     130     140

                                40      50      60      70      80      90
m519.pep      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASQREAE
                                |||||
a519      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASQREAE
                                150     160     170     180     190     200

                                100     110     120     130     140     150
m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESRLVAEANA EAIRQIAAALQTQGGADAV
                                |||||
a519      IQQSEGEAQAAVNASNAEKIARINRAKGEAESRLVAEANA EAIRQIAAALQTQGGADAV
                                210     220     230     240     250     260

                                160     170     180     190     200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                                |||||
a519      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                                270     280     290     300     310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

g519-1.seq

```

1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA -CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAGTCC TCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACGCG CGAAGCGGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCAA GCGGGGGCGG ATGCGGTCAA

```


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801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVPGFKSFV VIPQQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLSYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEI LRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVARANAERAI
 251 RQIAAALQ TQ GGADAVNLKI AEQYVAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GCGGTTTCCA TCGCGCCCTG ACGGcCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTTGCG GCTTTGGACG AGGCGGCGCG GGCTTGGGGT
 451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGCGCG AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTGTTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVPGFKSFV VIPQQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLSYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVARANAERAI
 251 RQIAAALQ TQ GGADAVNLKI AEQYVAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVPGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS L					
m519-1	MEFFIILLVAVAVPGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS L					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLSYGS SNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLSYGS SNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep						
m519-1						

780

```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGGACGAA
401 TCAACAGCAC CGTCGTCCTC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACCGCAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTGTGTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTGCGCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFQKSFV VIPQEVHVV ERLGRFHRAL TAGLNILIPP
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGLIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQILRS MQAQITAERE KRARIAESG RKIEQINLAS
201 QREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFQKSFVVIPQEVHVVVERLGRFHRALTAGLNILIPPIDRVAYRHSI
              |||||
m519-1      MEFFIILLVAVAVFGKSFVVIPQEVHVVVERLGRFHRALTAGLNILIPPIDRVAYRHSI
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGLIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGLIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQILRSMQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQILRSMQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

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```

m519-1      KRARIAESEGRKIEQINLASQGREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAPNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAPNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in E.coli. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1   atgcctgctc ttctttcaat acgtcgggca aacgcgctgc ctttttcgct
51  catttcggaa aggatgaagt tgctgggtgcc gtttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccc ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccc tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgccaacagt tcgaacggat cttttgacaa ggcgggcgca cgggccgatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgccccaa gcggcgaggaa atttctctct cgttgtcccc caacacggca
501 gccgcaccgc cgccgaccgt acctaacgct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1   MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1   ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTCGCG
51  CATTTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGCGCATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCC CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCAGACAGT TTTTGTGTTG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

```


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```

301  GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351  TGCGACCACT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
401  TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451  CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCsCG CAACACGGCA
501  GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551  CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
1   MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILILFAA KPSRRALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151 RAPSDGKFPF RCXATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520
      10      20      30      40      50      60
m520.pep  MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW
          |||||::|||||
g520      MPALLSIRANALPFSRISERMKLLVPLIMPAMDILILFAAKPSRTALMIGIPPATAASNW
          10      20      30      40      50      60

      70      80      90      100     110     120
m520.pep  TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
          |||||
g520      TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTKTSTSLRANS
          70      80      90      100     110     120

      130     140     150     160     170     180
m520.pep  SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPFRCXATRQPYRRRPYNLKDR
          |||:|::|:| ||||:| ||||| ||||| |||||:||||:|
g520      SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPPLRCPATRQPHRRRPYLSLKDR
          130     140     150     160     170     180

      190
m520.pep  CLLASLCLLVSRKCKY
          |||||
g520      CLLASLCLLVSRKCKY
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
1   ATGCTGCGC TTCTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
51  CATTTTCGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTAAGTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTTG
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTTG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCGACCACT TCGAACGGAT CTTTGACAAA GGCTG.CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCsCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
1   MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRRALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```


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151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSILTAAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
151 TVPKPKRPMF TGFI VSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACAGTGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```


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101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRAFSS	SLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKR	REISSALSRNTAA	PPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTAA	PPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq
1 ATGAAGTTGC TGGTGCCGT AATAATGCCG GCGATGGATT TAATCCTGTT
51 TGCCGCCAAA CCTTCGCCGA GGGCTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCCG CAGCGGGAAG
151 ATTTCTGTTG CGTATTCGGC GAGCAGTTTT TTGTTGCCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTCACGTGC GACCAGTTTCG
301 AACGGATCTT TGACAAAGGC TGCGGACGGG CAGGTTGTCT GGGCTTTTTC
351 TTCACTCAAA TCGCACACGG CAGAAATACG GATTTGCGCG CCCAAGCGAC
401 GGGAAATTTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep
1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKR	REISSALSRNTAA	PPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTAA	PPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq
1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTCAG
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTTC

g521n.pep

1 MKSKLPLILI NLSLISSPLG ANAAKIYTC INGETVYTTK PSKSCHSTDL
51 PPIGNYSSER YILPQTPEPA PSPSNGGQAV KYKAPVKTVS KPAKSNTTPQ
101 QAPVNSRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL*
151 SNVLDROONI QALQRELGRM *

m521.seq

1	ATGAAATCAA	AACCTCTCTT	AATCCTAATC	AACCTTTCCC	TGATTTCAAG
51	CCCATTGGGT	GCGAATGCGG	CCAAAATCTA	ACCTGACACA	ATCAACGGAG
101	AAACCGTTTA	CACCAACAAG	CCGTCCAAAA	GCTGCCACTC	AACCGATTTG
151	CCCCAATCG	GCAACTACAG	CAGCGAACCG	TATATCCCCG	CCCCAACGCC
201	CGAACCGGTA	TCATCACCGT	CAACCGGCGG	ACWGGTGTGC	AAATATAAAG
251	CCCCGGTCAA	AACAGTATCC	AAGCCGGCAA	AATCCATATAC	CGCCGCGCGC
301	CAACAAGCAC	CCTCAAACAA	CAGCAGACGC	TCCATTCTCG	AAACAGAATT
351	GAGCAACGAA	CGCAAAGCAT	TGGTTGAAGC	CCAAAAATATG	TTATCACAAAG
401	CACGCTCTGG	AATGGGCGGC	AACATCAACC	ATCAAGAAAT	AAATGCATTA
451	CAAGCAATATG	TATGGGACAG	GCAGCAAAAT	ATTCAAGCCC	TGCAAAGGGA
501	ACTGGGCGGT	ATGTAA			

m521.pep

1 MKSKLLLLI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTDL
51 PPIGNYSSER YIPPQTPEPV SSPSNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 OSNVLDROON IOALORELGR M*

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m521/q521

		10	20	30	40	50	60
m521.pep		MKSKLLILINFLISPLGANA	AKIXTCTINGETV	YTXKPSKSCHSTD	LPPIGNYSSER		
			:		:		
g521		MKSKLPLILINLSLISPLGANA	AKIYTCTINGETV	YTTKPSKSCHSTD	LPPIGNYSSER		
		10	20	30	40	50	60
		70	80	90	100	110	120
m521.pep		YIPPQTPEPVSSPSNGGXV	VKYKAPVKTVSKPAKSXT	PPPPQAPSNNRRS	SILETELSNE		
			:	:			:
g521		YILPQTPEPAPSPSNGGQAV	KYKAPVKTVSKPAKSNT	PP-QQAPVNNRRS	SILEAELSNE		
		70	80	90	100	110	
		130	140	150	160	170	
m521.pep		RKALVEAQKMLSQARLAKG	NINHQEINALQSNVLD	RQONIQALQRELGRMX			
			:	:			
g521		RKALTEAQKMLSQARLAKG	NINHQKINALXSNVLD	RQONIQALQRELGRMX			
		120	130	140	150	160	170

a521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAAG

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```

51 CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAAA GCTGCCTCTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAT ATCCAAGCAC TGCAAAGAGA
501 ATTGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYCT INGETVYTTK PSKSCLSTD
51  PPIGNYSSER YIPPQTSEPT PPSNNGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNRRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQQN IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFSLISSPLGANAAXIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER					
	:					
a521	MKSCLPLILINFSLISSPLGANAAXIYCTINGETVYTTKPSKSCLSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRRSILETELSNE					
	: :					
a521	YIPPQTSEPTPSNNGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcacccat cgcatttgg gcgtgggtca
101 ttttgcggtt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatattcc
201 gtttgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccg tctcgccgtc gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtc
351 acaagaacag cttgacctgc tcggcggcgc aaacgcgttt gaaactcgag
401 acaacaatg tgcgcggat ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAM
51  KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGCG GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCCTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAAA ACGATTTCG GGCCTCGCGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```


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301 TTGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKMWEQ
 101 LDRLSEKQIR SFGKLGAEQ LDLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKMWEQPLDRLSEKQIRSFSGKLGAEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKMWEQPLDGLSEKQISSFGKLGAEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLGGANAF EARDKQCVAD LKSEX					
	: : :					
g522	LDLGGANAF ETRDKQCVAD LKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAGCA AAAGCCAAA TCCGACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCCTGA AGAATATTCC
 201 GTTGGCGGAA AAATGGCAA ACGATTGCGG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCG CTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKMWEQ
 101 LDRLSEKQIS SFGKLGAEQ LDLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKMWEQPLDRLSEKQIRSFSGKLGAEQ					
	:					
a522	SCVKNIPFAEKWQNDLRARGLDSNNTRLTVDYCKMWEQPLDRLSEKQISSFGKLGAEQ					
	70	80	90	100	110	120

788

```

                130      140
m522.pep      LDLLGGANAFEARDKQCVADLKSEX
                |||||:|||||
a522          LDLLGGANAFETRDKQCVADLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51  gacgggaacg gtttatcttt tggttgtcag cgcggctttg gcgggttcgg
101 g cattgccta cgggctgact ggcagcacgc ctgcgcgcgt cttgaccgcc
151 g cactgcttt ccgcgtggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaagt gaaacggatt catatcagga tttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcatcgctc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYEILRYT GGNRYEVFYY
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL LIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
1  ..GCCGTCCTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGT CCGGCATGTC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GncGCTCTGC TTCCGCGCT GGTATTtng
151 TTCGTACACG CCAAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTtGGAT GCCGGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTTACGA AGTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCAT TG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLDT AGQYVEILRH TGGNRYEVFY RgTHWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng)

from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTXALLSALGIXF
                |||||:|||||
g523          MTVWFVAAVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
                |||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||:|

```


789

g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

a523.seq
1 ATGACTGTAT GGTGTGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51 GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

a523.pep
1 MTWVFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGT VYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTWVFVAAVAVLIIELLTGT VYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

g525.seq
1 atgaagtacg tccggttatt ttctctcggc acggcactcg ccggcactca
51 agcggcggt ggcgaatgg ttcaaatacga agcggcgagc taccgcccgc
101 tttatctgaa aaaagatacc ggcttgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaaccggtt
251 acctgaagca ttgatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggccaattga aacagccggt taccaatatt tcctgggttg ccgccaacgc
351 ctattcgccc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttccgcc acgcagaaaa aacggctcaa acgaaccggg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaagca ccgcccgaac tactgggggtg tttatgat
551 gcacgggctg a

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

g525.pep
1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKRLKRTR
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

790

```

m525.seq
1  ATGAAGTATG TCCGGTTATT TTWCCTCGGC GCGGCACTCG cCrrCACTCA
51  ArCGGCGGCT GcCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCrC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGc GCCGAAGgCG
301 GgCGAATTAA AACAAACCGGT AACCAATGTT TCCTGGwTTG CCGCCAACGC
351 CTAtTGC GCCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGA CTGCTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
501 TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

```

m525.pep
1  MKYVRLFXLG AALAXTOXAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GELKQPVNTV SWXAAANAYCA AQQKRLPTID EWEFAGLASA TQKXRLKRTR
151 LQPHYSRLVC RRRTERPARC RXKAARTTGA FMICTG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

```

m525/g525

      10      20      30      40      50      60
m525.pep  MKYVRLFXLG AALAXTOXAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          |||||  ||: |||  ||  ||||| ||||| ||||| ||||| ||||| ||||| |||||
g525      MKYVRLFFLGTALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
          10      20      30      40      50      60

      70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGELKQPVNTVSWXAAANAYCA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g525      AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGELKQPVNTISWFAANAYCA
          70      80      90      100     110     120

      130     140     150     160     170     180
m525.pep  AQQKRLPTID EWEFAGLASATQKXRLKRTRLQPHYSRLVCRRTTERPARCRXKAARTTGA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g525      AQQKRLPTID EWEFAGLASATQKXRLKRTRLQPHYSRLVCRRTTERPARCRQSTARTTGV
          130     140     150     160     170     180

m525.pep  FMICTGX
          |||||
g525      FMICTGX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

```

a525.seq
1  ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGATTAA AACAAACCGGT AACCAATGTT TCCTGGTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGA CTGCTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGTCTG A

```


This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1 MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AOGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

	10	20	30	40	50	60
m525.pep	MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF					
a525	MKFTRLFLCAALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVNTVSWXAANAYCA					
a525	AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525.pep	AOGKRLPTIDEWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCRXKAARTTGA					
a525	AOGKRLPTIDEWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCRQXVARTTGA					
	130	140	150	160	170	180
m525.pep	FMICTGX					
a525	FMICTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1 ATGAAGTACG TCCGGTTATT TTCTCTCGGC ACGGCACTCG CCGGCACTCA
 51 AGCGGGCGCT GCCGAAATGG TTCAAATCGA AGCGGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACATG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCAACGCG
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGACT TGCTTCCGCC ACGCAGAAA ACGGCTCAA CGAACCCGCG
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAGAGCC GCCCGAATA CTGGGGTGT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AOGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHLDV GKDRPNYWG VYDMHGLIEW TEDFNSSLLS
201 SGNANAQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLFGRFAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1 ATGAAGTATG TCCGGTTATT TTCTCTCGGC GCGGCACTCG CCGGCACTCA
 51 AGCGGGCGCT GCCGAAATGG TTCAAATCGA AGCGGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACATG
```



```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCGAACTA CTGGGCGGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTCG AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1  MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTVN SWFAANAYCA AQGRRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWG YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMEC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLFRCRCS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL DKYPVTNAEF					
g525-1	MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL DKYPVTNAEF					
	10	20	30	40	50	60
m525-1.pep	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA GELKQPVTVN SWFAANAYCA					
g525-1	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA GELKQPVTVN SWFAANAYCA					
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA GELKQPVTVN SWFAANAYCA					
g525-1	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA GELKQPVTVN SWFAANAYCA					
	70	80	90	100	110	120
m525-1.pep	AQGRRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYA DGGKRLHDV GKGRPNYWG					
g525-1	AQGRRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYA DGGKRLHDV GKDRPNYWG					
	130	140	150	160	170	180
m525-1.pep	AQGRRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYA DGGKRLHDV GKGRPNYWG					
g525-1	AQGRRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYA DGGKRLHDV GKDRPNYWG					
	130	140	150	160	170	180
m525-1.pep	YDMHGLIEWE TEDFNSSLLS SGNANAQMFCSGASIGSSDS SNYAAFLRYG IRTSLQSKYV					
g525-1	YDMHGLIEWE TEDFNSSLLS SGNANAQMFCSGASVGSASDS SNYAAFLRYG IRTSLQSKYV					
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWE TEDFNSSLLS SGNANAQMFCSGASIGSSDS SNYAAFLRYG IRTSLQSKYV					
g525-1	YDMHGLIEWE TEDFNSSLLS SGNANAQMFCSGASVGSASDS SNYAAFLRYG IRTSLQSKYV					
	190	200	210	220	230	240
m525-1.pep	LHNLFRCRCSRX					
g525-1	LHNLFRCASRX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```

1  ATGAAGTTTA CCCGTTACT CTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCGCG
101 TTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCT
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCC GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCGAACTA CTGGGCGGTT TATGATATGC
551 ACGGCTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTCG AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```


This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1 MKFTRLFLFC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGDRLDLHDV GKGRPNYWG VYDMHGLIEWE TEDFNSSLSS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLFGRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

```

              10      20      30      40      50      60
m525-1.pep  MKYVRLFFLGAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60
a525-1      MKFTRLFLFC AALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60
              70      80      90      100     110     120
m525-1.pep  AEFVNHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWFAANAYCA
              70      80      90      100     110     120
a525-1      AEFVNHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
              70      80      90      100     110     120
              130     140     150     160     170     180
m525-1.pep  AQGKRLPTIDEWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWG V
              130     140     150     160     170     180
a525-1      AQGKRLPTIDEWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYWG V
              130     140     150     160     170     180
              190     200     210     220     230     240
m525-1.pep  YDMHGLIEWE TEDFNSSLSSGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV
              190     200     210     220     230     240
a525-1      YDMHGLIEWE TEDFNSSLSSGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV
              190     200     210     220     230     240
              250
m525-1.pep  LHNLFGRCTS RX
              250
a525-1      LHNLFGRCTS RX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1 atggttttac cagtctcctt ttttcagcct gtccagttgg cggcgggtcgc
51 gcttggtcgg tctgccgtcg ggatgggagg aagtgatgcg gctgaattgg
101 tcgagctgtt tgcaactctc cctcaatgct gccgttttcg cgtctcttc
151 atacagaagc cgcgcctcgg gtgccgggag gcgttggttg ttcaaacctt
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tggttttact gtttttgact ttcgagccgt ttacttgaac
301 cctaccagtg tcgatatgct tttgcgcaag ggaacggggtc ttgaaaaaac
351 gtgccgccca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatac gattttggtt gaaataattg aatttggttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1 MVLPSVFFQP VOLAAVALGR SAVGMGGS DA AELVELFALF PQCCRFRVFF
51 IQKPRLGCR ALVVQTFNLD FMGKGIERQV DNIADVYGF VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1 ATGTTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51 GCTTGGTTCG TCTGCCGTCT GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```


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201 TAACCKTGAT TTTATAGGGA AGGG.AATTk AgCkTCaGty GrTwATaTCG
 251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTGTAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTGTT GAAATAATTG AATTTGTTTC GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep
 1 MVLVPSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLFP
 51 IQKPRXGCRA ALVVQTFNND FIGKXNXASV XXIADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLVPSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLFIQKPRXGCRA					
g527	MVLVPSFFQP VQLAAVALGR SAVGMGGSDA AELVELFALF PQCCRFRVFFIQKPRLGCR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNND FIGKXNXASV XXIADVYGFT VFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
g527	ALVVQTFNLD FMGKIERQVDNIADVYGFT VFDPRAVYLNPTQFDMLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGR IVLVFHTILFEIIEFVSSLA					
g527	KPFVQPHGGR IVLVFHTILFEIIEFVSSLA					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq
 1 ATGTTTAC CAGTCTCCTT TTTTACAGCT GTCCAGTTGG CGGCGGTCGC
 51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
 101 TCGAGCTGTT TCGCTCTTC CCTCAATGTT GCCGTTTTCG CGTCTCTTTC
 151 ATACAGAAGC CGCGCTTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
 201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
 251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTGTAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTGTT GAAATAATTG AATTTGTTTC GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep
 1 MVLVPSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLFP
 51 IQKPRLGCR ALVVQTFNLD FIGKIERQV DNIADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLVPSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLFIQKPRXGCRA					
a527	MVLVPSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLFIQKPRLGCR					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.pep	ALVVQTFNXXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTTGLEKTCRP					
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc  gggttaataaa  atatacggca  acggctgcgt  tgtttgcatt
51  tacggttgca  ggctgccggc  tggcggggtg  gtatgagtgt  ttgtccttgt
101  ccggctgggt  taagccgaga  aaacctgccg  ccatcgattt  ttgggatatt
151  ggcggcgaga  gtcgcgtgtc  tttagaggac  tacgagatac  cgctttcaga
201  cggcaatcgt  tccgtcaggg  caaacgaata  tgaatccgcg  caaaaatctt
251  acttttatag  gaaaataggg  aagtttgaag  cctgcggggt  ggattggcgt
301  acgctgacg  gcaaaccttt  gggttagagg  ttcaaacagg  aaggtttcga
351  ctgtttgga  aagcaggggt  tgccggcgaa  cggcctgtcc  gagcgcgtcc
401  gatggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA  TAALFAFTVA  GCRLAGWYEC  LSLSGWCKPR  KPAAIDFWDI
51  GGESPLSLED  YEIPLSDGNS  SVRANEYESA  QSYFYRKIG  KFEACGLDWR
101  TRDGKPLVER  FKQEGFDCLE  KQGLRRNGLS  ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAATTC  GGGCAATAAA  ATATACGGCA  ATGGCTGCGT  TGCTTGCAAT
51  TACGTTGCA  GGCTGCCGGC  TGGCGGGGTG  GTATGAGTGT  TCGTCCCTCA
101  CCGGCTGGTG  TAAGCCGAGA  AAACCGGCTG  CCATCGATT  TTGGGATATT
151  GCGCGCGAGA  GTCCGCCGTC  TTTAGGGGAC  TACGAGATAC  CGCTTTCAGA
201  CCGCAATAGT  TCCGTCAGGG  CAAACGAATA  TGAATCCGCA  CAACAATCTT
251  ACTTTTACAG  GAAAATAGGG  AAGTTTGAAG  C.TGCGGGCT  GGATTGGCGT
301  ACGCGTGACG  GCAAACCTTT  GATTGAGACG  TTCAAACAGG  GAGGATTTGA
351  CTGCTTGGA  AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA  MAALLAFTVA  GCRLAGWYEC  SSLTGWCKPR  KPAAIDFWDI
51  GGESPPSLGD  YEIPLSDGNS  SVRANEYESA  QSYFYRKIG  KFEXCGLDWR
101  TRDGKPLIET  FKQGGFDCLE  K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

```

m528/g528
10      20      30      40      50      60
m528.pep  MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
g528      MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
10      20      30      40      50      60
m528.pep  YEIPLSDGNSSVRANEYESAQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
g528      YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
70      80      90      100     110     120

```


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```

m528.pep      K
              |
g528          KQGLRRNGLSERVRW

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

```

a528.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CCGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

```

a528.pep
1   MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

m528/a528 95.0% identity in 121 aa overlap

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
a528	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSSLTGWCKPRKPAAIDFWDIGGESPPSLED					
	10	20	30	40	50	60
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
a528	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE					
	70	80	90	100	110	120

```

m528.pep      K
              |
a528          KQGLRRNGLSERVRW
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

```

g528-1.seq
1   ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCTTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAAATCTT
251 ACTTTTATAG GAAATAGGG AAGTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GGTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGAAA AAGCAGGGGT TCGGCGCAA CCGCCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

```

g528-1.pep
1   MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

```

m528-1.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

```


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```

51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTGGGATATT
151 GCGCGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGA AAGCAGGGGT TGCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51 GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

              10      20      30      40      50      60
g528-1.pep  MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
              |||||:|||| |||:|||||:|||||:|||||:|||||:||||| || |
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              10      20      30      40      50      60

              70      80      90      100     110     120
g528-1.pep  YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
              |||||:|||||:|||||:|||||:|||||:|||||: || | |||||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
              70      80      90      100     110     120

              130
g528-1.pep  KQGLRRNGLSERVRWX
              |||||:|||||
m528-1      KQGLRRNGLSERVRWX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
151 GCGCGCGAGA GTCCGCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TGCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

              10      20      30      40      50      60
a528-1.pep  MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
              |||||:|||||:|||||:|||||:|||||:||||| || |
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              10      20      30      40      50      60

              70      80      90      100     110     120
a528-1.pep  YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
              |||||:|||||:|||||:|||||:|||||:|||||: || | |||||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
              70      80      90      100     110     120

              130
a528-1.pep  KQGLRRNGLSERVRWX
              |||||:|||||
m528-1      KQGLRRNGLSERVRWX
              130

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
  1 atgaccata tcaaacccgt cattgccgcg ctgcactca tcgggcttgc
  51 cgctgtctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
 101 ggtcgaccg cctgatcaaa ctggaagtcc cgctgattt gaacaacccc
 151 gaccaaggca acctctaccg cctgcctgcc gggtcgggag ccgtccgcgc
 201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
 251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
 301 gccaacgcct ggcttgtcgt tgacggcaaa tccccgcgcg aaatctccgc
 351 cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
  51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
 101 ANAWLVVDGK SPAEISAAF..
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
  1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
  51 CGCTGTCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
 101 GGTGCGACCG CCTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
 151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCCGGCG CCGTCCGCGC
 201 CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
 251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
 301 CAACGCTGGC TCGTTGTCTG CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
 351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
 401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
 451 CCCCAAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
 501 CTACTCCACC GCGGAGCGCG ACAAAATCAT CGTCCGTATC GAACAGGGCA
 551 AAAACGGCGT TTCCGACATC TTCTTCGCC ACAAAGCCAT GAAAGAAGTG
 601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
 651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTTGGGCG
 701 TTGACGGACA GCAGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
 751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
 801 CGACTACGGC AGAAACTGGC GCGCACCGT GTCGCCCTC GACCGCATCG
 851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTT CCTGGTTCAA
 901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAC CCGGCCTGTT
 951 CAAACGCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTCGCCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGCCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
  51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAELKSV KGVRLERDGS
 101 QRWLVVDGKS PAEIWPLLKA FWQENGFDIK SEEPAGQME TEWAENRAKI
 151 PQDSLRLRFD KVLGGIYST GERDKFIVRI EQKNGVSDI FFAHKAMKEV
 201 YGGKDKDTTV WQSPSPDNL EAAFLTRFMQ YLGVGQQAE NASAKKPTLP
 251 AANEMARIEG KSLIVFGDYG RNWRTVLAL DRIGLTVVGQ NTERHAFLVQ
 301 KAPNESNAVT EQKPLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
 351 LNKDGSAYAG KDASALLGKL HSELR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

          10          20          30          40          50          60
g529.pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
```



```

m529      |||||
          MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDAQNLRYRLPA
          10      20      30      40      50      60

          70      80      90      100     110     120
g529.pep  GSGAVRAGDLEKRRTPAVQQPADAGSIEKQRRLPLRAATAANAWLVVDGKSPAIEISAAFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m529      GSGAVRASDLEKRRTPAVQQPADAFLKSVKGVRLER-DGSQRWLVDGKSPAIEIWLPLK
          70      80      90      100     110

m529      AFWQENGFDIKSERPAIGQMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVR
          120     130     140     150     160     170

```

```

a529.seq
1  ATGACCCATA  TCAAACCCGT  CATTGCCGCG  CTCGCACTCA  TCGGGCTTGC
51  CGCCTGCTCC  GGCAGCAAA  CCGAACAGCC  CAAGCTCGAC  TACCAAAGCC
101 GGTGCGCACCG  CCTGATCAAA  CTCGAAGTCC  CACCTGATT  GAACAACCCC
151 GACCAAGGCA  ACCTCTACCG  CCTGCCTGCC  GGTTCGGGCG  CCGTCCGCGC
201 CAGCGATTGG  GAAAAACGCG  GCACACCCGC  CGTCCAACAG  CCTGCCGATG
251 CCAGAAGTATT  GAAAAGCGTC  AAAGGTGTCT  GCCTCGAGCG  CGACGCCGAGC
301 CACGCTTGGC  TCGTGTGCGA  CGGCAAGTCT  CATGCCGAAA  TTGGCCGCTT
351 CCTGAAAGCC  TTTTGGCAGG  AAAACGGCTT  CGACATCAAA  TCCGAAGAAC
401 CCGCCATCGG  ACAAAATGAA  CCGAGTGGG  CGGAAAAACG  TGCCAAATC
451 CCCCAGACA  GCTTGCGCCG  CCTATTGCAG  ACAGTCGGTT  TGGCGGCATC
501 CTACTCCACC  GCGGAGCGCG  ACAAAATTCAT  CGTCCGTATC  GAACAGGGCA
551 AAAACGGCGT  TTCCGACATC  TTCTTCGCCC  ACAAGCCAT  GAAAGAAGTG
601 TACGGCGGCA  AAGACAAAGA  CACGACCGTA  TGGCAGCCCT  CCCCGTCCGA
651 TCCCAACGTC  GAAGCCGCTT  TCCTGACGCG  CTTTATGCAA  TATTTGGGCG
701 TTGACGGACA  GCAGCGGAA  AACGCATCGG  CAAAAAAACC  TACCTTTCCC
751 GCCGCCAACG  AAATGGCGCG  TATCGAAGGC  AAAAGCCTGA  TTGTCTTTGG
801 CGACTACGGC  AGAAACTGGC  GAGCAGCCGC  GCTCCGCTC  GACCGCATCA
851 GGCTGACCGT  CGTCGGTCAA  AACCCGAAC  GCCACGCTTT  CCTGGTTCAA
901 AAAGCCCCGA  ACGAAAGCAA  TGCAGTTACC  GAACAAAAAC  CCGGCTGTGT
951 CAAACGCCTG  CTGGGCAAAG  GCAAAGCGGA  GAAACCTGCC  GAACAGCCGG
1001 AACTGATTGT  CTATGCCGAG  CCTGTGCCCA  ACGGCTCGCG  CATCGTCTTG
1051 CTCAACAAG  ACGGCAGCGC  ATATGCCCGC  AAAGACGCAT  CCGCATTATT
1101 GGGCAAACTC  CATTCCGAAC  TGGCTTAA

```

```
a529.pep
  1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
51  DQGNILYRLPA GSGAVRASDL EKRRTPAVQQ PDAEVLKSV KGVRLERDGS
101 QRWLVVDGKS HAETVPLLK LFWQENGFDIK SEEPAIGOME TEWAENRAKI
151 PQDSLRLRLFD YVLGGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDQTTV WQPSFSDPNL EAAFLTRFMQ YLGVDDQQA E NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRTALAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVY EQKPLGFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDSALLGKL HSEL*
```

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA					
	10	20	30	40	50	60
m529.pep	70	80	90	100	110	120
	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDGKSPAEIWPPLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDGKSHAETWPPLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180

800

```

m529.pep  FWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVRI
a529       FWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDTVLGGIYSTGERDKFIVRI
           130      140      150      160      170      180

           190      200      210      220      230      240
m529.pep  EQGKNGVSDIFFAHKAMKEVYGGKDKDttVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
a529       EQGKNGVSDIFFAHKAMKEVYGGKDKDttVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
           190      200      210      220      230      240

           250      260      270      280      290      300
m529.pep  NASAKKPTLPAANEMARIEGKSLIVFGDYGRNRRRTVLALDRIGLTVVGQNTERHAFLVQ
a529       NASAKKPTLPAANEMARIEGKSLIVFGDYGRNRRRTALALDRIGLTVVGQNTERHAFLVQ
           250      260      270      280      290      300

           310      320      330      340      350      360
m529.pep  KAPNESNAVTEQKPGLFKRLLGKGAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
a529       KAPNESNAVTEQKPGLFKRLLGKGAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
           310      320      330      340      350      360

           370
m529.pep  KDASALLGKLHSELRX
a529       KDASALLGKLHSELRX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga gcgcggaat gacgggtttg atatgggtca tcgtgtcatc
51 ctgtgtgatg gatattaaag tgtttgtcat gttatgccgt ccgaacgggt
101 cagacggcat ggctatatat aaagttgtcc tgaggctttc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgacag
201 tgcgggtccgc atccgcccag ggcgataacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgcgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCV M DIKVFVMLCR PNGSDGMAIF KVLRLSGRR
51 GLLPVRPSPA ERAAGARAVR IRPRIPPIIS VRRDWVRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  WTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTCATC
51 sTGTGTGATG GATATTAAAG TGtYtGTTGC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGMtATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGAckTTGC WTGTCCGTTT yCCGTCAGCG GAACGAGCGG CAGGCGGACG
201 TGCgGTTTCG ATCTGCCCAg GGCGGATACC GCCATTTCG GTGCGGCGGG
251 GCTGGGTTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL -IWVIVSSCV M DIKvXVAXCR PNGSDGMXIF- KVLRLSGRR
51 GLLXVRFPSA ERAAGGRAVR ICPGRIPPIIS VRRGWVRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

```

m530.pep  XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVLRLSGRRGLLXVRFPSA
           |||

```


g530	MSASAAMTGLIWVIVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVRI C PGRI P PI S VRRGWVRR T WCRKSESVGR	99
	: : : : :	
g530	ERAAGARAVRIRPRRI P PI S VRRD V RR T WCRKSESAGR	99

```
a530.seq
1  ATGAGTGC GA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCATC
51  CTGTGTGATG GATATTAAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCATATATT AAAGTTGTCC TGAGGCTTTC AGGGCGGGCG
151 GGACTTTTGC CTGTCGCCCT TCCGTCACGG GAACAGACGG CAGGCGGACG
201 TCGGGTTCGC ATCTGCCGAC GCGGATACCC GCCCATTTCC GTGCGCGGGG
251 GCTGGGTTCC CAGAACATGG TGTCGTA AAT CGGAATCAGC CGGTCGTGTA
```

a530.pep

1	MSASAAMTGL	IWVIVSSCVM	DIKFVVALCR	PNGSDGMAIF	KVVLRLSGRR
51	GLLPVRLPSA	ERAAGGRAVR	ICPGRIPIIS	VRRGWVRTW	CRKSESAGR*

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVM	DIKVXVAXCRPNGSDGM	IFKVVLR	LSGRRL	LLXVRF	PSA
a530	MSASAAMTGLIWVIVSSCVM	DIKVFV	ALCRPNGSDGM	IAIFKVVLR	LSGRRL	LPVRLPSA
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAVRICPGRIPPIS	VRRGWVRR	TWCRK	SES	VGRX	
a530	ERAAGGRAVRICPGRIPPIS	VRRGWVRR	TWCRK	SES	SAGR	
	70	80	90	100		

g531.seq

1	ATGACCGCCC	TACTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CCGTCGGCAC
51	GGCAGGCATC	GTCTATCCCG	CCCTGCCCGG	CTTGGCATTG	ATGTTTGGCCG
101	GAACATGGCT	GCTTGCCAT	GCCGGCGGCT	ATCAAATCTA	CGGCGCAGGC
151	ATCTTGTTGA	CGGTCCGACT	CATCAGCCTT	GGCGGCATAC	TGGCGGACTA
201	TATGGCAGGC	ATGTTGGGGG	TAAATACAC	TGGGGCAGGC	AAACTCGCCG
251	TCCGAGGTGC	ATTGCCGGGC	AGCATCATCG	GCATATTTT	CTCCCTTCCC
301	GGACTAATAC	TCCGCCCTT	TATCGGCGCG	GCGGCAGGCG	AACCTGATCGA
351	TCGGCGCAAT	ATGCTTCAGG	CAGGTAAAGC	GGGCTTGGGT	ACGCTGTTGG
401	GGCTTGTCGT	CGGCACGGCG	TTCAAATCG	GCTGCGCGGT	ATCCATCTTG
451	TTTATCCTGT	TGGTAAATA	CATCGCATAC	CTGTTTTAA	

g531.pep

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPGLAL</u>	<u>MFAGTWLLAY</u>	<u>AGGYQIYGAG</u>
51	<u>ILWTVGLISL</u>	<u>GGILADYMG</u>	<u>MLGVKYTGAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFFSLP</u>
101	<u>GLILGPFIGA</u>	<u>AAGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTA</u>	<u>FKIGCAVSIL</u>
151	<u>FILLVKYIAY</u>	<u>LF</u>			

m531.seq

```
1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GCGGGGCATC GTTTaCCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGGCG
101 GAACATGGCT GCTTGCCCTAT GCCGGCGGCT ACCAAATCTA CCGCGCGGGC
151 GTTTTGTGGA CGGTCGGACT CATCAGCCTT GCCGGCATAC TGGCGGACTA
201 TGTGCGCAGC ATATGGGGGA CAAATATAC CGGAGCGGGC AAGCTCGCCG
251 TTCGCGGCGC ATTGSCCGGC AGCATCATCG GCATATTTTT CTCCCTTCCC
301 GGACTAATAC TCGGTCCCTT TATCGGCGCG GCGGCAGGCG AACTGATTCG
```


m531.pap

1 MTVLTVILAL ALIAVGTAGI VYPALPGLAL MFACTWLLAY AGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGKYGTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

Homology with a predicted ORF from *N. gonorrhoeae*

m531/q531

	10	20	30	40	50	60
m531.pep	MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL					
	:					
g531	MTALLVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGILWTVGLISL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGIWGTKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAGELIERRN					
	: : : :					
g531	GGILADYMAGMLGVKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAGELIDRRN					
	70	80	90	100	110	120
	130	140	150	160		
m531.pep	MLQAGKAGLGTLGLVVGTAFKIGCAVSILFILLVKYIAYLF					
g531	MLQAGKAGLGTLGLVVGTAFKIGCAVSILFILLVKYIAYLF					
	130	140	150	160		

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CCGCCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTTGCT	GCTCGCCTAC	TCCGCGCGCT	ACCAATCTA	CGCGCGGGC
151	GTTTGTGGA	CGCTCGGACT	CATCAGCCTT	GCCGCGATAC	TGGCGGACTA
201	TGTGGCAGAT	ATGTGGGGGA	CAAAATATAC	CGGAGCGGAG	CGGCTCGCGC
251	TTCGCGGCGC	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGSTCCCTT	TATCGGCGCG	GCGGCAGGCG	AACTGATCGA
351	ACGGCCCAAT	AGCTTTCAGG	CAGGTAAGC	GGGCTTGGGT	ACGCTGTTGG
401	GGCTTATCGT	CGGTACGGCG	TTCAAATACG	GCTGCGCGGT	ATCCATCTTG
451	TTTATCCTGT	TGGTGAATAA	CATCGCCTAC	CTGTTTTTAA	

a531.pep

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFA GTWLLAY SGGYQIY GAG
51 VLWTVGLISL AGILADYVAG IWGTYKTGAG KLA VRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERRN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

	10	20	30	40	50	60
m531.pep	MTVLT	VILAL	ALIAV	GTAGI	VYPAL	PGLAL
	MFAGT	WLLAY	AGGYQ	IYGAG	VLWTV	GLISL
	:		:			
a531	MTALL	VILAL	ALIAA	GTAGI	VYPAL	PGLAL
	MFAGT	WLLAY	SGGYQ	IYGAG	VLWTV	GLISL
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILAD	VYAGI	WGTYK	TGAGK	LAVRG	ALAGS
	IIGIFF	SLPGL	LILGP	FFIGA	AAGFI	FERBN

803

```

a531      |||||
          AGILADYVAGIWTGKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN
          70      80      90      100      110      120

m531.pep      130      140      150      160
          MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
a531      |||||
          MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acaggcggat tcgcctgatt tgggtgacgg
51  tttggaagac aggcgcgcgt tcggtaatgc gctcttgagc gcggttacct
101 atcttttggc gattttcgtg ccgatgatta cgccgcgct gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgcgatggc
201 gatggttgcg tcgggtgctg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGTTTGGC TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGTGCGCATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTCTGCGCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTCG GCGGCGGCTT CGGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCCG CTGTTGCGCA TGAGCGGCAT
651 TCGCGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACGAGCCG ATTGAAGCGG AGGAATACAC CAAACGCCCTG
901 CGCGGCGGCG TGTTGGCTGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTACAG
1001 TGACCGCGCT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCT CGTTGTGGT CGGCGGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGTTTTT GATGTTTCGGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGAG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCT CGTTTGAGCC
1251 GGAAGTGTTT AAAAACTGC CCGTCTGTG CCAAACTCT ATTTCGCGC
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVVL IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVILLI

```


Homology with a predicted ORF from *N. gonorrhoeae*

q532/m532

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

1	ATGAGCGGTC	AGTTGGGCAA	AGGTGCGGAT	GCGCCTGATT	TGGTGTACGG
51	TTTGGAGGAT	AGGCCGCCGT	TCGGTAATGC	GCTCTTGAGC	GCGGTTACCC
101	ATCTTTTGGC	GATTTTTGTG	CCGATGATTA	CGCCCGCGCT	GATTGTGGGC
151	GGCGCGCTGG	AATTGCCGGT	GGAGATGACG	GCGTATCTCG	TGTCGATGGC
201	GATGGTTGCC	TCGGGTGTCG	GCACTTATTT	GCAGGTCAAC	CGCTTCGGGC
251	CGGTCCGGTT	GGGGATGCTG	TCCATCCAGT	CCGTGAATTT	CTCGTTCTGT
301	ACCGTCATGA	TTCGCGTCCG	CGCGGGGATG	AAAGAGGGCG	TTTGACTAA
351	GGATGCGATG	ATTTTCGACGC	TCTTGGGCGT	ATCGTTTGTC	GGCGCGTTTT
401	TGGTGTGTTT	TTCGGCGTGG	CTTCTGCCGT	ATTTGAAAAA	AGTGATTACG
451	CCGACGGTCA	GCGGTGTGGT	GGTGATGCTG	ATCGGCTTGA	GTTTGGTACA
501	CGTCCGTATT	ACCGATTTCG	GCGGCGGCTT	CGGCGCAAAG	GCGGACGGCA
551	CGTTCCGGTC	GATGAAAAAC	TGGGGCTGG	CATCGCTGGT	GCTGTGATT
601	GTGCTGGTGT	TCAATTGCAT	GA AAAAACC	CTGCTCGGGA	TGAGCGGCAT
651	TGCGGTCGGT	CTGATTGCCG	GCTATATCGT	CGCGCTGTTT	TGGGCA AAGG
701	TGGATTTTTT	GGCACTGCAA	AACCTGCCGC	TGGTTACGCT	GCCCGTACCG
751	TTTAAATATG	GTTTTGCTTT	TGACTGGCAC	GCATTTATTG	TGGCGGGTGC
801	GATTTTCTTG	TTGAGCGTGT	TTGAGGCGGT	CGGCGATTTG	ACGGCGACGG
851	CAATGGTGTC	CGACCAGCCG	ATTGAAGGCG	AGGAATACAC	CAAACGCTTG
901	CGCGGCGGCG	TGTTGGCGGA	CGGCTTGGTG	TCCGTGATTG	CGACGGCTTT
951	GGGTTTCGTG	CCCGTCAGCA	CGTTTGCACA	AAACAACGGC	GTGATT CAGA
1001	TGACCGGCGT	GGCTTCGCGC	CATGTGGGCA	AATATATTGC	CTGATTTTTC
1051	GTGCTGTTGG	GTCTGTTCCC	CGTTGTCCGA	CGCGCGTTTA	CGACGATTCC
1101	GAGTCCGGTG	TTGGGCGGCG	CGATGTTTTT	GATGTTCCGC	TTGATTGCGA
1151	TTGCGGGCGT	GCGGATTTTG	GTCAGCCACG	GCATCCGCAG	GCGCGAAGCG
1201	GTAATTGCGG	CAACGTCGGT	CGGTCTTGGG	TTGGGTGTCT	CGTTTGAGCC
1251	GGAAAGTGTT	AAAAACCTCG	CCGTCTTGTT	CCAAAAC TCT	ATTTCCGCCG
1301	GCGGCATTAC	GGCAGCTTTG	CTGAATTTGG	TCTTGCCCGA	AGATAAAACC
1351	GAGGCGGCGG	TCAAGTTTGA	TACCGACCAC	TTGAACACT	GA

a532.pep

1 MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51 GALELPVEMT AYLVSAMAMVA SGVGYTLQVN RFGPVGSGML SIQSVNFSFV

805

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
 151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
 201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
 251 FKYGFADFWDH AFIVAGAI FL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
 301 RGGVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREAR
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
 451 EAAVKFDTDH LEH*

m532/a532 100.0% identity in 463 aa overlap

	10	20	30	40	50	60
m532.pep	MSGQLGKGADAPDLVYGLEDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
a532	MSGQLGKGADAPDLVYGLEDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m532.pep	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
a532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m532.pep	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK					
a532	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLRMSGIAGVGLIAGYIVALFLGKVDFSALQ					
a532	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLRMSGIAGVGLIAGYIVALFLGKVDFSALQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m532.pep	NLPLVTLVPVFFKYGFADFWDHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
a532	NLPLVTLVPVFFKYGFADFWDHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m532.pep	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASRHHVVGKYIAVILVLLGLFPVVG					
a532	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASRHHVVGKYIAVILVLLGLFPVVG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF					
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF					
	370	380	390	400	410	420
	430	440	450	460		
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

1 atgccctttc ccgttttcag acaantattt gcttngtcct tgctacggtt
 51 ttttgcgcta ggtcggattc tcgaatccga catttccaac agcgggtttt
 101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
 151 gcctgcattt caaatttaca tcgcttccaa ttctgcaaac ttggtatcca
 201 gttctttcac gccctgtttg ccgaagtga tggcagtcg ggcggattcg
 251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
 301 gacgttttgt ccgatgcgga agcctgcgta ggtttcgccc tgtttgaagt

g535.pep

1	MPPFPVFRQXF	AXSLLRFFFAV	GRILESDISN	SGFSETINAS	NVFFVGYEYP
51	ACISNLHRFQ	FRKLGIQFFH	ALFAEVDGQS	GGFAFVCGID	NHAGAEFGVT
101	DVLSDAEACV	GLRLFEVIDD	FVPLYGGLAR	VAVAVEGGFF	DQGVVQYFWR
151	DFFDEAGCDA	ELGTSVQHAL	LCHGDVEAFA	GAGDGDVHEA	APFFFAAALG
201	KAHFAGETPL	FHLTGEEDGVE	FQAFGGVDGH	QLD <u>GGFFACPC</u>	<u>LVFAGFEGGV</u>
251	AOEGEDGEGG	IV*			

m535.seq

1	aTGCCCTTtC	CCGTTTTcAG	ACGGCCTTTT	GCTTTGCTCT	TACTtACGTT
51	TTTTGCCGTA	AGTCAGATTc	TTGTATCCGA	CAITTTCCAAC	AGCGGTGTTT
101	CGGAAACAAT	AGACGCGTCA	AATGTTTTTG	TCGGATACGA	ATATCCGACC
151	TACATTTCAA	ATTTACATCT	CTTCCAATTt	CGCAAACITG	GTGTCCAACt
201	CTTTTcAGCC	CTGTTTGCGG	AAATTGATGG	TCAGTCGGGG	GGATTcGCCT
251	TTATCTGCGG	CATCGATAAT	CACGCCGGTG	CCGAATTtGG	CGTGGCGGAC
301	GTTTTGTCCG	ATACGGAAAC	CTGCGTAGGT	TTGGGGCTGT	TGTGTAGTcGT
351	CGATCAITTT	ATCTTTGGAT	GCGCGGGTTT	GGCGCGTGTt	GCCGTAACTG
401	TCGTAGGCAG	GCTTTTTGAC	GGACAGGTA	TGCAATACTt	CGGGTGGGAT
451	CTCTTCCGAC	AAGCGGGAGA	CGATGCGCAA	TGGGTTTtTG	CCGTGCAGCA
501	TGCGTtGTTG	CGCCATGGTG	ATGTAGAGGC	GTTTGGCGGC	GCGGGTGTATG
551	GCGACGTACA	TGAGGCGGCG	TtCTTCTTCG	AGGCCGCGCG	GTTcGGCAAG
601	GCTCAITTCG	CTGGGGAAGC	GGCCTTCTTC	CATGCCGGTG	AGGAAGACGG
651	CGTTAAATTC	CAGCCTTTTG	GCGGCGTGGA	CGGTcATGAG	TTGGACGGCC
701	TTTTCGCCTG	CGCCTGCCTG	GTTTTcACCG	GATTCcAGGG	CGGCATTGCT
751	TAGGAAGGCG	AGAATGGGGA	AGGCGGGGTC	GTCtGA	

m535.pap

1	MPFFVFRRP	ALSILTFFAV	SQLVSDISN	SGVSETIDAS	NVFGVEYPT
51	YISNLHLQF	RKLGVQLFHA	LFABEIGDQG	GFAFIGCIN	HAGAEEFQVAD
101	VLSDTETCV	LGLFVWVDF	IFCGGLLAR	AVTVVGRLED	QGVVYQFPGD
151	LFDEAGDDAE	LGLSVQHALL	RHGDVEAFAG	AGDGDVHEAA	FFFEAAAFGK
201	AHFAGEAAFF	HAGEEDGVKF	QAFGGVDGHE	<u>LDGLFACAL</u>	<u>VFTGFEGGIA</u>
251	XHGEGGEGV	V*			

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/q535

	10	20	30	40	50	59
m535.pep	MPFPVFRFPFALLSTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ					
	: : : : :					
g535	MPFPVFRQXFAXSLRFFAVGRILESDISNSGFSETINASNVFVGYEYPACISNLHRFQ					
	10	20	30	40	50	60
m535.pep	60	70	80	90	100	119
	FRKLGVLFLHALFAEIDGQSGGFAPICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDD					
	: : : : : :					
g535	FRKLGIQFFHALFAEVDGQSGGFAPVCGIDNHAGAEFGVTDVLSDAEACVGLRLFVIDD					
	70	80	90	100	110	120

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	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	: : : :						
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACAC						
	: : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVEFQAFGGVDGHELDGLFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIAXEGENGEGGVV						
	: : : :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

a535.seq (partial)

1	TTCAGACGGC	CTTTTGCTT	GTCCTTGCTA	CAGTTTTTTG	CCATAGGTCG
51	GATTCTCGAA	TCCGACATTT	CCAACAGCGG	TTTTTCGGAA	ACGATAGACG
101	CGTCAAATAT	TTTTGTCCGA	TACGAGTATC	CAGCCTGCAT	TTCAAATTTA
151	CATCGCTTCC	AATTCGCAA	ACTTGGTGTC	CAACTCTTTC	ACGCCCTGTT
201	TGCCGAAATT	GATGGTCAGT	CGGGCGGATT	CGCCTTTATC	TGCGGCATCG
251	ATAATCACGC	CGGTGCCGAA	TTTGGCGTGG	CGGACGTTT	GTCCGATACG
301	GAAACCTGCG	TAGGTTTGGG	GCTGTTTGTA	GTCGTCGATG	ATTTTGTCTT
351	TGGGCGCGGC	GGTTTGCGCG	GTGTTGCCAT	AGCGGTCGTA	GGCGGGTTT
401	TTGACGGACA	GGTAGTGCAA	TACTTCGGGC	GGGATTCTT	CGACGAAGCG
451	GGAGACGATG	CCGAATTGGG	TTTGTCCGTG	CAGCATGCGT	TGTTGCGCCA
501	TGGTGATGTA	GAGGCGTTTG	CGGGCGCGGG	TGATGGCGAC	GTACATCAGG
551	CGGCTTCTT	CTTCGAGGCC	GCCGCGTTCG	GCAAGGCTCA	TTTCGCTGGG
601	GAAGCGGCCT	TCTTCCATGC	CGGTGAGGAA	TACGGCGTTA	AATTCCAAGC
651	CTTTGCGGCG	GTGCACGGTC	ATGAGTTGTA	CGGCTTTTTC	GCCCGCGCCT
701	GCTTGGTTTT	CGCCGATTTC	GAGAGCAGCA	TTGCTTAGGA	AAGCGAGGAT
751	GGGAAGGCG	GGGTCGTCTG	A		

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

1	FRRPFALSLL	OFFAIGRILE	SDISNSGFSE	TIDASNIFVG	YEYPACISNL
51	HRFQFRKLG	QLFHALFAEI	DGQSGGFAFI	CGIDNHAGAE	FGVADVLSDT
101	ETCVGLGLF	VVDDFVFRG	GLARVAIAV	GGFFDGQVVQ	YFGRDFFDEA
151	GDDAELGLSV	QHALLRHGDV	EAFAGAGDGD	VHQAFFFEA	AAFKAHFAG
201	EAAFFHAGEE	YGVKFQAFGG	VHGHLYGFF	ARACLVFAGF	ESSIA*ESED
251	GEGGVV*				

m535/a535 88.7% identity in 256 aa overlap

	10	20	30	40	50	60
m535.pep	MPFPVFRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGVEYPTYISNLHLFQF					
	:					
a535	FRRPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGVEYPTYISNLHLRFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
a535	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	: : : :					
a535	VFGRGGLARVAIAVVGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

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	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIAXEGENGEVGVX					
a535	VFAGFESSIAXESEDGEVGVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1  atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51  tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatcagg gacggcggcg atgcgctgca ctacctcaac
151 cgcattccga cacaatcggg ttgcacgcg ctggcacacg cgccggtttt
201 ggaaaattcc gcccgaggc acgcacgcta tctcacgctc aatcccgaag
251 agcgcgcccg cgaaacacat ccgacaatc cgcactacac cgcacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgtccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcaggtgcgg catttgctgc
501 cgaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
551 agcgcgcccg tgcaaaaagg agcgggcagc cggaagcagg acggaaatat
601 taccgcaacg cttgccacaa cgggtgcggc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttgge ggcggcgcgc
701 tgccttattt ttacggggaa cgtcccagac cgtgcccgga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gaggcggcag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 ggggttttaac cgccggcaac gaccctaacg gcaggctgac cgcgcaccaa
901 ttgcgccctt tcccgctcaa acctttggaa tacggcacgc tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatggcagt
1001 ttagaaccgg aaaaccgat tacccttatt ttgaggtaaa cggcggcgag
1051 acacttgccg ttagaaaagg cgaaaaatat ttcattccact ggcgcggacg
1101 ctggtgtctg gaagcgtgta ccggttatac ctaccggcgg cagttcggca
1151 acagcctgtc catactccgg cacgaagcgg gcggcattgt cttcagcgtc
1201 agcggaatgg cgggaagccg catcaggctt actccggaag acagcccgga
1251 acgcggtgta accctttatt tgcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1  MKSLFIWLLL LGSAAGVFYH TONQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DALMSAIYHR
151 LSLDDRHTDE AGAAVFRENG KTVLVFNQGN GSFERACAKG RRQPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDVPPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGLRLTAHQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1  ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCCG CGGCAGGCGT
51  TTTCTACCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGCGGCGC ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGTTTTT
201 GGGAAACTCC GCCCGCAGGC ACGCAAGCTA CCTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

```


301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)
 1 MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNVHENIS TEEAAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIR DGGDALHYLN RIRAQIGLHK					
g537.	MKSLFIWLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIR DGGDALHYLN RIRITQIGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNVHENIS					
g537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDEAGAAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g537	GSFERACAKGRROPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq
 1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAAACC AATCCCTGCC CGCGGGCGAA CTGTCTATC
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
 151 CGCATCCGCG CCCAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTT
 201 GGAAAATTCC GCCCGCAGGC ACGCACGCTA TCTCAGCTC AATCCCGAAG
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCG
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTG
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
 651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGGCGGA ATATGAAATC
 751 ACGGGCAATC CTGCCAGCAT TGATTTTTCC GAGGCGGCAG GCAAAATTAC
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCCGTCA
 851 GGGTTTAAAC CGCCGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
 951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
 1001 TTAGAACCCG AAAACCCGAT TACCTTATT TTGAGGTAAA CGGCGGCGAG
 1051 ACACCTGCGG TTAGAAAAGG CGAAAATAT TTCATCCACT GGCGCGGACG
 1101 CTGGTGTTTG GAAGCGTGTA CCCGTATAC CTACCGGCAG CGACCCGGCA

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1151 GCCGCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTACAGCGTT
 1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLLDRHTDE AGAAVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPVEYEI
 251 TGNPASIDFS EAAGKITMKS FKLQCKNEI RPRVLTAGN DPNGRLTAYQ
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFTRKPD YPYFEVNGGE
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPSRLSISR HKAGGIVFSV
 401 DGMAGSRITL APEGETERG V TLYLQD*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIR DGGDALHYLN RIRAQIGLHK					
a537	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIR DGGDALHYLN RIRAQIGLHK					
	10	20	30	40	50	60
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHH PDNPHYTAQK LTERTRLAGY LYNVHENIS					
a537	LAHAPVLENSARRHARYLTLNPEDGHGEHH PDNPHYTAQK LTERTRLAGY LYNVHENIS					
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHH PDNPHYTAQK LTERTRLAGY LYNVHENIS					
a537	LAHAPVLENSARRHARYLTLNPEDGHGEHH PDNPHYTAQK LTERTRLAGY LYNVHENIS					
	70	80	90	100	110	120
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDEAGAAVRENGKTVLVFNQGN					
	130	140	150	160	170	180
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDEAGAAVRENGKTVLVFNQGN					
	130	140	150	160	170	180
a537	GRFERHCAQGRNQPEAGRKY YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq
 1 atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
 51 cgtcatgctg gtggcgctaa tgttgataa agatgatac ggcagcaatg
 101 ccgcccgtct gaacgggttt cagacggcat tggcggaagc cgtcgagctg
 151 gtcaaagcgg cgggcgcgga ttccgtacgc gtggagactg ccaaacgcga
 201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
 251 cggaagcagt tgccgcagac ggcattgatt tggctgtatt caaccacgaa
 301 cttactccca cgcaggaacg caatttgaa aaaatcctcc aatgccgcgt
 351 attggacaga gtggggctga ttctggcgat ttctgccgc cgcgccgca
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttgccg
 451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
 501 cggcatgaaa gggccgggcy aaacaaact ggaaccgac cgcggattaa
 551 ccgcccacg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
 601 cagcgcgccc tgcccgcaa gtcccgcgag tcgggcagaa tcaaacgtt
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
 751 acgacggcgc gggcgctgta catcagtcgc gcatgcagca ttatcctgac
 801 cgataccgct ggattcgtca gcgactgcc gcacaaactg atttccgcct
 851 tttccgccac cttggaagaa accgtgcaag ccgattgtgt gctgcacgtc
 901 gtcgagctg ccgcccggaa cagcgggcag cagattgaag acgtggaaaa
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcatc aagggtgtaca
 1001 acaaaaccga cctgctgccc tctgaagaac aaaacacggg catatggcgc
 1051 gacgctgcgg gaaaaattgc cgcgctccgc atttccgttg ctgaaaaatac

1	MSGRTGRNSA	TQAQPERVML	VGVLMDKDDT	GSNAARLNGF	QTALAAEVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEAVAAD	GIDLTVFNHE
101	LTPTQERNLE	<u>KILQCRVLDR</u>	<u>VGLILAI</u> FAR	RARTQEGRLQ	VELAQLSHLA
151	GRLIRGYGHL	QSQRGGIGMK	GPGETKLETD	RRLTAHRINA	LKKQLANLKK
201	QRALRRKSRE	SGRIKTFALV	GYTNVGKSHL	FNRLTKSGIY	AKDQLFATLD
251	TTARLLYISP	ACSIILTDTV	GFVSDLPKSL	ISAFSATLEE	TVQADVLLHV
301	VDAAARNSGQ	QIEDVENVLQ	EIHADHDPCI	KVYKNTDLLP	SEBQNTGIWR
351	DAAGKIAAVR	ISVAENTGID	ALREAIAEYC	AAAPNTDETE	MP*

m538.seq

1	ATGACAGGCA	GAACAGGCGG	CAACGGCAGT	ACCCAAGCGC	AACCCGAACG
51	CGTCATGCTG	GTCGGCGTAA	TGTTGGACAA	AGATGGTACG	GGCAGTAGTG
101	CCGCCAGTCT	GAACGGTTTT	CAGACGGCAT	TGGCGGAAGC	TGTCGAGCTG
151	GTCACCGGCT	CGGGCGGCGA	TTCCGTGCGC	GTTGGAGACTG	CCAAACCGCA
201	CCGTCCGCAC	ACCGCGCTGT	TTGTGCGCAC	GGGCAAGCGC	GCGGAGCTGT
251	CAGAAGCAGT	TGCCGCAGAC	GGCATCGATT	TGGTCGTATT	CAACCACGAA
301	CTCACGCCCA	CGCAGGAAACG	CAACCTTGAA	AAAGAACTsA	AATGCCCGGT
351	ATTGGACAGG	GTAGGGCTGA	TTCCTGGCAT	TTTCCTGTCG	CGCGCCCGCA
401	CGCAGGAAGG	CAGGCTGCAA	GTCGAGTTGG	CGCAATTGAG	CGATTTTGGC
451	GGACGCTTGA	TACGCGGTTA	CGGCCATCTG	CAGAGCCAGC	GCGCGGTAT
501	CGGCATGAAA	GGCCCCGGCG	AAACCAAAC	GGAAACCGAC	CGCCGATTGA
551	TGCCCCATCG	GATCAATGCC	TGTATAAAAC	AGCTTGCCAA	CCTCAAAAAA
601	CAGCGCGCCG	TGCGCCGCAA	GTChCGCGAA	TGGGCGACAA	TCAAACCGTT
651	TGCGCTGGTC	GGCTATACAA	ATGTGCGGAA	ATCCAGCTTG	TCAACCCGGC
701	TGACAAAGTC	GGGCATATAT	GCAAAGGACA	AGCTTAGTCC	CGAATGCAGC
751	ATTATCCGCA	CCGATACCGT	CGGATTCGTn	AGCGATCTGC	CGCacAAACT
801	GATTTCCGTC	TTTTCTgCC .A	CGCTGGAAGA	AACCGCGCAA	GCCGATGTGC
851	TGCTGCACGT	CGTCGATGCC	GCGCTCCGGA	ACACGCGACA	GCAGATTGAA
901	GACGTGGAAA	ACGTACTGCA	AGAAATCCAT	CCGCGCGATA	TTCCGTGTCAT
951	cAAGGTGTAC	AACAAAACCG	ACCTGCTGCC	GTCTGAAGAA	CAAAACACGG
1001	GCATATTGGCG	CGACGCTGCG	GGAAAAATTG	CCGCGCTCCG	CATTTCCGTT
1051	GCTGAAAAAT	CGCGTATAGA	CGCACTGCGC	GAGGCcATTG	CCGAGTCTTG
1101	TGCCCGCGCA	CCAAACACAG	ACGAAACCGA	AATGCCATGA	

m538.pep

1	MTGRTGGNGS	TOAQPERVML	VGVLMDKDG	GSSAARLNGF	QTALARAVAL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEAVADA	GIDLVPVFHE
101	LTPTQERNLE	KELKCRVLRD	VGLLAIATFR	RARTQEGRLQ	VELAQLSHLA
151	GLRLIRGYGHL	QSQRQKIGMK	GPGETKLETD	RLRLTAHRINA	LIKQLANLKK
201	QRALRRKSRE	SGTIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDKLSPECS
251	IILTDTVGVF	SDLPHKLISA	FSXTLEETAQ	ADVLLHHVDA	AAPNSGQQIE
301	DVENVLQEIH	AGDIPCIKIV	NKTDLLPSEE	QNTGIWRDAA	GKIAAVRISV
351	AENTGIDALR	EAIASACAAA	PNTDETEMP*		

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTSAAARLNGFQTALAEAVELVKAAGGDSVR					
	:	:	:	:	:	:
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDGTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLVPFNHSLTPTQERNLEKELKCRVLDR					
	:	:	:	:	:	:
g538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLVPFNHSLTPTQERNLEKILOCRLDR					

812

	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSORGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSORGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQALRRKSRESGRIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLPKHLISAFSXTLEETAQADVLLHV					
	:					
g538	AKDQLPATLDTTARRLYISPACSIILTDTVGFVSDLPKHLISAFSATLEETVQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREIAESCAAAPNTDETEMPX					
g538	ISVAENTGIDALREIAEYCAAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1   ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCCG TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCCGCAC GGGCAAGCGC GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTGGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCGCCCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTCCCGCGAA TCGGGCACAA TCAAAACGTT
651 TGCGCTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAACTG ATTTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CTGACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CCGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1   MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEVAAD GIDLVVFNHE
101 LPTPTQERNLE KILQCRVLDL VGLILAI FAR RTQEGRLQ VELAQLSHA
151 GRLIRGYGHL QSORGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

```


813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDTV GFVSDLPKLI ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
a538	MTGRTGRNGSTQAQPERVMLVGVMLDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLNVFNHELTPTQERNLEKELKCRVLDL					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLNVFNHELTPTQERNLEKILQCRVLDL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAIFARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
a538	VGLILAIFARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLENRLTKSGIY					
a538	RRLIAHRINALKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLENRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLPKLIISAFSXTLEETAQADVLLHV					
a538	AKDQLFATLDTTARRLYISPECSIILTDTVGFVSDLPKLIISAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCAAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccagtc ccgcaacggca
101 aggcggacga tgtattgttt gcgttctttt tggttggcgg cttcgatttt
151 ttgcccgtca tagggcgagg cggtgttagc tgtctgccgg attttcaaca
201 gaatgtcggg gagggcgatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaaag
301 ctgctgttcg atcagccaga cgcaggcgcc gcaggtaatg ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg ttccacaaa gtccgatttg
401 acttcgggca ggtcgtacag gcggatttgg tcgaggattt cttggggcgg
451 cagttcgggt tttttcgcgt cggcggtgcg tcgtttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcggggt cttcgccttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtggg aacagggttt tttcatggca tttcggtttc

```


814

```

651 gtctgtgttt ggtgcggcgg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgttcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgtt gttccgggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgacagg tttcttccaa
951 ggtggcggaa aaggcggaaa tcagtttgtg cggcagatcg ctgacgaatc
1001 cgacggatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgcgctcg tgtcgagagt ggcgaaaagc tggcttttcg catatatgcc
1101 cgacttggtc agccggttga acaggtgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

g539.pep

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQONVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVQ ADLVEDFLGR
151 QFGFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFVF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPLEFR
301 AASTTCSSTS ACTVSSKVAE KAEISLCGRS LTNPVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLP LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

m539.seq (partial)

```

1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGCGGACGA TGTATTGTTT GCGTCTTTT TGGTTGGCGG CTTTCGATTTT
151 TTGCGCGTCA TAGGGTGCAG CCGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCaGCgG
251 TCGGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTTAAACCGC CTCGCGCGTG CCGCGTGGG TTTCCACAAA GTCGGAAGTG
401 ACTTCGGGCA GGTGCTACAG GCGGATTGCG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTGCGCGT CCGCGGTGCG TTGTTTGTA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaCagG
551 GTTTCGCGGT CTTGCTTTTC GTAACGGACA GTCAGGTGGA GGTGTTCCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTTCATGCA TTTTCGTTTC
651 GTCGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTTT
751 CCGCAGCGT CGGCCATAT GCCGTGTTT TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCAGG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CCGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTcAGGATA ATGCTGCATT CCGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

m539.pep (partial)

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQONVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFRLVGGG LFVITAQARV NNALCDRLTA GAQGFVVFVF VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLEFGA
301 AASTTCSSTS ACAVSSSVAX KAEISLCGRS LTNPVSVRI MLHSG....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

m539/g539

```

          10      20      30      40      50      60
m539.pep  MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          |||
g539      MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```


815

	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAVGFKVGLDFGQVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGFKVGLDFGQVQADLVEDFLGRQFGFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFGNVQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSSTFSTSSICCPFLGA					
g539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSSTFSTSSICCPFLRA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVVSRAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRLNRLDPLTV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTTTT TGGTTGGCGG CTTGATTTT
151 TTGCGCGTCA TAGGGTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TCGGTGCTGT AATTGAGGTC GATCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGAAGTG
401 ACTTCGGGCA GGTGCTACAG GCGGATTGG TCGAGGATT CTTGGGGCGG
451 CAGCTCGGTT TTTGCGCGT CGGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACT CCTGACAACC GGCGCAGCAG
551 GTTCGCGGT CTTGCTTTT GTAACGACG GTCAGATGCA GGTTCGCGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTT TTTTCATGGA TTTGCGTTT
651 GTCTGTGTTT GGTGCGGCGG CACAATACT GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGCAGCGT CGCGCCATAT GCGCGTGTG TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTC TTGTACACCT TGATGCACG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCAGG TTTCTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CGGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTTCG CATATATGCC
1101 CCACTTGGTC AGCCGTTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEI GFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

```


816

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGLRVGGA LFVITAQARV NNALCDCLTT GAAGFAVFVF VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSSSVAE KAEISLCGRS LTNPTVSVRI MLHSGLMYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

	10	20	30	40	50	60
m539.pep	MEDLQEIGFDVAAVKVGQRQEHRLHHPQPGNGEADDVLF AFFL VGGFDFLRVIGCGGVA					
a539	MEDLQEIGFDVAAVKVGQRQEHRLHHPQPGNGEADDVLF AFFL VGGFDFLRVIGCGGVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
a539	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGLRVGGALFVITAQARVNNALCDRLTA					
a539	LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGLRVGGALFVITAQARVNNALCDCLTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
a539	GAAGFAVFVFTDGMQVFGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA					
a539	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
a539	AASTCSSTSACAVSSSVAEKAEISLCGRSLTNPTVSVRIMLHSGLMYSRRRAVVSSVAKS					
	310	320	330	340	350	360
a539	WSFAYMPDLVSRLNRLDLPTLVX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

```

g540.seq
1  atgccgccct cccgacgcgg caacggggtg ttttatcaaa acggcaaaact
51  tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101  tgccggtgcc gaaccgatg cgtctgaac cttcagacgg catcggtgtg
151  ttatttgctc actcgacgg gtgcaggttc gtattgtgtc gattcgtcgc
201  cgtaatacag caccgcgagt ttgacgggga tgcgtccctg cgatttgcg
251  tggcggttgg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg
301  gtagaagttt tcgctgttgc tgatttcaat catacgcgcg ccgcccgcgc
351  ctttcgcgca gttgaagtc caataggcca catcatcgta aggcgcggcg
401  gcacggtgtc cgcagtcgtt gatttcgcgc atatttttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

```

g540.pep
1  MPPSRRGNGV FYQNGKLANA VSACRLPNRQ TFPVPVPNPM PSEPSDGIGC

```


817

51 LFVHSDGCRF VLCRFVAVIQ HAEFDGDASL RFAVGVGIAQ GIRAAAVFLL
 101 VEVFAFADFN HTRAAAFAP VEVPIGHIIV RRGTVSAVV DLRHIFPA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1569>:

m540.seq (partial)
 1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTTGT
 51 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTTCGTC GCCGTAATAC
 101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT
 151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
 201 TTTCACGTTT GCTGATTICA ATCATGCGCG CGCTGCCGCC GCCTTTGCGC
 251 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
 301 TCCGAGTCG TTGATTGCG CCATATTTT CCAGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1570; ORF 540>:

m540.pep (partial)
 1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
 51 GIPOGIGTTA IFLLVEVFTF ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
 101 SAVVDLRHIF PA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 540 shows 85.7% identity over a 112 aa overlap with a predicted ORF (ORF 540.ng) from *N. gonorrhoeae*:

m540/g540

				10	20	30
m540.pep				PNMPSEPSD	GIGCLFVHPD	GGRFVLCRFV
g540	GNGVFYQNG	KLAVSACRL	PNRQTFPVP	PNMPSEPSD	GIGCLFVHSD	GCRFVLCRFV
	10	20	30	40	50	60
	40	50	60	70	80	90
m540.pep	AVIQHAEFDG	DSALXFAVG	IGIPIQGIGTTA	IFLLVEVFTF	ADFNHARAAA	AFAPVEIPIH
g540	AVIQHAEFDG	DASLRFVGV	GIAQGIRAAV	FLLVEVFAF	ADFNHTRAAA	AFAPVEVPIG
	70	80	90	100	110	120
	100	110				
m540.pep	HIIVRRGGAV	SAVVDLRHIF	PAX			
g540	HIIVRRGGTV	SAVVDLRHIF	PAX			
	130	140				

L' estremita' N-terminale di meningococco e' assente perche' interviene la fine del contig

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1571>:

a540.seq
 1 ATGCCGTCTT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAACT
 51 TGCCAATGCG GTTTCCGATT GCAGATTGCC AAACCGGCAA ACCTTTCCCG
 101 TGCCGATGCC GAACCCGATG CCGTCTGAAC CTTAGACGCG CATCGGGTGT
 151 TTATTTGTCC ACCCGGATGG GTGCAGGTTT GTATTGTGTC GATTCGTCGC
 201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTTGCGC
 251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG
 301 GTAGAAGTTT TCACGTTTGC TGATTTCAT CACACGCGCG CTGCCGCCGC
 351 CTTTGCGCCA GTTGAAATCC CAATACACCA CATCATCGTA AGGCGCGGCG
 401 GCGCGCGGCG CGCAGTCGTT AATCTGGTTC ATGTTTTTCC A

This corresponds to the amino acid sequence <SEQ ID 1572; ORF 540.a>:

a540.pep (partial)
 1 MPSSRRNGV FYQNGLANA VSDCRLPNRQ TFPVPMNPM PSEPSDGIGC
 51 LFVHPDGRF VLCRFVAVIQ HAEFDGDSAL *FAVGVGIPO GIGTTAIFLL
 101 VETTFADFN HTRAAAFAP VEIPIHHIIV RRGGAAAADV NLVHVFP

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

10 20 30 40 50 60
 m542.pep MPKWSRIRRCSVLSLMFSASVSRSLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGMPMS
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 g542 MPKWSRIRRCSVLSLMFSAAVSRSLTWCAPPSNAAFRVRLKSSDGIASASAVCPAAGSMPS
 10 20 30 40 50 60
 70 80 90 100 110
 m542.pep ETVSHKSDSSRNTSASXRNVS PKCPFGTAFRQDAAKPRRFGGKSHILTGSRX

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g542 ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

a542.seq
1 ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
51 CAGCGTGTCT GCCAGCCGGT TGACTTGATG TGCGCCGCCG GCAAACGCGG
101 CATTGAGGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTCCGCC
151 GTTTGCCCGG CCGCCGGCCC GATGCCGCTT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTT
301 GGGGGCAAAT CCCATATCCT GACCGGTTTC CGGTAA

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

a542.pep
1 MPKWSRIRRC SVLSLMFSVS ASRLT*CAPP ANAAFRMLK SSDGIASASA
51 VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
101 GSKSHILTS R*

m542/a542 94.6% identity in 111 aa overlap

	10	20	30	40	50	60
m542.pep	MPKWSRIRRC	SVLSLMFSVS	ASRLTWCAPS	ANAAFRVLK	SSDGIASAS	AVCPAAGPMPS
a542	MPKWSRIRRC	SVLSLMFSVS	ASRLTXCAPP	ANAAFRMLK	SSDGIASAS	AVCPAAGPMPS
	10	20	30	40	50	60

	70	80	90	100	110
m542.pep	ETVSHKSDSSRNTSASXRN	VSPKCPFGTAF	RQDAAKPRRF	GGKSHILTGSRX	
a542	ETVSHKSDSSRNTSASRRNV	SPKCPFGTAF	RQDAAKPRRF	GGKSHILTGSRX	
	70	80	90	100	110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

g543.seq
1 atggtttgtc gggtatttgc cgccgttttt ggctttcaac tcggcaatca
51 gcccgctgat gcctttggct ttgatgattt cgccgaattg gttgcggtac
101 acggtaacca ggctcgtgcc ttgatggcg acgttgtagg tacggtattt
151 gccgcccgtt tggtaggtgg taaagtccat attgacgggc ttctgaccgg
201 ggatgccgac ttccggcagg acgacgattt ccttgccgcc cttattgacg
251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattccttg gccaacgctt
351 gtttttgccg gtcggacgcg gtacgccaaag gggtgccgac cgccaatgcg
401 gtcatacgtt ggaaatcgaa atagggaacc gcataggcct cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggtcaaa acctgtgtgg
501 cgttttgccg gatttgctcc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgtca aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttcttgaaaa tggatgtgta tgtttattct gcggcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
701 ccgatcaggt ttccagaac cattgcagaa ctggttacgg agatggtgtc
751 gccggcagca aggttttccg tatcgccgcc ctgctgcagc ccgatgtact
801 gtgcgcccga aagtcccga gtcaggattt gcgcggaaac gtcactgctg
851 aactgatact tgccgtccaa atcaaggcgc accctgcct gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgcc gaccaatacg cctgcggatt
951 tgacgggggc attgacctc aaaccgcca tgcgcgcaa atcggcataa
1001 acggcgtaag tttgtccga accgccaac gccgcgccg ccgccacgcg
1051 gaaagcgaga aaggcaaccg ccgcgcgcc gatcaagacg aacagtcgca
1101 cccaaaattc caatatgttc tttttcatta a

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

g543.pep
1 MVCRLFAAVF GFQLGNQPDV AFGFDDFAEL VAVHGNQARA FDGDVVGTVF

820

51 AAALVGGKVH IDGLLTGDAD FGTDDDLFLAA LIDDGIVFDV DGRVFEFQHR
 101 AGIGADQQGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW
 151 ACRSRVAAFE DGQNLGCVLA DLSCVVRGG KCHADAQNTD AQCADEGGFF
 201 HDVFPENGCV CLPCGFPRIA ALSVFLGEAG HEFTDQVFQON HCRTGYGDGV
 251 AGSKVFRIAA LLQPDVLFQA KRSRQDLRGN VTAEILILAVQ IKAHPRLIGF
 301 RVKPDSDAD DQYACGFDGG IDLQTADVAE IGINGVSFVR TAERRAARHA
 351 ESEKGNRRRA DQDEQSDPKF QYVLFH*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1581>:

m543.seq
 1 ATGGTTTGTG GGTATTGTC CGCCGTTTTT GGCTTCAAC TCGGCAATCA
 51 GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
 101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACCTTGATAGG TACGGTATTT
 151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
 201 GTACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
 251 ATGGGATGTG CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
 301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
 351 GTTTTTGCGC GTGCGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATGCG
 401 GTCATACGTT GGAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
 451 GCGAGCGGTG TTGGCATCGC CGTTTTTTAA GATGCTCAAT ACTTGAGTGG
 501 CGTTTTGACG GATTTGGCTT ACCGCGTCGG CAGGGGCGCG AAATGCCATG
 551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGGG AGGATTTTTT
 601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
 651 CTTTTTCCGC ATTGCCCGCG TCGGCATTTT TCTCGGCAA ACTCGTCATG
 701 AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
 751 GGTGTCGCGG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
 801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCG
 851 CTGCTGAAC TATACTTGCC GTCCAAATCG AGGCGCACCC TCGCTGATA
 901 GGATTTGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
 951 CGGATTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
 1001 GCATAAACGG CGTAAGTTTT GTCGAACCG CCGAACGCG CACCGCCGGC
 1051 CACGCGGAAA GCGAGAAAG CAACCGCGCG CGGCCAATC AGGACGAACA
 1101 GTCCGACCCA AAATTCCAAT ATGTTCTTCT TCATTAA

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

m543.pep
 1 MVCRLFAAVF GFQLGNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
 51 TAALVGGEVH VDGFLPGYAD FGADDDFFAA FIDDGIVFDV DVGVFQFQHR
 101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
 151 ASGVGIAVFX DAQYLSGVL TDLAYRVGRGG KCHADAQNTD AQCADEGGFF
 201 HDXVSXFEYD GIRLFGGFFR IAAVGIFL GKTRHEFADKVF QNHCRITYGD
 251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAELILA VQIEAHPRLI
 301 GFRVKSADSAD APDQYACGFD GGIDLTADV AEIGINGVSF VRTAERRTAG
 351 HAASEKGNRR RANQDEQSDP KFQYVLLH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

m543/g543

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFVGFLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
g543	MVCRLFAAVFVGFLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGKVH					
	10	20	30	40	50	60
m543.pep	VDGFLPGYADFGADDDFFAAFIIDDGIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR					
g543	IDGLLTGDADFGTDDDLFLAALIDDGIVFDVDGRVFEFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIIDDGIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR					
g543	IDGLLTGDADFGTDDDLFLAALIDDGIVFDVDGRVFEFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180

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m543.pep  VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIADVFXDAQYLSGVLTDLAYRVGRGG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGVLADLSHCVGRGG
          130      140      150      160      170      180

          190      200      210      220      230      239
m543.pep  KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIAIVGIPLGKTRHEFADKV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      KCHADAQNTDAQCADEGGFFHDXV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
          190      200      210      220      230

          240      250      260      270      280      290      299
m543.pep  FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAELILAVQIEAHPRL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVTAEILILAVQIKAHPR
          240      250      260      270      280      290

          300      310      320      330      340      350      359
m543.pep  IGFRVKSADSADAPDQYACGFDGGIDLTADVAEIGINGVSFVRTAERRTAGHAESEKGNR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      IGFRVKSADSADAPDQYACGFDGGIDLTADVAEIGINGVSFVRTAERRAARHAESEKGNR
          300      310      320      330      340      350

          360      370      379
m543.pep  RRANQDEQSDPKFYVLLHX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      RRANQDEQSDPKFYVLFHX
          360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TCGATGGCG ACCTTGATAG TACGGTATTT
151 ACCGCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGCGCGCG ACGATGATT CTTGCGCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTG AAATCTTTG GCCAACGCTT
351 GTTTTGGCGC GTGCGACGCG GTGCGCCAAG GGTGCGCGAC CGCCAATGCG
401 GTCATACGTT GGAATTCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTGT
451 GCGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTGAGTGG
501 CGTTTGTACG GATTGTGTTT ACCGCGTCGG CAGGGCGGCG AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCCGC ATTGCGCGCG TCGGCATTTT TCTCGGCAAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCGC GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TCAGACCCGA
801 TGTACTGCTC GCCCAAAAGT CCCGAAGTCA GGATTGCGC GGAACGCTC
851 CTGCTGAAT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTGCGG TCAAGTCCGA TAGCGCCGAC GCGCCGACC AATACGCCTG
951 CGGATTTGAC GGGGGCATG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLAHVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQLG KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIPLGK TRHEFADKVF QNHCRITGYD
251 GVAGSKVFRV AALLQPDVLL AQKSRSDLR GNVAELILA VQIEAHPRI
301 GFRVKSADSAD APDQYACGFD GGIDLTADV AEIGINGVSF VRTAERRTAG

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	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQ	LGNQSVHAFRFD	NFAELVAVHGNQ	ARAFDGDVVGTV	FTAAALVGGEVH	
a543	MAYGLLA	AVXSLQLXNQSV	HAFRFDNFAELV	AVHGNQARAFDGD	VVGTVFTAAALVG	GEVH
	10	20	30	40	50	60
m543.pep	70	80	90	100	110	120
a543	VDGFLPGYADFG	ADDDFFAAFI	DDGIVFDVDVG	VFXFQHRAGI	GADQQGLKFFG	QRLFLR
	70	80	90	100	110	120
m543.pep	130	140	150	160	170	180
a543	VGRGAPRVADRQ	CGHTLEIEI	GNRIGFGFLAS	GVGIAVFXDAQ	YLSGVLTDLAY	RVRGRG
	130	140	150	160	170	180
m543.pep	190	200	210	220	230	240
a543	KCHADAQNTDAQ	CADEGGFFHDX	VSXFEYDGIRL	FGGFFRIA	AVGIFLGKTR	HEFADKVF
	190	200	210	220	230	240
m543.pep	250	260	270	280	290	300
a543	QNHCR	TGYGDGVAGSK	VFRVAALLQPD	VLLAQKSR	SDLRGNVAAEL	LILAVQIEAHERLI
	250	260	270	280	290	300
m543.pep	310	320	330	340	350	360
a543	GFRVKS	DSADAPDQYAC	GFGGIDLTAD	VAEIGINGVS	FEVVRTAERR	TAGHAESEKGNRR
	310	320	330	340	350	360
m543.pep	370	379				
a543	RANQDEQSDPK	FQYVLLHX				
	370					
	RANQDEQSDPK	FQYVLFHX				

```

g544.seq
1  atgaaaaaaa tactcaccgc cgccgccgtc gactgatcg gcatcctcct
51  cgccaccgtc ctcatccccc acagtaaaac cgcccccgcc ttctcctctg
101 ccgaccctga cggaaaaaac ttttccaacg ccgacctgca aggcaaagtc
151 accctgatta atttttgggt tctctcctgt cgaggttgtg tgagcgaaat
201 gcccaaagtc accaaaacgg caaacgacta caaaaaataa gattccaag
251 tcttcgcgtg tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gttaccgtc attatgatg cggacaaagc
351 cgtcggagac gcattcggca cacaggttta tccgacttcc gtcttctatg
401 gcaaaaaagg cgaaatcctc aacacttatg tcggcgcaacc cgatttcggc
451 aaactctacc aagaatcga taccgcgtcg qcqcaataq

```

g544.pep

1	MKKILTAAAV	ALIGILLATV	LIPDSKTAPA	FSLPDLHGKT	VSNADLQGV
51	TLINFWFPSC	PGCVSEMPKV	TKTANDYKNK	DFQVLAVAQP	IDPIESVRQY
101	VKDYGLPFTV	IYDADKAVGQ	AFGTQVYPTS	VLIGKKGEIL	KTYVGEPEDFG

151 KLYQEIDTAL AQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

m544.seq

```

1   ATGAWAAAAA TACTCACCGC CGCCGTCGTC GCACTGATCG GCATCCTCCT
51  TGCCATCGTC CTCmTCCCCG ACAGCAAAAC CGCGCCCGCC TTCTCCmTGC
101 CCGACCTGCA CGGAAAAACC GTTCCAACG CCGACCTGCA AGGCAAAGTA
151 ACCCTGATTA ATTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAWAT
201 GCCCAAAATC ATTA AACCG CAAATGACTA TAAAwCAAA AACTTCCAAG
251 TACTTGCCGT CGCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301 GTCAAAGACT ACGGTTTGCC GTTACCGTC ATGTATGATG CGGACAAAGC
351 TGTCGGACAG GCGTTCGGCA CACAGGTTA TCCGACTTCC GTCCTTATCG
401 GCAAATAAGG CGAAATCTC AAAACCTACG TCGGCGAACC CGATTTCGGC
451 AAACCTACC AAGAAATCGA TACGCGCGTG GCGCAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1588; ORF 544>:

m544.pep

```

1   MKKILTAADV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGV
51  TLINEFWFPC PGCVSXMPKI IKTANDYKXK NFOVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIgK*GEIF KTYVGEPDFG
151 KLYQEIDTRV AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60
m544.pep	MKKILTAADVVALIGILLAIVLXPDSKTAPAFSXPDLHGKT VSNADLQGVTLINFWFPC					
g544	MKKILTAADVVALIGILLATVLPDSKTAPAFSLPDLHGKT VSNADLQGVTLINFWFPC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSXPMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTV MYDADKAVGQ					
g544	PGCVSEMPKVTKTANDYKKNDFQVLAVAQPIDPIESVRQYVKDYGLPFTVIYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
g544	AFGTQVYPTSVLIGKXGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1589>:

a544.seq

```

1   ATGAAAAAAA TACTCACCGC CGCCGTCGTC GCACTGATCG GCATCCTCCT
51  TGCCATCGTC CTCATCCCCG ACAGCAAAAC CGCGCCCGCT TTCTCCCTGT
101 CCGANCTGCA CGGAAAAANC GTTTCNAACG CCGACCTGCA AGGCNAAGTT
151 ANCCTGATTA ANTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAAAT
201 GNCCANAATC ATTA AACCG CAAATGACTA TAAAAACAAA AACTTCCAAG
251 TCTTGCCGT CGCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301 GTCAAAGACT ACGGTTTGCC GTTACCGTC ATGTATGATG CGGACAAAGC
351 TGTCGGACAG GCGTTCGGCA CACAGGTTA TCCGACTTCC GTCCTTATCG
401 GCAAAAAGG CGAAATCTC AAAACTTATG TCGGCGAACC CGATTTCGGC
451 AAACCTACC AAGAAATCGA TACGCGCGTG GCACAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1590; ORF 544.a>:

a544.pep

```

1   MKKILTAADV ALIGILLAIV LIPDSKTAPA FLSXLHGKX VSNADLQGVX
51  XLIXFWFPC PGCVSEMXXI IKTANDYKXK NFOVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIgKKGEIL KTYVGEPDFG

```


151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544.pep	MXKILTA	AVVALIGILLAI	VLXPDSKTAPAF	SXPDLHGKT	VSADLQ	GKVTLINEFWFPSC
a544	MXKILTA	AVVALIGILLAI	VLIPDSKTAPAF	SLSXLHGKXV	XNADLQ	GKXVXLIXFWFPSC
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVS	XMPKIIKTANDY	KXKNFQVLAVA	QPIDPIES	VRQYVKDYGL	PFTVMYDADKAVGQ
a544	PGCVSEM	XXIIKTANDY	KXKNFQVLAVA	QPIDPIES	VRQYVKDYGL	PFTVMYDADKAVGQ
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVY	PTSVLIGKXGEI	FKTYVGE	PDFGKLYQEID	TRVAQX	
a544	AFGTQVY	PTSVLIGKKGEI	LKTYVGE	PDFGKLYQEID	TALAQX	
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547.seq
 1 atgttcgtag ataacggatt taataaaacg gtagecgagtt ttgccccaaat
 51 cgtcgaaact ttcgacgtat tcttcttttag gaacgattgc gcctttttta
 101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggat atatctcggt
 151 gatataattta caagatgctg cttcgagatt ccgaaccgct ccttttaaaga
 201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
 251 ccgaagtcga gatggatgcc cattaactcc ccttactcag aaaatattta
 301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
 351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaaccgaa
 401 aaaagcgggt tggtttttgt tggttaa

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547.pep
 1 MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
 51 DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
 101 KFIMLHIVTN IRVFCVCVKE LLTILVKNL PNGKKRFVFC C*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq
 1 ATGTTCTGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCCAAAT
 51 CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTSTA
 101 CGCAGATGAA ACAGCGGTGC GGTGCGGTCT GCTCGTTGGT ATATCTCGTT
 151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCTT CCTTTAAAGA
 201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
 251 CCGAAGTCGA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA
 301 AAATTATATA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTTGTGT
 351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
 401 GAAAAAAGCG GTTTGTTTTT TGTTGTAA

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547.pep
 1 MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
 51 DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
 101 KFIMLHIFTN IKVFXCVCK ELLTILVKNL SPNGKKRFVF CC*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

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	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRRKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRRKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCK					
g547	ELLTILVKNLSPNGKKRFVFCCK					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCTAG  ATAACGGATT  TAATAAACG  GTAGCGAGTT  TTGCCCAAAT
51  CGTCGAACT  TTCGACGTAT  TCTTCTTTAG  GAACAATTGC  ACCTTTTTTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTACATAT  ATTTACAAAT  ATTAAGTTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRRKYL
101 KFIMLHIFTN  IKVFXCVCVK  ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRRKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRRKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCK					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  tacttgccgc
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgcggcgcaa  gccgcttctt
101 caagtgcac  cgcgcggct  gcggaatat  cggcaagcc  gcaaacgcgc
151 ggtacggata  tgcgtaagga  agacatcgcc  ggcgatttca  cactgaccga
201 cggcgaaggc  aagcctttca  gcctgagcga  tttgaaaggc  aaggtcgtga
251 ttctgtcttt  cggctttacg  cactgtcccg  atgtctgcc  gacagggtt
```


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```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acggggcgcc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccggtgc gtatcttatc gataaaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLLP GVFLAALAA CKPDNSAAQ AASSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GQAKDKVQV FVSIDPERDT PEIIGKYAQ FNPDFIGLTA
151 TGGQNLPIVK QYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CCGCTCGGCT GCGGAAATG CCGCAAAGCA AnACACGCGC
151 GGTACGATA TGCGTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CGCGGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCG GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTAGCA TCGATCCGA ACGCGACAGC CCTGAAATCA
401 TCGGCAAGTA TGCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAACATTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CTTACGGAA GCGAGCCGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLLP GVFLAALAA CKPDNSAAQ VASSASASA AENAAKQXTR
51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSIDLKQL GQAKDKVQV FVSIDPERDT PEIIGKYAQ FNPDFIXLTA
151 TGGQNLPIVK QYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLLPGVFLAALAAACKPDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG					
g548	MFSVPRSFLLPGVFLAALAAACKPDNSAAQAASSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDKVQV					
g548	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTGLLTYSDTLKQLGGQAKDKVQV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTP EIIGKYAQFNPDFIXLTATGGQNLPIVKQYRVVSAKVNQXDDSENYL					
g548	FVSIDPERDTP EIIGKYAQFNPDFIGLTATGGQNLPIVKQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

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	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGGTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAATATTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTGCG CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSFPLGVFVLAALAA CKPDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*
  
```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSFPLGVFVLAALAA CKPDNSAAQVASSSASASA AENAAKPQTRGTD MRKEDIG					
a548	MFSVPRSFPLGVFVLAALAA CKPDNSAAQVASSSASASA AENAAKPQTRGTD MRKEDIG					
	10	20	30	40	50	60
m548.pep	70	80	90	100	110	120
	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYS DTLKQLGGQAKDVKV					
a548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYS DTLKQLGGQAKDVKV					
	70	80	90	100	110	120
m548.pep	130	140	150	160	170	180
	FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
a548	FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGDQNLPIVKQQYRVVSAKVNQKDDSENYL					
	130	140	150	160	170	180
m548.pep	190	200	210			
	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc
  
```


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```

151 caaatctgca atcggacggg ttgccacgcc gctttccatc gctgctttgg
201 cggcagccgt agcgacgcga ggcagcaggc gggaaatcgaa cggagtagga
251 atcaggtatt ccgcgccgaa ttcgaaattc ttaccgtaag cggcaaccac
301 ttcttcgggt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
351 cgcgtttcat ttcttcgttg atggtggttg cgccgacatc caacgcgccc
401 cggagatga acgggaagca caatacgttg ttcacttggg tcgggaagtc
451 ggagcggcgg gtaccgataa ccacgtccgg acgggtttct ttcgccagcg
501 gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
551 tcgttcacgt tgttcaacat ttcaggcgtc agcaggtttg cgccggagag
601 gcccaagaag atgtctttgc ctttaaccgc atcggcaagt acgcgcggc
651 cgttgctctc aacggcgtag aatttttttg attcgtccat gcggtctttg
701 tcttcgcggg tttggtaaat cagcctttg gagttgcaaa cgggtacgtt
751 ttcacgtttc aagcccaaat ccacaggttg gttcaggcag gcaatcgcg
801 cggcacctgc gccggagcac accaaagtcg cttcttcgat tttacggccg
851 gtataacgca ggcggttcaa tacggcggcg gcggtaatga tggccgtgcc
901 gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

```

g550.pep
  1 MITDRFHLFH FPVSFIYQSD NKMPPENSSD GILTTNGLQL PFAQLGSVSF
 51 QICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFAE FEFLTVSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QYVHLVREV
151 GAAGTDNHVR TGFFRQRROD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
201 AQEDVFAPNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIQQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AFAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

```

m550.seq (partial)
  1 ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
 51 GTTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCACG
101 CCTTTGGAGT CGCAAACGGT CACGTTTTTCG CGTTTCAAGC CCAAATCCAG
151 CAATTGGWTC AAGCAGGCAA TCGCGGCCCG ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTITA CGGCCGGTAA AACGCAKGGC GTTCAATACG
251 CGGCGCGCGG TAATGATGGC CGTGCCGTGC TGGTCGTCTG GGAATACGGG
301 GATTTTGCAG CGTTTGCATA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

```

m550.pep (partial)
  1 ..DGIGKHALAV VENGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
 51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

```

m550.pep
          10      20      30
          DGIGKHALAVVFNGLVGLVHTVFVFAGLVN
          |||::| |||||::|::|::|::|::|
g550      DGFFVHRVQHFRQQVCAGEAQEDVFAPNRIGKYAPAVVFNGVEFFGFVHAVFVFAGLVN
          190      200      210      220      230      240

          40      50      60      70      80      90
m550.pep  HAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTGQVQYGGGGNDGRA
          |||||::|::|::|::| ||||| |||||::|::|::|::| |||||::|::|
g550      HAFGVANGYVFTFQAQIQQLVQAGNRGGTCAGAHQSRFFDFTAGITQGVQYGGGGNDGRA
          250      260      270      280      290      300

          100
m550.pep  VLVVVEYGDFAAFAX
          |||::|::|::|::|
g550      VLVIMKYGDFAAFAX

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTACCTC TTCCATCGCC AAATCCGCCA AAGCATAACAC
301 GCAGGCGCGT TTCATTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGACAATA CATTGTTTAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCAGC TCCGGACGGG TTTCTTTCGC
451 CAGCGGCGGC AGGATTTCGG GATTGCGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTT AGTATTTTCA GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTCGC GTTTCAAGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCCGTAA ACGCAGGGCG TTCAATACGG CAGCGCGCGT AATGATGGCC
851 GTGCCGTGCT GGTCTGCTG GATACGGGG ATTTTGCAGC GTTTGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQTAE DEREAYIVH LVREVGAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIKHA
201 LAVVENGVEL FGLVHTVFEV AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                10      20      30
m550.pep                      DGIGKHALAVVENGVELFGLVHTVVFVAGL
                                |||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVENGVELFGLVHTVVFVAGL
              170      180      190      200      210      220

              40      50      60      70      80      90
m550.pep    VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDG
              |||
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYSGGGNDG
              230      240      250      260      270      280

              100
m550.pep    RAVLVVVEYGDFAAFAX
              |||
a550      RAVLVVVEYGDFAAFAX
              290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttgcca cgttggtcgtg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggta gtccgtcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggatc ttggactgca
```


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451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
501 acggcgcatc atctgcggcg gtatagtggg ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA
201 AGCGAAAAA GATCAGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCCTT TACGGTTCGC CTGTCGGTCA GTCCTGCTGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAG TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGCGG GTAAAAATCC CGATGCGGGC TGTAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPdag CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
g552	MKLKTLLLPFAALALCANAF AAPPGDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPdag					
g552	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA

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201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 TCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAGT
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRIKKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

```

              10      20      30      40      50      60
m552.pep      IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
              |||||||
a552           IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m552.pep      ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              |||||||
a552           ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              70      80      90      100     110     120

              130     140     150     160     170     180
m552.pep      YGSPVGQSVVAKNPRIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
              |||||||
a552           YGSPVGQSVVAKNPRIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
              130     140     150     160     170     180

              190
m552.pep      CKQAGQVGKRHHQKX
              |||||||
a552           CKQAGQVGKRHHQKX
              190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCGG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGAAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 INIKLKTLLL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLLKNAREI YTQEEIDGMI AFYGSVPVQS VVAKNPRIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

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```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCC GCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTATA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLTLLL PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLDL ITPEVKQAVR
101 NTLLENAREI YTQEEIDGMI AFYGSVVGQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYA					
m552-1	LNIKLTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYA					
	10	20	30	40	50	60
a552-1.pep	DKALAEMPEARKDQAAEAFNRYRENVLDLITPEVKQAVRNTLLKNAREIYTQEEIDGMI					
m552-1	DKALAEMPEARKDQAAEAFNRYRENVLDLITPEVKQAVRNTLLKNAREIYTQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	AFYGSVVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD					
m552-1	AFYGSVVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD					
	130	140	150	160	170	180
a552-1.pep	AGCKQAGQVGKRHQKX					
m552-1	AGCKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaaacct gtctttgggc ttgacaaaaa agctgcccgt
51  tatactgcaa acagaagtag cggagtgttg cttggcatgt ctagcggctg
101 tggccggatt ttatggttcc taccggaatt tgcgcgact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacgggcgtt gaggttgat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcggatcc ttcggacggg gctgcccgtca tggatccggc
351 ttcgggacga cgcaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtttcgagc aggggaagaa
451 aagcaggaaa tccgcaccc acccatgttg cgcgggattt ctgggtggg
501 gcggacattg tttcagcttt tggtttggc agcagcaatg gaagtgttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaat catgataaa gggcagcaca
701 tttacagctt accgccacct ttattccgc aatttgagtg cgatgggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaacgggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep


```
m553.bseq (partial)
  1  ATGGATTATT  TATCAAGACT  GTCCTTTGGA  TTTAACAAAA  AGCTACCTGT
51  CATTCTGCCAA  ACAGAAGCTG  CTGAATGTGG  TTTAGCATGC  CTGACATCCA
101 TCTTGTCCATA  TTATAGCTTT  CACTCTGATT  TAAGAACGTT  AGCCCAAAAA
151 TACACCTGTGT  CATTAAAGGG  CGCAAATCTT  GCAGACATCA  TGAGATTTGG
201 CAATGAAATG  AATTTAACGC  CAGAGCTTT  GCGTTTAGAG  TTAGATGAGC
251 TGTCAAATTT  ACAACTACCC  TGCATTCTCC  ATTGGAACCT  AAACCATTTT
301 GTTGTACTTT  GTTCCATTTC  CAAAGACAGT  ATGTCACATT  TGACCCTCGC
351 TTTCGGTAGT  CGAAAAATCA  AAATGGACGA  AGTTTCACAA  AAATTCACAG
401 GGATTGCCCT  AGAATTATTC  CCCAATACCC  ATTTTGAAGA  GAAAAAAGAA
451 ACAAAAGAAA  TCAAAATATT  ATCTCTATTA  AGGGGGGG.  T  CAGGCTTAAA
501 ACGCTCTTTA  ATTCAAATGC  TTATATTAGC  TATTCTTTTG  GAAGTCTTTG
551 CATTG...
```

```
m553.ppep (partial)
  1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYGYF HTDLRTLROK
 51 YTLSLKGANL ADIMRFGNEM NLTPRALRL ELDLSNLQLP CILHWNLNHF
101 VVLCSISKDS IVIMDPAVGM RKIKMDEVSG KFTGIALELF PNTHFEKKKE
151 TKKIKILSLI RGXSGLKRSI IQMLILAIIS EVFAL...
```

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
g553.pep		MDYLQNL	SLGLTKKLPVILQTEVAECGLACLA	AAVAGFYGFYTDLRALRSKYCLSLKGENL			
		:	: :			:	: :
m553		MDYLSRLS	SFGFNKKLPVILQTEVAECGLACLS	SILSYGFHTDLRTL	RQKYTL	SLKGANL	
		10	20	30	40	50	60
		70	80	90	100	110	120
g553.pep		ADIVRFADDMGLTGRALRLDLDELGSLRL	PCILHWDLNHFVVLESVSSDGA	AVMDPASGR			
		:	: :	:	: :	:	: :
m553		ADIMRFGNEMNLTPRALRL	ELDELSNLQLPCILHWNLNHFVVLCS	SISKDSIVIMDP	PAVGM		
		70	80	90	100	110	120
		130	140	150	160	170	180
g553.pep		RKVKTEEISRKFTGIALELWP	NTRFEAGEEKQEIRILPMLRGISGLGR	TLFQLLALAAAM			
		: :	: :		: :	:	: :
m553		RKIKMDEV	SQKFTGIALELFPNTHFE	EKKETKKIKILSLLRGX	SGLKRS	LQMLIL	LAISL
		130	140	150	160	170	180
		190	200	210	220	230	240
g553.pep		EVFAFLQNV	SFKIGRGESLALIGRSGCGKSTLLDILSGNLP	PPESGKVMINGHDI	YSLPPP		
		:					
m553		EVFAL					

```
a553.seq
  1  ATGCCCCATC  TGCAAAACCT  GTCTTTGGGC  TTAAGAAAA  AGCTGCCTGT
51  TATCCTGCAA  ACAGAAATAT  CAGAATGCGG  CTTGGCATGT  CTGGCGGCTG
101 TGGCGGGATT  TCATGGTTTC  CATAACGAAT  TACGCGCACT  GCGTTCAAAA
151 TAC
```


This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

a553.pep
1 MPHLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
51 Y

m553/a553 62.7% identity in 51 aa overlap

	10	20	30	40	50	60
m553.pep	MDYLSRLSFGFNKKLPVILQTEVAECGLACLSILSYYGFHTDLRTLRLRQKYLTLKGANL					
	: : : : : : : : : : :					
a553	MPHLQNLSLGLKKKLPVILQTEISECGLACLAAGVAGFHGFHTNLRALRSKY					
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLTPRALRLEDELSNLQLPCILHWNLNHFVVLCSISKDSIVIMDPAVGM					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

g554.seq..
1 atgacagcac ataaaatcct gcccgctcctt cttcccatca tcttaggcgt
51 ttctcacgca acggtgcat cgcccgcgcc caacagaccg acggtacacg
101 ccgccccac gctccaaaca cccgaaaccc tcacggcggc acacatcggt
151 atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
201 tgtcgaaccg gcggcactaa cccaactgat gaccgcatat ttgggttttca
251 aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaataccc
301 gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccgcgca
351 tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
401 acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
451 aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
501 caccgtattc aaaaaccgca caggcttggg tagagaagga caggtttcca
551 ccgccaaaga cctctccctg ctgtctgaag cattgatgcg cgactttccg
601 gaatattacc cgctgttttc catcaaactc ttcaagtttg aaaacataga
651 acaaaacaac cgcaatatcc tttatatag ggacaacaat gtaaacggcc
701 tgaaagccgg gcacacagaa agcggcggtt acaaccttgc cgtgtcatac
751 tcgggcaacg gcaggcacat cctgtcatc acactagggt cggaatcggc
801 ggaaaccgca gcatcggaac acagcaagct gctgaaccgg gcattgcagg
851 ccttcgatac gcccaaaata tatccgaaag gcaaaaccgt tgcccaaatc
901 caaatttccg gaggcagcaa aaaaaccgtc cgcgagggt tcctcaaaga
951 agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
1001 tggaaacatc acagccgatt cccgccccgg taaaaaaagg gcagatttta
1051 ggaaaaatca aaatcaggca aaacggacat accattgccg aaaaagaat
1101 cgtcgactg gaaaacgtag aaaaaagaag ccggtggcaa aggctttgga
1151 cgcgtctgac aggcagtaa

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

g554.pep..
1 MTAHKILPVL LPIILGVSHA TAASPAPNRP TVHAAPTLQT PETLTAHIV
51 IDLQSRQTL AKNTNTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LCANDAALT ADRLNGSIE
151 NFVQQMKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLIIVI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGH TIAEKEIVAL ENVEKRSRWQ RLWTRLTGQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

m554.seq..
1 ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51 TTCTCACGCA ACGGTGCTG CATCGCCGCGCC CAACAGACCG ACGGTACACG
101 CCGCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTTGAACCG GCGGCACTAA CCAACTGAT GACCGCATAT CTGGTTTTC
251 AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACCT AAAAATACCC

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301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCGGCCCGG TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTC CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCTATC
751 TCCGGCAACG GCAGGCACAT CCTGTGTCATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTQPT PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IQSEENLKIP
101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LSANDAALTL AGRLGNGSIE
151 NFVQQMKEA RRLGMKNVTF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKT V RAGFLKEAYI TLPKKEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554.pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTQPTPETLTAAHIVIDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTQPTPETLTAAHIVIDLQSRQTL					
	10	20	30	40	50	60
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTVS					
	70	80	90	100	110	120
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTVS					
	70	80	90	100	110	120
m554.pep	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMKEARRLGMKNTVFKNPTGLSREG					
g554	TDKLLKGMIALCANDAALTLADRLGNGSIENFVQQMKEARRLGMKNTVFKNPTGLGREG					
	130	140	150	160	170	180
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554.pep	SGGYNLAVSYSGNRHLIVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
g554	SGGYNLAVSYSGNRHLIVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
m554.pep	SGGYNLAVSYSGNRHLIVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
g554	SGGYNLAVSYSGNRHLIVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					

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g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASNKLLNRLAQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300
           310      320      330      340      350      360
m554 . pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGY
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGH
           310      320      330      340      350      360
           370      380      390
m554 . pep TIAEKEIVALENVKKRSRWQRLWACLTGQX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g554      TIAEKEIVALENVKKRSRWQRLWTRLTGQX
           370      380      390
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```
a554 . seq
1  ATGACAGCAC ATAAAATCCT GCCCGTCTTG CTTTCCATCA TCTTAGGCGT
51  TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAACA TCAATACCCC
201 TGTGCAACCG GCGGCACTAA CCAACTGAT GACCGCATAT CTGGTTTTCa
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAACTT AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTGTAC GTCCCGCGCA
351 TACGGTCAGC ACCGACAAAC TCTTAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCAG CTGTCTGAAG CATGATGCG CGACTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTCA AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGCGGGCT ACAACCTTGC CGTGTATAC
751 TCCGGCAACG GCAGGCACAT CCTGTGTCAT ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAAG
851 CCTTCGATAC GCCAAAATA TATCCGAAAG GCAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCCTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```
a554 . pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGDTV TDKLLKGMIA LSANDAALT AGR LGNGSIE
151 NFVQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKEKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SNGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRONGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*
```

m554/a554 99.2% identity in 389 aa overlap

```
           10      20      30      40      50      60
m554 . pep MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQFPETLTAAHIVIDLQSKQILS
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a554      MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQFPETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60
           70      80      90     100     110     120
m554 . pep AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTV
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSNGIRSEENLKIPESAWASEGSRMFVRPGDTV
```


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	70	80	90	100	110	120
	130	140	150	160	170	180
m554.pep	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQOMNKEARRLGKMKNTVFKNPTGLSREG					
a554	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQOMNKEARRLGKMKNTVFKNPTGLSREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKEKNIEQNNRNILLYRDNNVNLKAGHTE					
a554	QVSTAKDLAQLSEALMRDFPEYYPLFSIKSFKEKNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554.pep	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m554.pep	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGY					
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGY					
	310	320	330	340	350	360
	370	380	390			
m554.pep	TIAEKEIVALENVKKRSRWQRLWACL TGQX					
a554	TIAEKEIVALENVKKRSRWQRLWACL TGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatcctgct tgcgcgcgtc atcgtcgccc cgcgtgcggg cggctttggt
151 tggacatccc gccgacagca acgccagttt atcgaacgct tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

m556.pep.

```

1  MDNKTCLRIG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPRTR QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTGTG
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCGGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTGCGCAA AATGTTTCGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTCLRIG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```


101 LSQKCSVDEA HAMFKKRPT R QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLLILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
g556	MDNKTCLRGLLILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT R					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT R					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
g556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAAAC	GCGCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTTTA	AGCCTCATT	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT
201	CGACATCGAT	CCCGAAAAAG	GCAGAATCAA	CGAGGCAAAC	CTGCGCCGTA
251	TGTACCACAG	CGCGGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC
301	CTGTGCGCAA	AATGTTCCGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG
351	CCCACACG	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC
401	AGAAACGTCC	GCACCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKTCLRGL	GLILLTTAVL	SLIIVLIVDS	WPLAILLAIV	IVAAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HQKDAITLIC
101	LSQKCSVDEA	HAMFKKRPT R	QEINQMAAKQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLLILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
a556	MDNKTCLRGLLILLTTAVLSLIIVLIVDSWPLAILLAIVIAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT R					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPT R					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
a556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

This corresponds to the amino acid sequence <SEQ ID 1640: ORF 557>:

m557.pap..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

a557.seq
 1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
 151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
 201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
 301 GTATTGAAAC GCGGCGAGCC GGTGGGCAAA CCGATGACCG TGTCCGTCCG
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
 451 CGCCGCCTGA CCTTCTGAA GCGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

a557.pep
 1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51 LYQASGRVDD AAGAQMTLRI DSVSQNKETY TVTRA AVINE YLLILTVEAQ
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
 151 RRLTFLKAE*

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFFLETAL YQASGRVDD					
a557	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETAL YQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTL RIDSVSQNKETY TVTRA AVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
a557	AAGAQMTL RIDSVSQNKETY TVTRA AVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEIL GKQEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
a557	AYADNEIL GKQEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

g558.seq..
 1 ATGGATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCCGAT TCTTGCCGGT GCGGGAATGA
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
 201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

g558.pep..
 1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMMPYTFE ELYMLQOGTA
 51 HQAPHCVLPE RGPPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP
 101 LSDGIV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

m558.seq..
 1 ATGAATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCCGAT TCTTGCCGGT GCAGGAATGA
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
 201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

Computer analysis of this amino acid sequence gave the following results:

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMPLYTFSELYMFQOGTAHQAPHCVLPE					
	: : : : :					
g558	MDACFFVIPAQAGIRRFGIVFKRSGRILAGAGMPLYTFSELYMLQOGTAHQAPHCVLPE					
	10	20	30	40	50	60
	70	80	90	100		
m558.pep	RDYPPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSPLSDGIVX					
	: : : :					
g558	RGCPPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSPLSDGIVX					
	70	80	90	100		

a558.seq

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

a558.pcp

m558/a558 70.2% identity in 141 aa overlap

[illegible]

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEO ID 1649>:

g560.seq

1 atgctcatca tccgcaacct gatttactgg ctgatactct qttccagcct

g560.pap..

1	<u>MLTIIRNLIYW</u>	<u>LILCSSLIFL</u>	<u>FPFMLLASPF</u>	RDGAHKMARV	VWGILNWSLK
51	HIVGLKYRII	GAEHIPDRPS	VICAKHQSGW	ETLALQEIFP	PQVYVAKREL
101	FKIPFPFGWL	KLVTGTGIDR	NNREANEQL	IKQGLARKN	GYWITFPEG
151	TRLAPGKRGK	YKLGGARMAC	MFEMDIAPVA	LNSGFAPWPN	SLFKITYPEGIT
201	VIICPTIPHA	SGSEAEIMEK	CEHLIETQOP	LISGAGPPAA	EMPSET*

m560.seq

1	ATGCTCATCA	TCCGCAACCT	GATTTACTGG	CTGATACTCT	GTTCACCCCT
51	GATTTTCCTC	TTTCCCTTTA	TGCTGCTGCG	CTCGCCTTTC	CGGGACGGGG
101	CGCACAAAGAT	GGCGCGGGTC	TGGGTCGGCA	TTCTCAACTG	GTGCGTCAAA
151	CACATCGTCG	GGCTCAAATA	CCGCATCATC	GGCGCGGAAA	ACATCCCAGA
201	CGCCGCCGCC	GTGATCTGCG	CCAAACACCA	AAGCGGCTGG	GAAGACGCTCG
251	CCCTTCAGGA	CATTTTTCGG	CCGAGGTTT	ACGTTGCCAA	ACGCGAGTTG
301	TTCAAAATCC	CCTTTTTCGG	CTGGGGCTTG	AAACTGGTCA	AAACCATAGG
351	CATAGACCGC	AAACAACCCG	GCGAAGCTCA	CGAGCAGCTC	ATAAAAACAGG
401	GGTTGGTGGC	CAAAAACGAA	GGCTATTGGA	TTACCATTTT	CCCCGAAGGC
451	ACGCGCCTTG	CGCCCGGAAA	ACGCGGCAAA	TACAAACTCG	CGGCGCGCGC
501	CATGGCGAAA	ATGTTTGAGA	TGGACATCGT	CCCCGTCGCC	CTCAACAGCG
551	GCGAATTTTG	GCCGAAAAAC	TCCTTTCTGA	AATATCCGGG	GGAATCACC
601	GTGCTCATCT	GTCCGACCAT	CCCGCACGCA	AGCGGCAGCG	AAGCCGAATT
651	GATGGAAAAA	TGCGAATCAT	TCTCGAAAG	GCAACAACCG	CTTATTTCCG
701	GCGCAGGCCC	GTTTGCCGCC	AAAATGCCGT	CTGAACCGC	ATGA

m560.pep

1	MLIIRNLIYW	LILCSTLIFL	PPFMLLASPF	RDGAHKMARV	VWGILNWSLK
51	HIVGLKYRII	GAENIPDRPA	VICAKHQSGW	ETLALQDIFP	PQVYVAKREL
101	FKIPFFGWGL	YLVKTGIDIR	NMRREANEPL	IKQGLVRKNE	GYWITFPEG
151	TRLAPAGKRG	KYLKGARMK	NNFEDIAPVA	LNSGEFVWPKN	SFLKYPGEIT
201	VVICPTIPHA	SGSEAELEMEK	CEHLEIETQOP	LISGAGPFPA	KMPSETA*

Homology with a predicted ORF from *N.gonorrhoeae*

m560/q560

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWILLCSTLIFLPFPMLLASPFRDGAHKMARVWVGILNWSLKHIVGLKYRII					
	:					
g560	MLIIRNLIYWILCSSLIFLPFPMLLASPFRDGAHKMARVWVGILNWSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAQHSGWETLALQDIFPPQVYVAKRELFKIPFGWGLKLVKTIGIDR					
	: : :					
g560	GAEHIPDRPSVICAQHSGWETLALQEIFPPQVYVAKRELFKIPFGWGLKLVKTIGIDR					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFPA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFPA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```
a560.seq
1  ATGCTCATCA  TCCGCAACCT  GATTACTGCG  CTGATACTCT  GTTCCACCCT
51  GATTTTCCTC  TTTCCCTTTA  TGCTGCTCGC  CTCGCCTTTC  CGAGACGGGG
101 CGCACAAAGAT  GGCGCGGGTC  TGGGTCAAAA  TCCTCAACCT  CTCGCTCAAA
151 CACATCGTCG  GGCTCAAATA  CCGCATCATC  GCGCGGAAA  ACATCCCCGA
201 CCGCCCCGCC  GTCATCTGCG  CCAAACACCA  AAGCGGCTGG  GAAACGCTCG
251 CCCTTCAGGA  CATTTTTCGG  CCGCAGGTTT  ACGTTGCCAA  ACGCGAGTTG
301 TTCAAAATCC  CCTTTTTCGG  CTGGGGCTTG  AAATGGTCA  AAACCATAGG
351 CATAGACCGC  AACCAACGCC  GCGAAGCCAA  CGAGCAGCTC  ATAAACAGG
401 GGTGGCGCG  CAAAACGAA  GGCTATTGGA  TTACATTTT  CCGCAAGGC
451 ACACGCCTTG  CGCCCGGAAA  ACGCGGCAA  TACAACTCG  GCGCGCGCG
501 CATGGCGAAA  ATGTTTGAGA  TGGACATCGT  CCCGTCGCC  CTCAACAGCG
551 GCGAATTTG  GCCGAAAAC  TCCTTCTGA  AATATCCGG  GGAATCACC
601 GTCGTCATCT  GTCGACCAT  CCCGACGCA  AGCGGAGCG  AAGCCGAAT
651 GATGGGAAA  TGCGAACACC  TCATCGAAC  GCAGCAGCG  CTCATTTCCG
701 GCGCAGGCC  GTTGCCGCC  AAAATGCCGT  CTGAAACCG  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```
a560.pep
1  MLIIRNLIYW  LILCSTLIFL  FPFMLLASPF  RDGAHKMARV  WVKILNLSLK
51  HIVGLKYRII  GAENIPDRPA  VICAQHSGW  ETALQDIFP  PQVYVAKREL
... 101  FKIPFGWGL  KLVKTIGIDR  NNRREANEQL  IKQGLARKNE  GYWITIFPEG
151  TRLAGKRGK  YKLGARMAM  MFEMDIVPVA  LNSGEFWPKN  SFLKYPGEIT
201  VVICPTIPHA  SGSEAELEMG  CEHLIETQQP  LISGAGPFPA  KMPSETA*
```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAQHSGWETLALQDIFPPQVYVAKRELFKIPFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAQHSGWETLALQDIFPPQVYVAKRELFKIPFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMGKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

m561.seq.

```

1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCCT
301 TCGGACACCC CTCTTGCTTA TGATTTGATA CAATCCATCG TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCGCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCTGC TGTACTGATG CTGTTTGGC
551 ACCAGATTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATCAAA CAGGTCGGGC GTTGTTCCTA TCAATGAGG GGCAGGTTGA
701 AAATTTTATA TGATGATTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTT CATTATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTG GGAAGTACC ATGAGGAAAT CTCCCCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GCGCAAAAC AGGAGGAAGA AAAACGCCTG CTGTCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTACGT TCCTAACCT ACAGGTACAG ATGCTGGAAA CCGCCTTTGC
1251 CGAAAAACAA CGGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTTCCGT
1351 ACCAAAAATCA GCAATAAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCCG
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCGTTTCT GCGCCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCCCGCGCCA CCCATGTAAA
1551 ATTCACCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTGACACG GAGAAAATAG GAGAACCAC GGGCAGCCAT
1651 GTCGGACTGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

m561.pep

```

1  MILPARFSDG ISLSLRKLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIEFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFHWQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNOMG GRKLKYDDL EGQVAEQTRS
251 LEKQONQLTL LYQTTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLL LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFAENK REEAENISF IKTVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFARFT QQTGITVETA WENGSLFPQ EAQLQMIFIL

```


845

501 QESLSNIRKH ARATHVKFTL SEHGGRTMT IQDNGQFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQQGTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS	SVVLTLLLSRL	LENAASVIEE	EAGNLR	MQAY	
	:					
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALS	SVVLTLLLSRL	LENAASVIEE	EAGNLR	MQAY	
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAE	FEKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA			
g561	RLAYMAGEGSPRAQIDNQIAE	FEKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIE	LFQALENANEKNTWWLRRFQWAIM	MLMTLVSSVLM			
g561	NILPPLQAYRRPTQIELYRFAGNIE	LFQALENAGEKNTWWLRRFQWVIM	MLMTLVSSVLM			
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRR	CFDIPVPEGGTP	PEFKQVGRCFNQMGGR	LKILYDDL		
g561	LFWHQIWVIRPLQALREGAERIGR	HFDPVPEDVRPNSNRSGGVST	KWRS	SGX		
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQONQLTLLYQT	TRDLHQSYIPQQA	AHFLNRLIPAVGADSGR	VC	LDG	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCCT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAACA	TCGAACTGTT	TTTGCAGGCA
451	TTGGAAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTACTGATG	CTGTTTGGC
551	ACCAGATTTG	GGTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAAATTCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCTG	CTGTACCAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAAGACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCCGATTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGAAAAAC	AGGAGGAAGA	AAAACGCCTG	CTTGCAGTAT
1151	TCGAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACTG	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCCTTTGC
1251	CGAAAAACAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTCCGT
1351	ACCAAAATCA	GTAATAAGA	ATTCCCCGAA	GCGTTGCCG	ACCTATTCTC

846

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1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
  1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
 51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRKILYDDL EGQVAEQTRS
251 LEKQNQNLT LLYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFFI EYQNETLGRLLSFPNGISL
351 DEDDRILLQT LGRQLGVSIA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFENK REEAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFDT ENIGEPSGSH
551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

      10      20      30      40      50      60
m561.pep MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY
      |||
a561      MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY
      10      20      30      40      50      60

      70      80      90      100     110     120
m561.pep RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP SDTPLAYDLI QSMLIIDWQA
      |||
a561      RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP SDTPLAYDLI QSMLIIDWQA
      70      80      90      100     110     120

      130     140     150     160     170     180
m561.pep HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIM LMTLVSSVLM
      |||
a561      HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIM LMTLVSSVLM
      130     140     150     160     170     180

      190     200     210     220     230     240
m561.pep LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKILYDDL
      |||
a561      LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKILYDDL
      190     200     210     220     230     240

      250     260     270     280     290     300
m561.pep EGQVAEQTRSLEKQNQNLT LLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
      |||
a561      EGQVAEQTRSLEKQNQNLT LLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
      250     260     270     280     290     300

      310     320     330     340     350     360
m561.pep GSDVYVSIHHADCGTAASDLGKYHEEIFFIEYQNETLGRLLSFPNGISLDEDDRILLQT
      |||
a561      GSDVYVSIHHADCGTAASDLGKYHEEIFFIEYQNETLGRLLSFPNGISLDEDDRILLQT
      310     320     330     340     350     360

      370     380     390     400     410     420
m561.pep LGRQLGVSILAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK
      |||
a561      LGRQLGVSILAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK

```


847

	370	380	390	400	410	420
	430	440	450	460	470	480
m561.pep	REEAAENISFIKTGVQECYEDVRELLLNERTKISNKEFPEAVADLFARFTQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNERTKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m561.pep	WENGSLFLPPQEAQLQMIFILQESLSNIRKHARATHVKFTLSEHGGRFTMTIQDNGQGFD					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLLKQDGSFTMTIQDNGQGFD					
	490	500	510	520	530	540
	550	560	570	580	590	
m561.pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSOAQQGTTVSLTVASEESLKK					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSOAQQGTTVSLTVASEESLKK					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1 atggcaagcc cgtcgagtct gcctttcaat tcgggcaaga ccaaaccgac
51 ggcttttgcc gcgccggttt tggtcggaat catgttttcc acgccgctgc
101 gggcgcggcg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtcgct ggatgggtgg cttgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaaacgac ggtcatgtcg gcggtcagga cgctgtcgtt caccgctac
301 acgacggttg catcgacatc gtcgcgccc ggtgcggaaa tgaggacttt
351 ttccgcgcgg ctttcgaggt ggattttggt tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tgcgggtcga gaagaagggg attttgtcgc cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcgttg
601 acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1 MASPSSLPFN SGTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51 VSAWMVVIAP LTMP TSLNT LATGERQLVV QEALTTVMS AVRTLSFTFY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVEKKG ILSPLTMRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1 ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51 GGCTTTTGCC GCGCCGGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTGATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCGCGCCG CTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TCGGGGTGGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501 GAGGTGCGG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
551 TGTCGAATTT GGTGAGATGG GCGTTGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1 MASPSSLPFN SGTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51 VSAWMVVIAP LTMP TSLNT LATGERQLVV QEALTTVMS AVRTLSFTFY

```


848

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
 201 TATSWWS*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*.

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLFPNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	:					
g562	MASPSSLFPNSGKTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
g562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTSASKR					
g562	LSRWILAFSLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTSASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
g562	PCTVSNLVRWALVSRLPLALTATIWSWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq

1	ATGGCAAGCC	CGTCGAGTTT	GTCTTTCAAT	TCGGGCAGTA	CCAAACCGAC
51	GGCTTTTGCC	GCGCCAGTTT	TGGTCGGAAT	CATGTTTTCC	ACGCCGCTGC
101	GGGCGCGCG	CAGGTCTTTG	TGGCGCACGT	CGGTAACGGT	TTGGTCGTTG
151	GTCAGCGCGT	GGATGGTGGT	CATCGCGCCT	TTGACGATGC	CGACGCTTTC
201	GCTCAACACT	TTGGCAACCG	GCGAGAGGCA	GTTGGTGGTG	CAGGAAGCGT
251	TGGAAACGAC	GGTCATGTCG	GCGGTCAGGA	TGCTGTCGTT	CACGCCGTAC
301	ACGACGGTTG	CATCGACATC	GTCGCCGCC	GGTGCGGAAA	TGAGGACTTT
351	TTTCGCGCCG	CTTCCAGAT	GACTTTGGC	TTTTCTTTC	CTGGTGAACG
401	CGCCGGTGCA	TTCCATGACC	AAATCGACAC	CGAGTTCTTT	CCACGGCAGT
451	TCGGCAGGGT	TGCGGGTCNA	GAAGAANGGG	ATTTTGTCGC	CGTTGACGAT
501	GAGGTTGCCG	CCGTCGTGGG	ATACGTCGGC	TTCAAAGCGT	CCGTGCACGG
551	TGTCGAATTT	GGTGAGGTGG	GCGTTGGTTT	CAAGGCTGCC	GCTGGCGTTG
601	ACGGCGACGA	TTTGAGTTG	GTCTTGA		

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep

1	MASPSSLSFN	SGSTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAWMVVIAP	LTMPTLSLNT	LATGERQLVV	QEALETTVMS	AVRMLSFTPY
101	TTVASTSSPP	GAEMRTFFAP	LSR*TLAFSL	LVNAPVHSMT	KSTPSSFHGS
151	SAGLRVXKXG	ILSPLTMLRP	PSWDTASAKR	PCTVSNLVRW	ALVSRLPLAL
201	TATIWSWS*				

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLFPNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
a562	MASPSSLFPNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60

849

	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
a562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRMLSFPTYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLVNAPVHSMTKSTPSSFHGSSAGLRVEKKGILSPLTMLRPPSWDTSASKR					
a562	LSRXTLAFSLVNAPVHSMTKSTPSSFHGSSAGLRVXXKGILSPLTMLRPPSWDTSASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
a562	PCTVSNLVRWALVSRLPLALTATIWSWSX					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

```

1  ATGAACAAAA  CCCTCTATCG  TGTGATTTTC  AACCGCAAAC  GCGGTGCTGT
51  GGTAGCTGTT  GCCGAAACCA  CCAAGCGCGA  AGGTAAAAGC  TGTGCCGATA
101 GTGGTTCGGG  CAGCGTTTAT  GTGAAATCCG  TTTCTTTCAT  TCCTACTCAT
151 TCCAAAGCCT  TTTGTTTTTC  TGCATTAGGC  TTTTCTTTAT  GTTTGGCTTT
201 GGGTACGGTC  AATATTGCTT  TTGCTGACGG  CATTATTACT  GATAAAGCTG
251 CTCCTAAAC  CCAACAAGCC  ACGATTCTGC  AAACAGGTAA  CGGCATACCG
301 CAAGTCAATA  TTCAAACCcc  tACTTCGGCa  ggGGTTTCTG  TTAATCAATA
351 TGCCAGTTT  GATGTGGGTA  ATcgcGGGGC  GATTTTAAAC  AACAGTCGCA
401 GCAACACCCA  AACACAGCTA  GGCGGTTGGA  TTCAAGGCAA  TCCTTGCTTG
451 ACAAGGGGCG  AAGCACGTGT  GGTGTAAAC  CAAATCAACA  GCAGCCATCC
501 TTCACAACCT  AATGGCTATA  TTGAAGTGGG  TGGACGACGT  GCAGAAGTCG
551 TTATTGCCAA  TCCGGCAGGG  ATTGCAGTCA  ATGGTGGTGG  TTTTATCAAT
601 GCTTCCCGTG  CACTTTGAC  GACAGGCCAA  CCGCAATATC  AAGCAGGAGA
651 CTTTAGCGCG  TTTAAGATAA  GGCAAGGCAA  TGCTGTAATC  GCCGGACACG
701 GTTTGGATGC  CCGTGATACC  GATTTACAC  GTATTCTTTT  GTATGCCAAC
751 AAAATCACCT  TGATCAGTAC  GGCCGAACAA  GCAGGCATTC  GTAATCAAGG
801 GCAGTTGTTT  GCTTCTTCCG  GTAATGTGGC  GATTGATGCA  AATGGCCGTT
851 TGGTCAATAG  TGGCACGATG  GCTGCCGCCA  ATGTGCAAGA  TATGAATAAT
901 ACAGCGGAAC  ACAAGTCAA  TATCCGCGAG  CAAGCCTTTG  AAAACAGCGG
951 TACGGCGGTG  TCGCAACAAG  GCACCTCAAAT  TCACAGTCAA  TCGATTCAAA
1001 ACACTGGCAA  ATTATTGTCG  GCAGGAACAG  AGGATTTAGC  CGTTTCAGGC
1051 AGCCTGAACA  ATCAAAATGG  CGAAATAGCG  ACCAATCAAC  AACTGATTAT
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 1301 QSN~~NEHTGST~~ VGS~~LKGD~~TTI VASKHYEQTG SNVSSPEGNN LISTQ~~SMDIG~~
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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq.

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 6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
 6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TCGGCAGCA
 6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
 6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
 6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
 6601 GGTCAAACG CGAATGGTAA ACTAACC GCC AGTCAAGAAA CCGCACACGT
 6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
 6701 ATGCTCTAGC AGGAGCATTG AGTGCGGCG GGTGCGAAGC GGCTGCGCCT
 6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
 6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
 6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
 6901 AATGCGCAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
 6951 TGCTCTTAGC CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
 7001 ATAGGTTAAA CACAAAAGAG CTAATATTG CCACAATTGC TTCAACTTTT
 7051 CAATTAAATT TATTTCTAA TAGTGAATT GGTGGTGAAG GTGGAGTTGG
 7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
 7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
 7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
 7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
 7301 ATAGGTTAAA CACAAAAGAG TTAGTTGGAT TAATTCTGGA AACTTATAAA
 7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
 7401 TGTAAGAAAA AGATTATCTG AAAAAGATTA CCAGAATACA AGCAATATAT
 7451 TGATTCACTT AGATAATACT GGTGCCGAT TTAATAATCA GCAGAGGAGA
 7501 AAACAAATCA GAGCACAAAT TTCAGCCAGA CAATGGAGAA GATAA

This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pcp..

1 MNKTLRVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVPFGTTH
 51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIIADKAAP KTOQATILQT
 101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIQ
 151 GNPWLARGEA RVVNVQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
 201 GGFINASRAT LTTGPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
 251 LSYHSKIDAP VWGQDVVVVA GQNDVVATGN AHSPILNNA ANTSNNTANN
 301 GTHIPLFAID TGKLGMYAN KITLISTAEQ AGIRNQQLF ASSGNVAIDA
 351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVENSGTAV SQOQTQIHSQ
 401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQGLSQ
 451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQGTNS YNASFHSSTT
 501 TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNGSGI IANGQTDVSA
 551 QOGLNAGOI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
 601 RQOLEIETDQ LDNAHGKLLS AETADLAVSG SLNNQNGEIA TNQQLIIHDG
 651 QOSTAVIDNT NGTIQSGRDV AIQAKSLNN GTLAADNKLD IALQDDFYVE
 701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
 751 DIGTQHNLTN RGLIDGQQTQ IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
 801 ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDTNGQATGK
 851 AORIHNAGAT IEAAGKMLQ VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
 901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
 951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
 1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
 1051 SHRKALSHHA PSQGTBLPOS NGISLPYTSN SFTPLPSSSL YIINPVNKG Y
 1101 LVETDPRFAN YRQWLGS DYM LDSLKLDPNN LHKRLGDGY EQLINEQIA
 1151 ELTGHRRLDG YQNDDEQPKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
 1201 DIVVLQKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTQINV
 1251 SGSLKNSGTI AGRNALINT DTLDNIGGRI HAQKSAVTAT QDINNIGGML
 1301 SAEQTLILLNA GNNINSQSTT ASSQNTQGS TYLDRMAGIY ITGKEKGVLA
 1351 AQAGKDNII AGQISNQSEQ QQTRLQAGR INLDTVQTSK HQATHFDADN
 1401 HWIRGSTNEV GSSIQTKGDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
 1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSSTFEGKQV
 1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTOTQSQS ETYHOTQKSG

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1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGSLKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLSNNT TQTYEQKGLT VAFSSPVTDL
1651 AQQAIIVAAQS SKQVGQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVVISITY GEQQNRQTTO VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKSAQ WNAGAAVSFG
1801 QGGWSLGVTA GGNVVGKGYGN GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKKG
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKLDKADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQGGKV ILNMLASGLA APTQSGAGIA AATASPAVSY AIGQHFKDLA
2201 GQNANGKLLTA SQETAHVLAH AVLGAAVAAG GDNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGAAVGN SATDAAQGS
2301 NAQSAVENND TVEQVKFALR HPRIAIAGS VHKDPGSTLE PNISTIASTF
2351 QLNLFNPSEF GEGGGVGNF RHVLWQATIT REFGKDIIVK VGNSHESGEK
2401 INYSIRRNLS LDKADEMIDQ LNNEIGREIA LNTNRLNTKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNLIHLNLT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

	10	20	30	40	50	
g563.pep	MNKTLRYVIFNRKRGA VVAE TTKREGKSCADSGSGSVYVKS VSFIPTH-----SKAFC					
m563.pep	MNKTLRYVIFNRKRGA VVAE TTKREGKSCADSDSGSAHVKS VPFPGTTHAPVCRSNI FS					
	10	20	30	40	50	60
	60	70	80	90	100	110
g563.pep	FSALGFS LCLALGT VNI AFADGI ITDKAAPKTQQATILQTGN GIPQVNIQTPTSAGVSVN					
m563.pep	FSLLGFS LCLAVGT ANI AFADGI IADKAAPKTQQATILQTGN GIPQVNIQTPTSAGVSVN					
	70	80	90	100	110	120
	120	130	140	150	160	170
g563.pep	QYAQFDVGNRGAILNNSRSNTQTQLGGW IQGNPWLTRGEARVVVNQINSSHPSQLNGYIE					
m563.pep	QYAQFDVGNRGAILNNSRSNTQTQLGGW IQGNPWLARGEARVVVNQINSSHSSQMNGYIE					
	130	140	150	160	170	180
	180	190	200	210	220	230
g563.pep	VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVIA GHGL					
m563.pep	VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVVIAGHGL					
	190	200	210	220	230	240
	240					
g563.pep	DARDTDFTRIL-----					
m563.pep	DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPILNNA AANTSNTANN					
	250	260	270	280	290	300
	250	260	270	280	290	
g563.pep	-----LYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGMT					
m563.pep	GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGMT					
	310	320	330	340	350	360

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      300      310      320      330      340
g563.pep  AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----
          |||::| :|||:|||||: |||:|||||:|||||: |||:|
m563.pep  AAANAKDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG
          370      380      390      400      410      420

g563.pep  -----
m563.pep  SLKNETSGTIEAARLAIDTDTLNNQKLSQTGSQKLHIDAQGKMDNRGRMGLQDTAPTAS
          430      440      450      460      470      480

g563.pep  -----
m563.pep  NGSSNOTGNSYNASPHSSTTTPTTATGTGTATVSISNITAPTTFADGTIRTHGALDNSGSI
          490      500      510      520      530      540

g563.pep  -----
m563.pep  IANGQTDVSAQQGLNNAGQIDIHQLNAGSAFDNHNGTIISDAVHIQAGSLNNQNGNITT
          550      560      570      580      590      600

      350      360      370      380
g563.pep  -----EDLAVSGSLNNQNGEIATNQQLIIHDGQQSTVVIDNT
          |||:|||||:|||||:|||||:|||||:|
m563.pep  RQOLEIETDQLDNAHGKLLSAEADIADLAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT
          610      620      630      640      650      660

      390      400      410      420      430      440
g563.pep  NGTIQSGRDVAIQAKSLSNNGTLAADNKLIDIALQDDFYVERKIVAGNELSLSTRGSLKNS
          |||:|||||:|||||:|||||:|||||:|
m563.pep  NGTIQSGRDVAIQAKSLSNNGTLAADNKLIDIALQDDFYVERNIVAGNELSLSTRGSLKNS
          670      680      690      700      710      720

      450      460      470      480      490      500
g563.pep  HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQIQAGQMNNIG
          |||:|||||:|||||:|||||:|||||:|
m563.pep  HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQIQAGQMNNIG
          730      740      750      760      770      780

      510      520      530      540      550      560
g563.pep  TGRIYGDNIAIAATRLDNQDENGTAIAAARENLNLGIEQLNNRENSLIYSGNDMAVGGA
          |||:|||||:|||||:|||||:|||||:|
m563.pep  TGRIYGDNIAIAATRLDNQDENGTAIAAARENLNLGIGQLNNRENSLIYSGNDMAVGGA
          790      800      810      820      830      840

      570      580      590      600      610      620
g563.pep  LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFG
          |||:|||||:|||||:|||||:|||||:|
m563.pep  LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFG
          850      860      870      880      890      900

      630      640      650      660      670      680
g563.pep  RHELLREGTQHELGWFFVYNNESDHLRTPDGAHENWHKYDYEKVTQETQVTTGTAPAKIIA
          |||:|||||:|||||:|||||:|||||:|
m563.pep  RHELLREGTQHELGWSVYNDES DHLRTPDGAHENWHKYDYEKVTQKTQVTTGTAPAKIIS
          910      920      930      940      950      960

      690      700      710      720      730      740
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g563 . pep	GSDLIIDSKAVFNSDSRIIAGGQLLVQTEKDGLHNEQTFGEKKVFSENGKLHNYWRARRK
m563 . pep	GNDLTIDGKEVFNTDSQIIAGGNLIVQTEKDGLHNEQTFGEKKVFSENGKLHSYWREKHK
	970 980 990 1000 1010 1020
g563 . pep	750 760 770 780 790 800
	GHDETGHRQNYTLPEEITRDISLGSFAYESHKALSRHAPSQGTLPQSNRDNIRTAKS
m563 . pep	GRDSTGHSEQNYTLPEEITRNISLGSFAYESHRKALSHHAPSQGTLPQSN-----
	1030 1040 1050 1060 1070
g563 . pep	810 820 830 840 850 860
	NGISLPYTPNSFTPLPGSSLYIINPANKGYLVETDPRFANYRQWLGS DYMLGSLKLDPNN
m563 . pep	-GISLPYTSNSFTPLPSSSLYIINPVNKG YLVETDPRFANYRQWLGS DYMLDSLKLDPNN
	1080 1090 1100 1110 1120 1130
g563 . pep	870 880 890 900 910 920
	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
m563 . pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
	1140 1150 1160 1170 1180 1190
g563 . pep	930 940 950 960 970 980
	SAEQAAQLTSDIVWL VQKEVKLPDGGTQT V LMPQVYVRVKNGGIDGKGALLSGSNTQINV
m563 . pep	SAEQVAQLTSDIVWL VQKEVKLPDGGTQT V LVPQVYVRVKNGDIDGKGALLSGSNTQINV
	1200 1210 1220 1230 1240 1250
g563 . pep	990 1000 1010 1020 1030 1040
	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQKSAVTATQDINNIGGILSAEQTL L LNA
m563 . pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQKSAVTATQDINNIGGMLSAEQTL L LNA
	1260 1270 1280 1290 1300 1310
g563 . pep	1050 1060 1070 1080 1090 1100
	GNNINNQSTAKSSQNAQGSSTYLDRMAGIYITGKEKGVLAQAQKDINI IAGQISNQSDQ
m563 . pep	GNNINSQSTTASSQNTQGSSTYLDRMAGIYITGKEKGVLAQAQKDINI IAGQISNQSEQ
	1320 1330 1340 1350 1360 1370
g563 . pep	1110 1120 1130 1140 1150 1160
	GQTRLQAGRDINLDTVQTKYQEIHFADNHTIRGSTNEVGSSIQTKGDVTL LSGNNLNA
m563 . pep	GQTRLQAGRDINLDTVQTSKHQATHFDADNHVIRGSTNEVGSSIQTKGDVTL LSGNNLNA
	1380 1390 1400 1410 1420 1430
g563 . pep	1170 1180 1190 1200 1210 1220
	KAAEVGSAKGT LAVYAKNDITISSGIHAGQVDDASKHTGRSGGKNKL VITDKAQSHHETA
m563 . pep	KAAEVSSANGT LAVSAKNDINISAGINTTHVDDASKHTGRSGGKNKL VITDKAQSHHETA
	1440 1450 1460 1470 1480 1490
g563 . pep	1230 1240 1250 1260 1270 1280
	QSSTFEKGQVVLQAGNDANILGSNVISDNGTRI QAGNHVRIGTTQTQSQSETYHQTKSG
m563 . pep	QSSTFEKGQVVLQAGNDANILGSNVISDNGTQI QAGNHVRIGTTQTQSQSETYHQTKSG
	1500 1510 1520 1530 1540 1550
g563 . pep	1290 1300 1310 1320 1330 1340
	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGS LKGDTTIVASKHYEQTGSNVSSPEGNN

	1950	1960	1970	1980	1990	2000
g563.pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDGGS LNAE					
	: : : : : :					
m563.pep	TASQETAHVLAHAVLGA AVAVGDNALAGALSAGGSEAAAPYISKWLYGKEKGS DLTAE					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049	
g563.pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFQTASDFASSFSYPINMX					
	: : : : : :					
m563.pep	EKETVTAITNVLTATGA AVGNSATDAAQGS LNQA SAVENNDTVEQVKFALRHPRIAIAI					
	2270	2280	2290	2300	2310	2320

m563.pep	GSVHKDPGSTLEPNISTIASTFQLNLPNSEFGGEGGVGNAFRHLVQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564.seq
1  ATGAACCGCA  CCTGTACAA  AGTTGTATTT  AACAAACATC  GAAACTGCAT
51  GATAGCCGTT  GCTGAAATG  CCAAACGCGA  GGGCAAAAC  ACAGCCGACA
101 CCCAAGCTGT  AGGTATTTTG  CCAAATGATA  TTGCGGGCTT  TCGGGGTTTT
151 ATCCATTCTA  TCTCTGTAT  CTCATTCTCC  CTTTCATTAC  TGCTCGGTTT
201 TGCCCTTATC  CTGACTTCTT  CTTCTGCTAC  TGCCCAAGGT  ATCGTTGCCG
251 ACAAAATCCG  ACCTGCACAG  CAACAGCCTA  CCATCCTGCA  AACAGGTAAC
301 GGCATACCGC  AAGTCAATAT  TCAAACCCCT  ACTTCGGCAG  GGGTTTCTGT
351 TAATCAATAC  GCCCAGTTTG  ATGTGGGTAA  TCGCGGGGCG  ATTTTAAACA
401 ACAGTCGCAG  CAACACCCAA  ACACAGCTAG  GCGGTTGGAT  TCAAGGCAAT
451 CCTTGGTTGG  CAAGGGGCGA  AGCACGTGTG  GTTGTA AAC  AAATCAACAG
501 CAGCCATTCT  TCACA ACTGA  ATGGCTATAT  TGAAGTGGGC  GGACGACGTG
551 CAGAAGTCGT  TATTGCCAAT  CCGGCAGGGA  TTGCAGTCAA  TGGTGGTGGT
601 TTTATCAATG  CTTCCCGTGC  CACTTTGACG  ACAGCCCAAC  CGCAATATCA
651 AGCAGGAGAC  CTTAGCGGCT  TTAAGATAAG  GCAAGGCAAT  GTTGTATCG
701 CCGGACACGG  TTTGGATGCA  CGTGATACCG  ATTACACACG  TATCTCAGT
751 TATCATTCCA  AAATTGATGC  ACCCGTATGG  GGACAAGATG  TTCGTGTCGT
801 CGCGGGACAA  AACGATGTGG  CCGCAACAGG  TGATGCACAT  TCGCCTATTC
851 TCAATAATGC  TGCTGCCAAT  ACGTCAACAA  ATACAGCCAA  CAACGGCACA
901 CATATCCCTT  TATTTGCGAT  TGATACAGGC  AAATTAGGAG  GTATGTATGC
951 CAACAAAATC  ACCTTGATCA  GTACGGTCTG  GCAAGCAGGC  ATTGTAATC
1001 AAGGGCAATG  GTTTGCCCTC  GCCGGCAATG  TGGCAGTGAA  TGCTGAGGGT
1051 AAAGTGGTCA  ACACGGGCAT  GATTGCAGCG  ACGGGAGAAA  ATCATGCGGT
1101 TTCACTTCAT  GCCCGCAATG  TTCATAATAG  CGGTACGGTT  GCCTCACAGG
1151 ATGATGCCAA  TATTCACAGC  CAGACGCTGG  ACAATTCAGG  TACGGTCTTA
1201 TCCTCAGGTC  GATTGACTGT  TCGTAATTTA  GGCCGTCTGA  AAAACCAAAA
1251 CAACGGTACG  ATCCAGGCTG  CCCGCTTAGA  TATGTCAACA  GGTGGTTTGG
1301 ATAACACAGG  TAATATTACT  CAAACAGGTT  CACAAGCATT  GGATTGGTA
1351 TCTGCCGCGA  AATTCGATAA  CAGTGGCAAG  ATTGGTGTA  GTGACGTTCC
1401 ACAGACCGGT  TTGAATCCCA  ATCCATCAGT  CATACCACAG  ATTCCGAGTA
1451 CTGCAACAGG  TTCAGGCAGC  AGCACTGTCT  CGGTATCTAA  GCCTGGTTCA
1501 AACAAATCCC  TTTCACCTAC  AGCACCTGCA  AAAA ACTAC  CCGTAGGACG
1551 CATTCAAACA  ACAGGAGCAT  TTGACAATGC  AGGATCAATT  AATGCGGGTG
1601 GGCAAAATTGA  CATTGCCGCC  CAAAACGGTT  TGGGAAATTC  GGGTAGTCTG
1651 AATGCGGCTA  AACTACGAGT  ATCAGGCGAT  TCATTTAACA  ATACGGTAAA
1701 AGGCAAACTC  CAGGCACACG  ATCTGGCTGT  TAACACTCAA  ACTGCTAAAA
1751 ACAGCGGTCA  CTTATTA ACT  CAAACCGGCA  AGATTGATAA  CCGTGAACTG
1801 CATAATGCCG  GAGAAATTGC  CGCCAACAA  CTGACACTAA  TTCATTCCGG
1851 CCGCTTGAGC  AATGATAAAA  AAGGCAATAT  TCGAGCTGCA  CATTACAGC
1901 TTGATACCGC  CGGTTTACAT  AATGCAGGTA  ACATTCTTGC  CGATAGTGGA
1951 ACCGTTACCA  CCAAGAATAA  TCTTCGCAAT  ACAGGAAAAG  TTTCTGTTGC
2001 ACGACTGAAT  ACCGAAGGTC  AGACTCTAGA  TAATACGCGC  GGACGTATAG
2051 AGGCTGAAAC  GGTAAACATC  CAAAGTCAGC  AACTGACTAA  CCAAAGCGCG
2101 CATATTACTG  CTACCGAACA  ACTGACTATC  AATAGTCGAA  ATGTAGACAA
2151 CCAAAACGGC  AAACCTCTAT  CTGCAAAACA  AGCACAATTA  GCTGTTTCAG
2201 ACGGCCTATA  CAACCAACAT  GGTGAAATTG  CCACCAACCG  GCAGTTGTCT

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2251 ATTACGATA AAAATCAAAA CACTTTGGCG TTAAACAATG CGGATGGCAC
 2301 GATTCAATCT GCCGGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACAA
 2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT
 2401 TTCGTCGTAG AGCGCGACCT CACTGCAGGC AAACAATTAA ATCTAAGCAT
 2451 AAAAGGCCGT CTGAAAAATA CCCATACCTT ACAAGCAGGC CATACGCTCA
 2501 AACTCAATGC CGGCAATATA GATAACCAAG TTACAGGCAA AATTATTGGT
 2551 GGAGAACAAA CGGACATCAC ATCCGAACAG CATGTTGACA ACAGGGGCTT
 2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGGTCAA ACCCTGACCA
 2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA
 2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGGC
 2751 AATAGCTGCA AGGAAACGTT TGGATATTGG AGCGAAAGAG ATTCTAACC
 2801 AAGAAGGTGC CCTACTATCC AGCGAAGGTA TTTTGGCCGT AgGTAATCGA
 2851 CTGGATGAAC AACATCATGC GGCAGGCATG GCCGATACCT TTGTTAATGG
 2901 CAGTGCCGGT TTGGAAGTAC AAGGTGATGC ATTGATGTCC GTTCGGAATA
 2951 TGCAGAATAT CAATAATCAC TTAAACACAG AGACATACTT AGCCAAAGCG
 3001 GAAAAGCAAG TCCGCGACTA CACCGTACTG GGGCAAAATA CCTACTATCA
 3051 GCGCGGAAAA GACGGTTTAT TCGACAACCT GCAAGGACAA AAAGACCAAA
 3101 CTACTGCTAC GTTCCATTTA AAAAATGGTT CTCGTATTGA GGCCAACCAA
 3151 TGGCATGTCC GAGACTACCA CATCGAGACT TATAAAGAAC GCATCATCGA
 3201 AAACCGGCCG GCACACATTA CTGTGGGCGG TGATTGACT GCCTCAGGTC
 3251 AAAATTGGCT GAACAAAGAC AGCCGGATTG TAGTAGGCGG GCGTATTATC
 3301 ACTGATGATT TAAACCAGAA AGAAATTACC AATCAAAGTA CAACAGGCAA
 3351 AGGTCGCACA GATGCTGTG GCACACAGT GGATTCAGTT ACAAAAAAG
 3401 GATGGTACAG CGGTAGAAAA AGACAACGCC GTACTGAAAG AAACCATACT
 3451 CCTTACCATG ATACCCAAT ATTTACCCAC GACTTCGACA CGCTGTATC
 3501 CGTCATCCAA CAGAATGCCG CCTCCCCTTC CTTTCAACCC GCCGCATCTG
 3551 CAATCAAAT GATTGACGGA GTATCCACGG CAGCCGTCAA TGGTCAGCGC
 3601 ATCCATACCG GTAATGTGGT CTCGTTAAAT AACGCTACTG TTACTCTGCC
 3651 TAACAGCAGC CTCTATACCA CCCATCCTGA CAATAAAGGC TGGTTGGTTG
 3701 AAACCGATCC TCAATTTGCA GACTACCGCC GCTGGTTGGG CAGCGACTAC
 3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG
 3801 CGACGGCTAC TACGAACAAA AACTTGTTAA TGAACAAATC CATCAGTTAA
 3851 CAGGCTACCG CCGACTCGAC GGCTACAGGA GTGATGAAGA ACAATTCAAA
 3901 GCTCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTGC GTCTCACCCC
 3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAACT TCAGATATCG
 4001 TTTGGATGGA AAATCAAACC GTCACCCTGT CTGACGGTTC GACTCAAACC
 4051 GTACTGGTTC CTAAAGTCTA TGCCCTGGCG CGCAAAGGTG ATCTCAATAC
 4101 CTCCGGTGGC CTGATTAGTG CCGAACAAGT CTTACTTAAA CTGCAAAACG
 4151 GCAACCTGAC TAACAGCGGT ACCATTGCCG GGCAGCAGGC CGTACTCATC
 4201 CAGGCACGGA ATATTAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG
 4251 CTTAAAGCT GAAAAAGTA TCAATATCGA CGCGGGCGAG GTACAAGCAG
 4301 GCAGACTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC
 4351 CAAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC
 4401 CGGCATTAAAC GTGGTCGGAA GCCATACTGA ACAAGTAGAT AACAGAATTT
 4451 CAGACGGCAT CCTATCCCTG CATGCCAGCA ACGATATCAA CCTCAATGCG
 4501 GGCACCGTCT CTAACCAAGT TAAAGACGGC ACTACCCAAA TTACCGCCGG
 4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG
 4601 GTACATTAGA TGACGAGAAC CATCGCCATG TCCGCCAAAG TACCGAAGTC
 4651 GGCAGCAGTA TCCGCACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA
 4701 CTTAAAAATC CGCCAAGGCG AACTGGAGGC CGAAGAAGGC AAAACCGTCC
 4751 TTGCCGAGG ACGTGATGTC ACTATCAGCG AAGGACGCCA AATAACCGAA
 4801 CTGGATACCT CGGTAAGCGG AAAAAGCAAA GGCATCCTTT CAGTACCAA
 4851 AACACACGAC CGCTACCGCT TCAGTCATGA TGAAGCAGTC GGCAGCAACA
 4901 TCGGCGGCGG CAAAATGATT GTTGCAGCCG GGCAGGATAT CAATGTACGC
 4951 GGCAGCAACC TTATTTCTGA TAAGGGCATT GTTTTAAAG CAGGACACGA
 5001 CATCGATATT TCTACTGCCC ATAATCGCTA TACCGGCAAT GAATACCAG
 5051 AGAGCAAAAA ATCAGGCGTC ATGGGTACTG GCGGATTGGG CTTTACTATC
 5101 GGTAAACCGGA AACTACCGA TGACACTGAT CGTACCAATA TTGTCCATAC
 5151 AGGCAGCATT ATAGGCAGCC TGAATGGAGA CACCGTTACA GTTGACGAA
 5201 ACCGCTACCG ACAAAACGGC AGTACCGTCT CCAGCCCCGA GGGCGCAAT
 5251 ACCGTCACAG CAAAAGCAT AGATGTAGAG TTCGCAACA ACCGGTATGC
 5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTCGCCCTCA
 5351 ATGTCCCGGT TGTCCAAGCT GCACAAAAT TCATACAAGC AGCCCAAAAT
 5401 GTGGGCAAAA GTAAAAATAA ACGCGTTAAT GCCATGGCTG CAGCCAATGC
 5451 TGCATGGCAG AGTTATCAAG CAACCAACA AATGCAACAA TTTGCTCCAA
 5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAAGCCC CAGTATCAGT


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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAAACCTAT CAGAGCAAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCG
6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCAC AGCCGCTACG AAGGCAGAAG
6351 CTTGGGCATA GCGCGCAGTT TCGACCTGAA CGGCGGCTGG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAACAGC ACCACCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAAAAGCT TCGACAAAGA
6651 CGCGGTGCGC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTTCG
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCT TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGCGCGC GGCACCTCCC
7001 TTGCCGCACC GTATTGCGAC AAAGCGGCGG AAAACCTCGG TCCGGCGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGTTGG AACAAATAGG
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAAATATG CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGTGCGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCGGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAAGTACGA GCCTTGTCAG CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GCGGGGTGCG GGAATATATC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

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m564.pep
1  MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALE LTSSSATAQG IVADKSAPAQ QQPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 FWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIROGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW QGDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWFFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNPSPVPIQ IPSTATGSGS STVSVSKPGS
501 NNPVSPAPTA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKLRVSGD SFNNTVKGKL QAHDLAVNTQ TAKNSGHLIT QTKIDNREL
601 HNAGEIAANN LTLHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLRN TKGVSVARLN TEGQTLDNTR GRIEATVNI QSQQLTNQSG
701 HITATEQLTI NSRNVNDQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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Homology with fha

SCORES Init1: 190 Initn: 524 Opt: 594
Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

		10	20	30	40	50	60	
m564	.pep	MNRTLYKVVFENKHRNCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS						
		: :: :: : : : : : : : : : : : : : : : : : : :						
fhfab_borpe		MNTNLYRLVFSHVRGMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA						
		10	20	30	40	50		
		70	80	90	100	110	119	
m564	.pep	LSLLLG-SALILTSSSATAQGIVADKSAPAAQQPTILQTGNGIPQVNIQTPTTSAGVSVNQ						
		: : : : :: :: : : : : : : : :						
fhfab_borpe		WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLOGGNKVPVVNIADPNSGGVSHNK						
		60	70	80	90	100		
		120	130	140	150	160	170	179
m564	.pep	YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSSHSSQLNGYIEV						
		: :: : :: : : : : : : : : : : : : : :						
fhfab_borpe		FQQFNVANPGVVFNNGLTDGVSRIIGGALTKNPNLIR-QASAILAEVTDTPSRILAGTLEV						
		110	120	130	140	150	160	

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	180	190	200	210	220	230	239
m564 .pep	GRRRAEVVIANPAGIAVNGGGFINASRATLTTAQPQYQAGDLSGFKIRQGNVVIAGHGLD						
	: :: : : : : : : : :						
fhab_borpe	YGKGADLIIANPNGISVNGSLTNASNLTLTTGRPSVNGGRI-GLDVQOGTVTIERGTVN						
	170	180	190	200	210	220	
	240	250	260	270	280	290	
m564 .pep	ARDTDYTRILSYHISKIDAPV---WGQ---DVRVVAGQNDVAATGDAHSPILNNAANTS						
	: : : : : : : : : : : : : :						
fhab_borpe	ATGLGYFDVVARLVKLGAVSSKQKPLADIAVVAGANRYDHATRRATPI----AAGARG						
	230	240	250	260	270	280	
	300	310	320	330	340	350	
m564 .pep	NTANNGTHIPLFAIDTGKLGGMYANKITLISTVEQAGIRNQGWQFASAGNVAVNAEGKLV						
	: : : : : : : : : : : : : :						
fhab_borpe	AAAGA-----Y AIDGTAAGAMYGKHITLVSSDGLGVRQLGS-LSSPSAITVSSQGEIA						
		290	300	310	320	330	
	360	370	380	390	400	410	
m564 .pep	NTGMIAATGENHAVSLHARNVHNSGTVASQDDANIHSQTLDNSTGLSSGRLTVRNLRGL						
	: : : : : : : : : : : : : :						
fhab_borpe	---LGDATVQRGRLSLKAGVVSAGKLASGGGAV---NVAGGGAVKIA---SASSVGNL						
	340	350	360	370	380		
	420	430	440	450	460	470	
m564 .pep	KNQNGGTIAAARLDMSTGGLDNTGNITQTSQALDLVSAGKFDNSGKIGVSDVPQTGLNP						
	: : : : : : : : : : : : :						
fhab_borpe	AVQGGGKVQATLLNAG-----GTLVSGRQAVQLGAASSRQALSVNAGGALKADKLSEA						
	390	400	410	420	430		
	480	490	500	510	520	530	
m564 .pep	NPSV-IPQIPSTATGSGSSTVSVPKPGSNNPVSPAPAKNYAVGRIQTTGAFD-NAGSIN						
	: : : : : : : : : : : : : :						
fhab_borpe	TRRVVDVGKQAVALSASSNALSVRAGG-----LKAGKLSATGRDLVDGKQAVTLGSA						
	440	450	460	470	480	490	
	540	550	560	570	579		
m564 .pep	AGGQIDIAAQNLGNSGLNAAKLRSVSG-----DSFNNT-----VKGKLAHDLAVNT						
	: : : : : : : : : : : : : : : : : : : :						
fhab_borpe	SDGALSVSAGGNLRANELVSSAQLEVRGQREVALDDASSARGMTVVAAGALAARNLQSKG						
	500	510	520	530	540	550	
	580	590	600	610	620	630	
m564 .pep	QTAKNSGHLTQTGKIDNRELH--NAGEIAANNLTLIHSGRLSNDKKGNIARAHLQDLTA						
	: : : : : : : : : : : : : : : : : : : : : : : :						
fhab_borpe	AIGVQGGAEVSVANANSDAELRVGRGQVDLHDLAARGADISGEGRVNIGRARSDDSVK						
	560	570	580	590	600	610	
	640	650	660	670	680	690	
m564 .pep	GLHNAGNILADSGTVTTKNNLRNTGKVSARLNTGQTLDNTRGRIEAEVTNIQSQQLTN						
	: : : : : : : : : : : : : : : : : : : : : : :						
fhab_borpe	-VSAHGALSIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGG-----AVNLGDVQ---						
	620	630	640	650	660		
	700	710	720	730	740	750	
m564 .pep	QSGHITATEQLTINSRNVNQNKKLLSANQAQLAVSDGLYNQHGIEATNRQLSIHDKNQ						
	: : : : : : : : : : : : : : : : : : : : : : : :						
fhab_borpe	SDGQVRATSAGAMTVRDV-----AAAADLALQAGDALQAGFLKSAGAMTVNGRDAV						
	670	680	690	700	710		

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m564 .pep 760 770 780 790 800 810
TLALNNADGTIQSAGNVSQAKSLANNGTTLTAGNKLDIALTDFFVVERDLTAGKQL-NLS
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe RL-----DGA-HAGGQLRVSSDGAALGSLAAKGELTVSARAATVA-EL---KSLDNIS
720 730 740 750 760

m564 .pep 820 830 840 850 860 870
IKGRLLK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLNSDGLT
: | : : : : : : : | : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-
770 780 790 800 810

m564 .pep 880 890 900 910 920 930
HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGAIAARKRLDI-GAKEIHN
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe --GSDGAISVSGRDVVRVDQARSADISLG---AEGGATLGAVEAAGSIDVRGSGTV--
820 830 840 850 860

m564 .pep 940 950 960 970 980 990
QEGALLSSEGIFAVGNRLDEQHHAGMADTFVNGSAGLEVQGDALMSVRNMQNNHFKT
: : | : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe AANSLHANRDVVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV
870 880 890 900 910 920

m564 .pep 1000 1010 1020 1030 1040 1050
ETYLAKAEK--QVRDYTVLGQNTYYQAGKDGLFDNSQGGKQDQTATFHLKNGSRIEANQ-
| | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe ALQSAKASGTLHVQGGHLDLGTAAVGAVDV---NGTGDVVRVAKLVSDAGADLQAGRS
930 940 950 960 970

m564 .pep 1060 1070 1080 1090 1100
--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLNKDSRIVVGGRIITDDINQKE
: | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe MTLGIVDTTGDLQARAQQKLELGSVKSDGGLQAAAGGALSAAAEEVAGALELS---GQGV
980 990 1000 1010 1020 1030

m564 .pep 1110 1120 1130 1140 1150 1160
ITNQSTTGKGRTDVAGTQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV
: : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFTPG
1040 1050 1060 1070 1080

m564 .pep 1170 1180 1190 1200 1210 1220
SVI---QQNAASPSFQPAASAIAKLIDGVSTAAVNGQRIHTGNVVSLLNNATVTLNSSLTYT
| : | : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe SVVVRAQGNVTVGRGDPHQGVLAQGDIIIMDA--KGGTLLLRNDALTENGTVTISADSAVL
1090 1100 1110 1120 1130 1140

m564 .pep 1230 1240 1250 1260 1270 1280
THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQDNLHLHKRLG DGYEQLVNEQI HQ
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe EHSTIESKISQSVLAAGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRQIDV
1150 1160 1170 1180 1190

m564 .pep 1290 1300 1310 1320 1330 1340
LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFGLTPG-IALSAEQVARLTSDIVWMENQTV
: | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
fhab_borpe VDGRPQI----TDAVTGEARKDES VVS DAALVADGGPIVVEAGELVSHAGGIGNGRNK--
1200 1210 1220 1230 1240 1250

		1350	1360	1370	1380	1390	1400
m564	.pep	TLSDGSTQTVLVPKYALARKGDLNTSGGLISAEQVLLKLQNGNLNNSGTIAGRQAVLIQ					
fhab_borpe	--ENGASVTVRTT-----GNLVNKGYISAGKQGVLV- GGALTNEFLVGSDGTQRIE						
		1260	1270	1280	1290	1300	
		1410	1420	1430	1440	1450	
m564	.pep	ARNINSNGNIQ-----ADQIGLKAEKSINIDGGQVQAGRLLTAQ---AQNININLTGTT					
fhab_borpe	AQRIENRGTFQSQA PAGTAGALVVKA AEAI VHDGVMA TKGEMQIAGKGG SPTVTATAGA KA						
		1310	1320	1330	1340	1350	1360
		1460	1470	1480	1490	1500	
m564	.pep	QTSGNERNGNTAI--DRMAGINVV-GSHTEQVDNRSTSD-GILSLHASNDINLNAAATVSNQV					
fhab_borpe	TTSANKLSVDVASWDNAGSLDIKKGAQVTVAGRYAEHGEVSIQGDYTVSADAIALAAQV						
		1370	1380	1390	1400	1410	1420
		1510	1520	1530	1540	1550	
m564	.pep	--KDGTQTITAGNNLNLGT-IRTE---HREAYGTLDDENHRHRVQRST-----EVGS					
fhab_borpe	TQRGGAANLTSRHDTRFSNKIRLMGPLOVNAGGPVSNNTGNLKVREGVTVTAASFNETGA						
		1430	1440	1450	1460	1470	1480
		1560	1570	1580	1590	1600	
m564	.pep	SIRTONGALLRAGNDLKI RQGELEAEEGKT VLAAGR DV--TI SEGRQITELDTS---VSG					
fhab_borpe	EVMAKSATLTTSGAARN--AGKM QVKEAATIVAA SVSNPGTFTAG KDITVTSRGGF DNEG						
		1490	1500	1510	1520	1530	
		1610	1620	1630	1640	1650	1660
m564	.pep	K---SKGILSSTKTHDRYRF---SHDEAV-GSNIGGGKMIVAAGQDINVRG SNLISDKGI					
fhab_borpe	KMESNKDIVIKTEQFSNGRVLD AKHDLTVTASQ ADNRGSLKAGH DFTVQAORI--DN SG						
		1540	1550	1560	1570	1580	1590
		1670	1680	1690	1700	1710	
m564	.pep	VLKAGHDIDISTAHNRYTG----NEYHESKKS GVMGTGGLGFTIGNRKTTDDTDRTNIV					
fhab_borpe	TMAAGHDATLKAPHLRN TGQVVAGHDII HINS AKLENTGRV--DARNDIALDVADFTN--						
		1600	1610	1620	1630	1640	1650
		1720	1730	1740	1750	1760	1770
m564	.pep	HTGSIIGSLNGDTVTVAGNRYRQT----GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA					
fhab_borpe	-TGSLYAEHDA-TLTLAQGTORDLVVDQHILPVAEGLRVKAKSLTTEIETGNPGSLIA						
		1660	1670	1680	1690	1700	1710
		1780	1790	1800	1810	1820	1830
m564	.pep	HTQEOKGLTVALNVFVQQAAQNFIQAAQNVGKSKNKRVNAMAAAANA-WQSYQATOQM					
fhab_borpe	EVQE-----NIDNKQA----IVVGKDLTLS-SAHGNVANEANALLWAAGELTVKAQN						
		1720	1730	1740	1750		
		1840	1850	1860	1870	1880	1890
m564	.pep	FAPSSSAGQGNNNQSPSISVSITYGEQKSRNEQKRHYTEAAASQIIGKGQTTLAATGSG					
fhab_borpe	ITNKRAALIEAGGNARLTA AVALLNKLGRIRAGEDMHLD---APRI---ENTAKLSGEV						
		1760	1770	1780	1790	1800	1810
		1900	1910	1920	1930	1940	1950
m564	.pep	EQSNINITGSDVIGHAGTALIADNHIRLQSAKQDGSEQSKNKSSGWNAGVAVKIGNGIRF					
fhab_borpe	QRKGVQDVGGEHGRWSGIGYVNYWLRAGNGKKAGT-----IAPWPYGDDLTAEQSLIEV						
		1820	1830	1840	1850	1860	

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKQGGSTTHRHVHGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
					:	:	:
fhab_borpe		GKDLVNLNAGARKDE-----HRHL-----LNEGVIQAGGHGHIIG-----DVDNRSV-					
		1870	1880	1890	1900		

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYQSKQONGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE				
		:	:	:	:	:
fhab_borpe		VRTVSAMEYFKTLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY				
		1910	1920	1930	1940	1950

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATLTASDIQNH--RYEGRSFGIGGS					
		:	:	:	:	:	:
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDLRGHTLESAEGRKI-FGEY					
		1970	1980	1990	2000	2010	

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYSGDSDSKNSTTRSGVNTNHIHITDEAG				
		:	:	:	:	:
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRRVHDQLG-----QRYGKALGMDAETKEVDGIIQ				
		2020	2030	2040	2050	2060

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKEFGRNAA					
		:	:	:	:	:	:
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRVT--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
		:	:	:	:	:	:
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQETVLAAGAGLTLSNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYDTWKEGGIGRSILHGAAGGLTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
		:	:	:	:	:	:
fhab_borpe		AQNRGRPEGLKIGAHSAATSVSGSFDALRDVGLEKRLDIDDALAAVLVNPFIIFRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccctgcgttt cgcacgcgcg aacgacaccg gctcgccctgc acttctggct
151 acctgcacgc gtgcgatgtc caagtcgagc gcgaaatacg gaatatactc
201 tttggcgcaa gacgcgtccg accgtctgcc cgccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgcag
301 atcgagcgac ttcatgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCGC AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCG GCCCCTGCCG AAGCCGACAA

```


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```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTGCG CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTGCG CGACCGAATG TTTCATTTT AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSF NTSSSIANSIN
 201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
               |||||||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              10      20      30      40      50      60

              70      80      90     100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDL LMVSTSILCRSSDFMSQLDLTKRPTSASLP
               |||||||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTCGTGCA TATTGTTGAG
  51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
 101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
 151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
 201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCTGCCC AAGCCGACAA
 251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
 301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
 351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
 401 CCGCCGTGCG CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCC
 451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
 501 AGCCGTTTTG AGGCTGTGCG CGACCGAATG TTTCATTTT AAGGCAATGG
 551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
 601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSF NTSSSIANSIN
 201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
               |||||||

```


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```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
           70      80      90     100     110     120
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           |||||
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           70      80      90     100     110     120
           130     140     150     160     170     180
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           |||||
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
           190     200     210
m565.pep  KAMANTTSAFNTSSIANSTCRQPPINAX
           |||||
a565      KAMANTTSAFNTSSIANSTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggtaac
51 ggttggtcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 ttaccctaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggct
151 gccggctttg tgggtgattt ccacgcgttc gccgtcggtg gcgaagaggg
201 cggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtgacct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTGTGTAT GGGGGTTAAC
51  GGTGTGTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACC GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGTC GCCGACGATG TCGCTGCGC GGACGTTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFAH AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||

```


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```

g566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCGCTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51 GGTGTGTTTACG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTTACCG
101 TTTACCCAAA CTGCGGCGCG GACGCGCCCG GCGGCAAAGG TCATGCGGCT
151 GCTTGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGGCCGT AAACGCGCGA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFTVYPNCGA DGAGGKGHAA
51  ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVAFAAVNGA
101 LFEVSAERAG DDFAHA*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||
a566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq..
1  atgcgacgac gggcagcggc atcgacaagg cgggtttgca gtccggcggt
51  tatcaggtct tattgggcga tgcggacgtg cagtcggcgg cggtacgcag
101 caaagagggc ggatacggcg tgttgggtgc gaacgcgcgc gcttgccggc
151 gcggaaatcg agctgggtgc ggaaatcgcc cgggaagtgc gtttgaaaaa
201 cgcgtcaag gcagtgccgg aagattacga cttatcctg atcgactgtc
251 cgccttcgct gacgctgttg acgcttaacg gcttgggtgc ggcggcggc
301 gtgattgtgc cgatgttgtg cgaatattac gcgctggaag ggatttccga
351 tttgattgcg accgtgcgca aaatccgtca ggcggtcaat cccgatttgg
401 acatcacggg catcgtgcgt acgatgtacg acagccgcag caggctgggt
451 gccgaagtca gcgaacagtt gcgcagccat ttcggggatt tgctttttga
501 aaccgccatc ccgcgcaata tccgccttgc ggaagcgccg agccacggta
551 tgccggtgat ggcttacgac gcgcaggcaa aggggtccaa ggcgtatcct
601 gccttggcgg acgaactggc ggcgaggggt tcggggaaat ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAATR RVCSPAFIRS YWAMRTCSRR RYAAKRADTA CWVRTRALAG
51  AEIELVQEIA REVLKNALK AVAEDYDFIL IDCPPSLTLL TLNGLVAAGG
101 VIVPMLCEYY ALEGISDLIA TVRKIRQAVN PDLDITGIVR TMYDSRSLV
151 AEVSEQLRSH FGDLLFETAI PRNIRLAEAP SHGMPVMAYD AQAKGAKAYL
201 ALADELAARV SGK*

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
  1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101  GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151  GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201  CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
251  CTGTGTTGGG TGCGAACC GC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301  CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGA
351  AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401  TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451  TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501  CAAAATCCGT CAGGCGGTCA ATCCCGATTT GGACATCACG GGCATCGTGC
551  GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601  TTGCGCAGCC ATTTGCGGGA TTTGCTTTT GAAACCGTCA TCCCGCGCAA
651  TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701  ACGCGCAGGC AAAGGTACC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751  GCGCGGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
  1  MSANILAIAN QKGGVGKTTT TVNLAASIAS RGKRVLVVDL DPQGNATTGS
 51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101  QEIAREVRLK NALKAVEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151  CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201  LRSHFGLLF ETVIPRNI RL AEAPSHGMPV MAYDAQAGT KAYLALADEL
251  AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

m567.pep      60      70      80      90      100      110      119
              GYVQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEED
g567          AFIRSYWAMRTCRRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKAVEED
              20      30      40      50      60      70

m567.pep      120      130      140      150      160      170      179
              YDFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
g567          YDFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
              80      90      100      110      120      130

m567.pep      180      190      200      210      220      230      239
              TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNI RLAEAPSHGMPVMAYDAQAG
g567          TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETAIPRNI RLAEAPSHGMPVMAYDAQAG
              140      150      160      170      180      190

m567.pep      240      250
              TKAYLALADELAARVSGKX
g567          AKAYLALADELAARVSGKX
              200      210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
  1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101  GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151  GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201  CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
```


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```

251 GCGTGTGGG TCGAACC GCCTGGCCG GCGCGAAAT CGAGCTGGT
301 CAGGAAATCG CCCGGAAGT GCGTTTAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGT GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTC GATTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATT GGATATCAC GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTGCGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYVGLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

10 20 30 40 50 60
m567.pep MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDL DPQGNATTGSGIDKAGLQSG
|||||
a567 MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDL DPQGNATTGSGIDKASLQSG
10 20 30 40 50 60

70 80 90 100 110 120
m567.pep VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
|||||:|||||:|||||
a567 VYQVLLGDADVQSAAVRSKEGGYVGLGANRALAGAEIELVQEIAREVRLKNALKAVAEDY
70 80 90 100 110 120

130 140 150 160 170 180
m567.pep DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
|||||
a567 DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
130 140 150 160 170 180

190 200 210 220 230 240
m567.pep GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAGT
|||||:
a567 GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
190 200 210 220 230 240

250
m567.pep KAYLALADELAARVSGKX
|||||
a567 KAYLALADELMARVSGKX
250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
1 atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
51 gataccttgc agaactctgcc gattaaagcg ttcgaggctg cccaatattt
101 tcaggcgcac attgttttcg tcaggcggc gtacctgtt ttgcaaagcc
151 tgtaaaaaca gcccacatcag gaacgaaact tcgtcttcg ggcgacgcca
201 gttttcggtt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgct tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```


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401 tgctgctctt catatctgcc ttctcgcggtt cggcggtcaa atgccgtctg
451 aacgccgcgc cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep
1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
151 NAAP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51 GATGCCCTTGC AGAATCTGCC GGTGAAGCG TTCGCGGCTG CCCAATATCT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CGGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAGGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTGAG
601 GAGTTTTTTG ATGTGGTTCG TGGCATCGCG GCGCACGTTG CGGATAGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep.
1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVGIA AHVADRDAEF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRIKRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVFGNVFVGQ					
g568	MCLGMVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	130	140	150			
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAEFFRFAAYDFNQVFAAFLGQHG					
g568						
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTGAC  GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAAACT TCGTCTTCGG GCGGCGGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTGTGTCCC
301 ATTAGCGCGG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCAGGCGG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CGGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAGGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CCGGCGCTTC TTCCGCTTCG CCGCGTACGA CTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1  MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLRNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADGDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMP	CRICRLKRSRLPNIF	RRILFSCR	RRTCFCKA	CKNSPIRNET	
a568	MLRVRPVLFAVKASASSMP	FRIKRLKRSRLPSI	FRILFSCR	RRTCFCKA	CKNSPIRNET	
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCT	PSLAQCFTIFS	SNASKPRLCP	IMRGRKRFFA	QRPLPSIITA	
a568	SSSGRRQFSVEKANTVRYCT	PSLAQCFTIFS	SNASKPRLCP	IMRGRKRFFA	QRPLPSIITA	
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSA	FRGSAFKCRLNAE	PCRLNCHQI	FFFGSQEFV	FGNVFVGQ	
a568	ICLGMVCSKTACVLLFMSA	FRGSAFKCRLNAE	PCRLNCHQI	FFFGSQEFV	FGNVFVGQ	
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFV	FEFFDVVVGIAAH	VADRDAAF	FRFAAYDFNQ	VFAAFLGQHG	
a568	FLNRFFAATCLVFGNFFV	FEFFDVVVGIAAH	VADRDAAF	FRFAAYDFNQ	VFAAFLGQHG	
	250					
m568.pep	HRHADQVADSCR	VQSQVX				
a568	HRHADQVADSCR	VQSQVX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1  atgctgaaac aacgggtaat aaccgctatg tggtgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgccggc
101 tgattgccct gaccgccttg tgggagtatg cccgatggc cggtttgtgc
```


874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa ttggtttggt tatgttggtt
251 tggcattttg gctcgccgtt atgcctttgt gggtgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat ccctggcgcc cgcattccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGMPLPNLVM YVVLAFWLAV MPLWLRPKWR
101 LGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCT GATTGCCCTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
201 TGCCATATGC GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCGGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCACCGCGG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGCTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCGGATAT TTGCGCGTAT
451 TTCAGCGGCA AGCGGTTCCG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGCTGTC TGGCATTGCA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGCTG ACCGTTGTCA GCGTATGCCG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GGCGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALLAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGMPLPNLVM YVVLAFWLAV MPLWLRPKWR
101 LGGWQVYAV GWLLMPFWF ALVSLRPHFD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRITDSL
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALLALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALLALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRPKWRLNGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRPKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHFPDDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEGAIGGAVC					
g569	ALVSLAPASRX -					
	130	140	150	160	170	180
m569.pep	ALVSLRPHFPDDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEGAIGGAVC					
g569	ALVSLAPASRX -					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCT GATTGCCCTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```


875

```

151 AAAATTAATA CCAACCATTA CCTCGCCGCA ACCTTGTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA CGGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAEFLAV MPLWLRFKWR
101 LGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLI GLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRDTSGL
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGGLCKIKTNHYLAA					
a569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGGLCKIKTNHYLAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAEFLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
a569	TLVFGVVAYAGGWMLPNLVWYVVLAEFLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
a569	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
	130	140	150	160	170	180
	190	200	210	220	230	240
m569.pep	VAVYMTAVRSAGWLAFDTGWFDTVLI GLVL TVVSVCGDLL ESWLKRAAGI KDSSKLLPGH					
a569	VAVYMTAVRSAGWLAFDTGWFDTVLI GLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH					
	190	200	210	220	230	240
	250	260				
m569.pep	GGVFDRDTSLIAVISVYAAMMSVLNX					
a569	GGVFDRDTSLIAVISVYAAMMSVLNX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1  atgatcgtt tgaccgcgc gtttgcgcc gccctgatcg gtttatgctg
51  caccacaggc ggcacgcgc acacctcca aaaaatcggc tttatcaaca
101 cggagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc cgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttggaaa ggcagctcgc cggcggcaaa cttaaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggt cgaagcggtc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgcca cgcgctcatc gtcaaaatcg

```


876

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
 451 acccaatacgy acgttaccga cagcgctcatt aaagaaatga acgcccgtg
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MTRLTRAF~~AA~~ ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
 101 RKKQAQFEED YNLRNNEBFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151 TQYDVTDSVI KEMNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCACGCGC ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGCAAA CTCAGAAACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MTRLTRAF~~AA~~ ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAP
 101 RKKQAQFEED YNLRNNEBFA SLQQNANRVI VKIAKQEGYD VILQNVIIYVN
 151 TQYDVTDSVI KEMNAR*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAF AA ALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MTRLTRAF AA ALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQRRGLDLERQLAEGKLRNAKKAQAEKWRGLVAAPRKKQAQFEEDYNLRNNEBFA					
g570	ELQKLQREGLDLERQLAGGKLKDAKKAQAEKWRGLVEAPRKKQAQFEEDYNLRNNEBFA					
	70	80	90	100	110	120
m570.pep	ELQKLQRRGLDLERQLAEGKLRNAKKAQAEKWRGLVAAPRKKQAQFEEDYNLRNNEBFA					
g570	ELQKLQREGLDLERQLAGGKLKDAKKAQAEKWRGLVEAPRKKQAQFEEDYNLRNNEBFA					
	70	80	90	100	110	120
m570.pep	SLQQNANRVIKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		
m570.pep	SLQQNANRVIKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCACGCGC ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGCAAA CTCAAAGACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

877

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRFAAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKOARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRNREEFA SLQONANRVI VKIAKQEGYD VILQDVIYVN
151  TQYDVTDSVI KEMNAR*

```

m570/a570 97.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKOARKIQKTLDSEFSARQD					
a570	MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKOARKIQKTLDSEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNREEFA					
a570	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNREEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQONANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX					
a570	SLQONANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttgtt gttaccgttt tcggcgccgg
 51  tataggttct gccgtccac acgtgctg cgtcgcaaa caggctcagg
101  cggacgggtg gtgcgtcttt cgcaccgggc atcgggaaga gcagctcggc
151  ggagacgttg gctttttgtg tgcgcggta gctgattttt tcgccgtatt
201  cgtcatacac tttcgggccc agcgtgccgc tttcgtagcc gcgcaccgaa
251  cccagggcgc cgcgtagaa gttttcaaag aaggggattt ctttggttct
301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHRBEQLG
 51  GDVGFVAAV ADFFAVFVIH FRAERAAFVA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTGG AACCTGCGCG CCGGTGCGCG
 51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAACAGGCG TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTCGCGC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTCG
251  TATCCGCGCA CCGAACCCAG GCCGCGCGCG TAGAAGTTT CAAAGAAGGG
301  GATTTCCTTG GTTCTGCCGT AGCCGCGCGC AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTGG CTCAGGGGGA AGAACCAGGT TTGGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCCGGCTT
451  CACGCCCGTC AGGTAGCCGC GCGTCGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLCGDVGF FVAADVADFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  DFFGSAVAAR NADFAAEHQE EGFAQGESEPG LVVGGGVVLQ FAARQGDGFGV
151  HARQVAARRP *

```


m571/g571 93.1% identity in 102 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

m571/a571 98.1% identity in 160 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 1713>:

g572.seq..

879

```

1  atgtgcgccca tcgtcggggc ggcggggctg ccttcgcgcg tcgcagcggc
51  gcaaaaaggc aaaaccattt atctggcaaa caaagaaacg ctggtggttt
101 cccgcgcggtt gtttatggaa accgcccgcg caaacggcgc ggcagtggtg
151 cccgtcgaca gcgaacacaa cgccatttcc caagttttgc cgcgcgatta
201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
251 cccgcgggcc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 cccgagcagg cgggtcaaaac ccccaattgg cgtatggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggctgtt caactgtccg cccgacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgctac cgcgacggct ccgtgctggc
501 gcaactgggc aatcccgata tgcgaacgcc catcgccctat tgtttgggct
551 tgcccgagcg catcgattcg ggtgtcggca aactcgattt cggcgccattg
601 tccgcgctga ccttccaaaa gcccgacttc ggccgcttcc cctgcctgaa
651 gttcgcttat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcgcgcaa gaaaccgcc gtcgcgcctt ttttggacgg acagattaag
751 tttaccgaca ttgccaaaac cgtcgcccac tgtcttgac aagacttttc
801 aaacggcatg ggcgatatag aaggactgtt ggcgcaagat gcccgacac
851 gcgcacaagc gcgggcattt atcggcacac tgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

g572.pep..

```

1  MCAIVGAAGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAVAL
51  PVDSEHNAIF QVLPRDYDTR LNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PEQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDGFAL
201 SALTTFQKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

m572.seq..

```

1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATT TCTTGGCAAA CAAAGAAACG CTGGTGGTTT
101 CCGCGCGGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGCCTG
151 CCGCTCGACA GCGAACACAA CGCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CGCGGGCGGT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGCGGCCCC GTTCTGACC GCGGATTAA ACACGTTTGA CCGCATTACG
301 CCGCCCCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTCTGGC
501 GCAACTGGGC AATCCCGATA TCGGAACGCC CATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCC GGTGTGCGCG ACCTGGATT CGACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCGCGACTTT GACCGCTTCC CCTGCTGAG
651 GCTCGCTTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TGCGTATTGA
701 ACGCCGCCAA CGAAGCGGCC GTCGCGCCT TTTTGGACGG ACAGATTAA
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTGAC AAGACTTTTC
801 AGACGGCATA GGCATATAG GGGGGCTCTT GGCGCAAGAT GCCCGGACAC
851 GCGCACAAGC GCGAGCATT ATCGGCACAC TCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

m572.pep..

```

1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAVAL
51  PVDSEHNAVF QVLPRDYAGR LNEHGIASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTTFQKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEA VAAFLDGQIK
251 FTDIKTVAH CLAQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/g572 92.9% identity in 295 aa overlap

```

          10      20      30      40      50      60
m572.pep  MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAVALPVDSEHNAVF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572       MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAVALPVDSEHNAIF
          10      20      30      40      50      60

          70      80      90     100     110     120
m572.pep  QVLPRDYAGRLEHNGIASIILTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572       QVLPRDYDTRLNEHGIDSIIILTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS

```


880

	70	80	90	100	110	120
	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDPKLEVVHHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
g572	ATMANKGLELIEAHWLFNCPDPKLEVVHHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDLFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGDLDLFDALSALTFQKPDFGRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIMGDI ELLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```

a572.seq
1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGCTG
151 CCGTCGACA GCGAACACAA CGCCGTTTTTC CAAGTTTTGC CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTTGACC GCCGATTTAA ACACGTTCTG CAGCATTACG
301 CCCGACCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCT GGTGTCGGCG ACCTGGATTT CGACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCTTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCCT TTTTGACCGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGGCATA GCGACATAG GGGGCTCTT GGCGCAAGAT GCCCGGACAC
851 GCGCACAAGC GCGGGCATTT ATCGGCACAC TCGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```

a572.pep
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPRDYGRL LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVHHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFQKPDF DRFPCLKLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

m572/a572 98.3% identity in 295 aa overlap

10 20 30 40 50 60
m572.pep MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF
|||||
a572 MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF
10 20 30 40 50 60

70 80 90 100 110 120
m572.pep QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
|||||
a572 QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS
70 80 90 100 110 120

```


881

	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSVMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgcccctgtt  tgtgccgcct  taatcgcaat  atcggcagtt  tccaaatcac
51  gaatctcacc  gaccataatg  atgtccgggt  cctgacgcag  gaaagacttc
101 aaagcagcgg  caaaagtcag  accctgctta  tcattgacgt  taacctgatt
151 gatgcccggc  aggttaatct  cggcagggtc  ttccgccgtt  gcaatattta
201 ccgactccgt  attcaaaata  ttcaaacagg  tatagagcga  caccgtctta
251 cccgaaccgg  tcggaccggt  taccagcacc  atcccgtaag  gacggtgaat
301 cgcttccaac  aacaattttt  tctggaacgg  ctcaaaaccg  agctggtcga
351 tgttcaaaag  cgccgcatcg  gaattcaaaa  tccgcatcac  gaccttttcg
401 ccaaacagcg  tcggcaatgt  gctgacacgg  aaatcgacag  gcttgccgcc
451 cttttgaaag  gtcagctgca  tcctaccgtc  ctgcccgtatc  cgtttttcgg
501 aaatgtccaa  acgcgacatt  accttaatcc  gggaagcaag  ctgccccttc
551 accgcaatgg  gcggctgaac  cacctcgcgg  agctgcccgt  ccacacggaa
601 acggatacgc  gcattgtgtt  cgtaaaactc  gaaatggatg  tcggatgccc
651 cgctacgcaa  ggcacccgac  aaagttttat  ggataaacct  cggaaacagg
701 ccgtcttctg  cctcctcgtc  gtcgatatac  aggggtgtgc  ttctctcttc
751 ctcttgcccc  tccccaagct  cctgaagcag  cgatgtcgaa  cgcgaaccca
801 cccaatcgag  caaaccgcgc  aactgggtcat  cctcgacaat  gaccaactca
851 accgcaatcc  ctgcccgcga  aaccgttttc  tgaatttgcg  gcattctggg
901 cggatcggaa  accgcaaaaa  atactttgtc  gcccccacgg  aaaaccggca
951 cacagtggaa  ctccaccatc  tgctcctcgg  tcaaacacccc  catcagcacc
1001 ctgtggcgcg  gataatgacg  caaatcaaga  atcgataaac  tgaacaccct
1051 cgcaatcaat  gccgcaagcg  acttgggcga  aatgacacgg  tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLRLNRN  IGSFQITNLT  DHNDVRVLTQ  ERLQSSGKSQ  TLLIIDVNLI
51  DARQVNLGRV  FRCNIYRLR  IQNIQTGIER  HRLTRTRRTG  YQHPVVRTVN
101 RFQQQFFLER  LKTELVDVQR  RGIGIQNPHH  DLFAQRRQC  ADTEIDRLAA
151 LLKGQLHPTV  LRYPPFGNVQ  TRHYLNPGSK  LPPYRNGRLN  HLAELPVHTE
201 TDTRIVFVKL  EMDVGCPTAQ  GIRQSFMDKP  RNRAVECLLV  VDIQGVAFLE
251 LLPLPKLLKQ  RCRTRTHPIE  QTRQLVILDN  DQLNRNPGCR  NRFLNLRHLG
301 RIGNRKKYFV  APTENRHTVE  LHHLLLRQHP  HQHPVARIMT  QIKNRITEHP
351 RNQCRKRLGR  NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT  TGTGCCGCCT  TAATCGCAAT  ATCGGCAGTT  TCCAAATCAC
51  GAATCTCACC  GACCATAATG  ATGTCCGGGT  CCTGACGCAG  GAAAGACTTC
101 AAAGCAGCGG  CAAAAGTCAG  GCCCTGCTTA  TCAITGACGT  TAACCTGATT
151 GATGCCCGGC  AGGTTAATCT  CGGCAGGGTC  TTCCGCCGTT  GCAATATTTA
201 CCGACTCCGT  ATTCAAAATA  TTCAAACAGG  TATAGAGCGA  CACCGTCTTA
251 CCCGAACCCG  TCGGACCGGT  TACCAGCACC  ATCCCGTAGG  GACGGTGAAT
301 CGCTACCAAC  aCaw.TTTT  TCTGAAACGG  CTCAAACCG  AGCTGGTCGA
351 TGTTCAAAGA  CGCGGCATCG  GAATTCAAAA  TCCGCATCAC  GACCTTTTCG
401 CCAAACAGCG  TCGGCAATGT  GCTGACACGG  AAATCGACAG  GCTTGCCCGC
451 CTTTGAAGAG  GTCAGCTGCA  TCCTGCCGTC  CTGCGGTATC  CGTTTTCGCG
501 AAATGTCCAA  ACGCGACATT  ACCTTAATCC  GTGAAGCAAG  CTGCCCCCTT

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882

```

551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAGTCTTAT GGATAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTC TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```

1 MPCLCLRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51 DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXPFLKR LKTELVDVQR RGIGIQNPHH DLFQKRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSIMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCLRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
g573	MPCLCLRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXPFLKRLKTELVDVQR					
g573	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXPFLKRLKTELVDVQR					
	70	80	90	100	110	120
m573.pep	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXPFLKRLKTELVDVQR					
g573	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXPFLKRLKTELVDVQR					
	70	80	90	100	110	120
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPFGNVQTRHYLNPXSK					
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPFGNVQTRHYLNPXSK					
	130	140	150	160	170	180
m573.pep	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSIMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSIMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSIMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSIMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

883

a573.seq

```

1  ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTAAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAAATTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGTGTGGC TTTCTCTTC
751 CTCCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCGACAAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKQYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
a573	10	20	30	40	50	60
m573.pep	70	80	90	100	110	120
a573	70	80	90	100	110	120
m573.pep	130	140	150	160	170	180
a573	130	140	150	160	170	180
m573.pep	190	200	210	220	230	240
a573	190	200	210	220	230	240
m573.pep	250	260	270	280	290	300
a573	250	260	270	280	290	300

884

	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1 atgtgctcga atctgccaaa cagccttaag aaagccgata tggacaacga
51 atttgggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
101 tgggctgggt tggcgcccg cgtggatatga aaaccgattt gaagcaggca
151 aaaagcatcc ctctcggtatt ttataaaaagc ctggacgctt tggtcgaccg
201 caacagcggg cgcgcggcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaa cttaccctcg gcaaaactta ccgtcagcgc
301 ggcgaaaacg acaaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaa ggcgggtttg gtcgatcgtg ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgctt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgcccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgccgcgctc
751 gaagcctatg ccgcatcgca gcagcaaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaacc tctgacagga tatatgcaga cgtttcccga acttgaccctg
901 atcaatgtcg tgtacgagaa atccctgctg ctttaaggcg agaaagaagc
951 cgcgcaaac gcegtcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgtacgcct gctcgggttg aaactcagcg atttgatcc ggcttgaaa
1051 gccgatgcgc acatgatgcg ttcggttatc ggacggcagc tccagcgcac
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1 MLPNLPNSLK KADMDNBLWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAENV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFV LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDLDPWAK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1 ATGCGCCCGA ATCTACCAAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51 ATTTGGGATT ATCTGCTGCG CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTGGGGATT TTATAAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GGCAGAAAACG ACAAAGCCAT CAACATACAC CCGACAATGC TCGATTCTCC
351 CGATACGGTC GGCAGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGACG GTAAAAATGGC GCGTGAAAGC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGCGTTT

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651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCGGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAAAC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACCTCAGC ATATGAATCC GGCTTGGAAA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCACCTGCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```
1 MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSTPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRRARVLF LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAAALFKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GKPEEGLNRLTG YMQTFPELDL
301 INVVEKSLLL KCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFWHCPACN KWQTFPNKI
401 EV*
```

m573/g573 97.8% identity in 402 aa overlap

m574.pep	10	20	30	40	50	60
	MRPNLPNSLKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
g574	MLPNLPNSLKADMDNELWIILLPIILLPVFFTMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
m574.pep	70	80	90	100	110	120
	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
g574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
	70	80	90	100	110	120
m574.pep	130	140	150	160	170	180
	GEKRRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
g574	GEKRRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	190	200	210	220	230	240
	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
g574	AQLLSHDEQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
m574.pep	250	260	270	280	290	300
	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
g574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
	250	260	270	280	290	300
m574.pep	310	320	330	340	350	360
	INVVEKSLLLKCEKEAAQTAVELVRRKPD LNGVYRLGLKLSDMNPAWKADADMRSVI					
g574	INVVEKSLLLKGEKEAAQTAVELVRRKPD LNGVYRLGLKLSDLDPWKADADMRSVI					
	310	320	330	340	350	360
m574.pep	370	380	390	400		
	GRQLQRSVMYRCRNCHFKSQVFWHCPACN KWQTFPNKIEVX					
g574	GRQLQRSVMYRCRNCHFKSQVFWHCPACN KWQTFPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1  ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTTGGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCCG GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GGCAGAAACG ACAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGGGG
451 GTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTCCCT TGCCGCGCTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGAAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTCAACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAATCAGCG ATTTGGATCC GGCTTGAAAA
1051 GCCGATGCCG ATATGATGCG TTCGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACA GTCTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1  MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLDSPDPT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSLDPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFSQ VFFWHCPACN KWQTFPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
a574	MRPNLPNSLEKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLDSPDTT					
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLDSPDTT					
	70	80	90	100	110	120
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKPEEGLNRLTGYMQTFPELDL					
a574						
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDMNPAWKADADMMSVI					
a574						
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFFTPKNKIEVX					
a574						
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1 ..atgcgctgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51 ccgtcaaaaca gtccgctttc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggaacttc actggtctgt tccgcaacag
151 gttcggaaac ggtgttacgg gtttcgtcgg tcggcggtgc gatggcagaa
201 gccggcggtt cttggggggg cggattcggc agcggtttcc gatgcggcag
251 tatttgacgc ggggtacagg ccgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggtcgggt cgaacggccg gtttttcgc
351 ttttgcctcg ggcgcggcaa cttttgcttc aggtttttca accggttttt
401 cgacaggttt ctctatcggt ttctccacag ttgcctgttt ggacggttca
451 gacggcatgg atgcagtttc ggctttgggt ttccgcgttt gcggtttggg
501 ttgttcgctt ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1 ..MPCLRRQAAR CTNRTDRQT VRFRLLRQK PVRQVRQVR RQLHLWLPQQ
51 VRKRCYFRFR SACRWQKRL LGGADSAAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGG RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACL DGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq .
1 ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51 GGCAGGTTTT CCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTGTGC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCCGGCGTG TCGATGACGA TTTCCACAGG
201 GTTGACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCTGTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCCGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGACG GGATTCTTCG GTACGGCGCG CGCGTTTGGG TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAAATGCC GCGCTCCGC CGGCAAGCAG
651 CAGGTTGATC GAACCGCGA ACAGACCGTC AAACAGTCCG CTTTCGGTTT
701 CTCTCTCGCG AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGTCG CGTGTGAT GGCAGAACCG GCGGCTTCTT GGGGGCGGA
801 TTGGGCGCG GTTTCCGATG CGGCAGTATT TGCAGCGGTT ACAGGTTCCG
851 GTCGAAOCCG CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTTCTT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTCCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCGTTTTCG GGTTTGGGTT
1001 GTTCCGCTTT GATCCTGTTT AGATTCCGAA TGTCGA

```


This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep

```

1 MVSGEAEFRK PASPEGEAGF AEAVSSVPIW LFEGLRSEKS VSTVSGLFSA
51 VWATDSGSGV SMRTISTGLYK LKVGSGSYTLS VDSMAFQSS ARFWVSSSCV
101 SAPDKMPFCA AARLSKSKSM RLGVGVSVTS NCVFADNSS DSPSKASVDF
151 TSFPFGAGCV AGVTSKAVI SMPSSAASSR SGSSSGTDSS VRRARLDWR
201 RKSSSRAINA APPASSKVY EPPNRPSPNSP LSVSSSAETC STGESATLPV
251 SSVGVSMAEA AASWGADSAV VSDAAVFAAG TGSGRARTG AFASGAATFA
301 SGFSTGFTSTV ACLDGGSDMD AVSALGFVAV GLGCSALLIF RFGM*

```

m575/q575 70.2% identity in 114 aa overlap

```

                240      250      260      270      280
m575 . pep  SSAETCSTGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFPAAGTG-----
                |||
g575        LHNLFPPQQVRKRCYRFRRSACRWQKRRLGADSAAVSDAAVFPAAGTGPGWRSVAEAGVS
                50      60      70      80      90      100

                290      300      309      310      320
m575 . pep  -----SGRTAGFSAPASGAATFASGFGSTGFST-----VACLDGSDGMDAVSALGFA
                |||
g575        DTAGLGSGRRTAGFSAPASGAATFASGFGSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA
                110     120     130     140     150     160

                330      340
m575 . pep  VCGLGCSALI-----LFRFGMX
                |||
g575        VCGLGCSALIFLGAAALILFRFGMX
                170     180

```

a575.seq

1	ATG GTT TCGG	GCG AGG AAGC	CTT CAG GAAG	CCT GCC AGTC	CGG AGG GTGA
51	GGC AGG TTTT	GCG GAAG CTGT	TTT CTCT CTGT	GCC GAT ATGG	TGT TTT GAGG
101	G CAG GTT GTC	GGAG AAAT CG	GTAT C GACGG	TTT CCG GTT	GTTT TCG CGCA
151	GTT TGGG CGA	CAGAT TCCGG	TT CGGG CGTG	TCGAT ACAGA	TTT CGAC AGG
201	GTT GTAC GGG	TTGA AGGT CT	CGGG CT CGTA	CAC GTCT CT	GTGG ATT CGA
251	TGG C GTTCCA	ATCGG CATCC	GCG CGT TTTT	GGG TTT CTTC	ATC CTG CGTA
301	AGT GCG CGGG	ATAAAAT GCC	GTTT GCG CGG	GCT GCC AGGC	TGT CGAAATC
351	CAAG TCGATG	CGG TTGAAG	CGT AT CCGT	TT CGACAT CG	AAGCT TGT TT
401	TTGCC GACAA	CTCT TCTTCA	GATT CCCCAT	CTA AGGCAAG	TGT GTCTG TT
451	ACAT CGTTTT	TCGG AGCGGG	TT CGGG CGTT	GCC GAG TTT	CGACT CTGGC
501	AAAG GTGATT	TCTAT GCCGT	CGT CT CCGCC	GTCTG CAAGG	TCAGG CTCTT
551	CCTC AGGGAC	GGATT CTTCG	GTACGG GCGCG	CGCG TTGGA	TTGGG CAAGG
601	CGCAA AAGCA	GCAG CAGGGC	GATCA ATGCC	GCG CCTCCGC	CGGCA AGCAG
651	CAAG GTGTAC	GAACC GCCGA	ACAG TCCGCT	TT CGG TTTCT	TCTT CCGCAG
701	AAAC GTTTTC	GACAG GTTCC	GAA ACCGCGT	TACCG GTTTC	GTCGGT CGGC
751	GTG TCGATGG	CAGA AGCGGC	GGCT TCTTGG	GGGG CGGATT	CGGC AGCGGT
801	TTCCG ATGCG	GCAGT ATTTG	CACGG CGGTAC	AGGT TCGGGT	CGA AGCGCGC
851	GTTTT TCCGC	TTTT GCTTCG	GGCG CGGCAA	CTTTT GCTTC	AGG TTTTTTCA
901	ACC GGTTTCT	CTACC GTTGC	CTG TTTGGAC	GGT TCGGACG	GCAT GGAATGC
951	GGT TCTGGCT	TGGG GTTTGC	CCG TTTGCGG	TTT GGGTTGT	TCCG CTTTGA
1001	TCCT GTTTCAG	ATT CGGAATG	TGA		

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep

1	MVSGEEAFRK	PASPEGEAGF	AEAVSSVPIW	LFEGRLSEKS	VSTVSGLFSA
51	VWATDSGSGV	SMTISTGLYG	LKVSGETYLS	VDMAFQSSAS	AREWVSSSCV
101	SAPDKMPFCA	AARLSKSKSM	RLEGVSVSTS	NVCFASSSSS	DSPSKASVWF
151	TSFFGAGSGV	AGVSTSAKVI	SMPSSAASSR	SGSSGDTDS	VRRARLDWAR
201	RKSSSRAINA	APPPASSKVY	EPPNPSLVS	SSAETCSTGS	ETALPVSSVG
251	VSMAEAAASW	GADSAADVDA	AVFAAGTGS	RTAGFASAFS	GAATFASGFS
301	TGFTVTACLD	GSDGMDAVSA	LGFAVCGLSG	SALILFRFGM	*

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m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEAEFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEAEFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m575.pep	SMTISTGLYGLKVGSGSYTLSDVSMAFQSASARFWSSSCVSAPDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVGSGSYTLSDVSMAFQSASARFWSSSCVSAPDKMPFCAAARLSKSKSM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m575.pep	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFAGAGSGVAGVSTSAKVISMPSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFAGAGSGVAGVSTSAKVISMPSAASSR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m575.pep	SGSSSGTDSSVRRRLDWARRKSSSRINAAPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSSVRRRLDWARRKSSSRINAAPPASSKVYEPN----SPLSVSSSAETC					
	190	200	210	220	230	
	250	260	270	280	290	300
m575.pep	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTSGRTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTSGRTAGFSAFASGAATFA					
	240	250	260	270	280	290
	310	320	330	340		
m575.pep	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaaagaaat caaaatgacc gaagagcagg cccagggaagt gatgatgaaa
151 ttcttcgagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccctccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtagggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcgggc acccgaaaac
601 gcgcccgcca agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAIED LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51 FLQEQQAKAV EKHKADAKAN KEKGAEFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```


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```

51   GCAAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GCGGCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501  AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVRTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

	10	20	30	40	50	60
m576.pep	MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ					
g576	MGVDIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ					
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVRTTASGL QYKITKQEG KQPTKDDIV					
g576	EQQAKAVEKH KADAKANKEK GEAFLENAA EDGVRTTASGL QYKITKQEG KQPTKDDIV					
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLID GTVFDSSKANG GPVTFPLSQ VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE					
g576	TVEYEGRLID GTVFDSSKANG GPVTFPLSQ VIPGWTEGVRL KEGGEATF YIPSNLAYRE					
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPN ATLVFDVKLV KIGAPENAPA KQPAQVDIKK VN					
g576	QGAGEKIGPN ATLVFDVKLV KIGAPENAPA KQPDQVDIKK VN					
	180	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTCCG CCGCTTGGC
51  ACTTTCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCG TTCTTCCGCG CAGGGCGACA CCTCTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCCCGG TCACCTTCCC TTTGAGCCAA

```


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601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
 701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

a576.pep
 1 MNTIFKISAL TISAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVTASG
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

		10	20	30
m576.pep		MQQASYAMGV DIGRSLKQMK EQGAEIDLKV		
a576	CGKKEAAPAS ASEPAASSA QGDTSSIGSTM	MQQASYAMGV DIGRSLKQMK EQGAEIDLKV		
	30	40	50	60
	40	50	60	70
m576.pep	FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA	80	90	
a576	FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA	90	100	110
	100	110	120	130
m576.pep	KDGVTASGLQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ	140	150	
a576	KDGVTASGLQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ	150	160	170
	160	170	180	190
m576.pep	VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV KIGAPENAPA	200	210	
a576	VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV KIGAPENAPA	210	220	230
	220	230	240	250
m576.pep	KQPAQVDIKK VN	260		
a576	KQPAQVDIKK VN	270		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

g576-1.seq
 1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
 101 CTGCCGCCG TCTGCCGCG CAGGCGGACA CCTCTTCAAT CGGCAGCAGC
 151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
 201 ACAATGAAG GAACAGGGCG CGGAATCGA TTTGAAAGTC TTTACCGATG
 251 CCATGCAGGC AGTGTATGAC GGCAGAGAAA TCAAAATGAC CGAAGAGCAG
 301 GCCCAGGAAG TGATGATGAA ATTCTGCGAG GAGCAGCAGG CTAAAGCCGT
 351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
 401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
 451 CTGCAGTACA AAATACCAA ACAGGGTGAA GGCAACAGC CGACAAAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
 551 TCGACAGCAG CAAAGCCAAC GCGCGCCCGG CCACCTTCCC TTTGAGCCAA
 601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
 701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPDQVDIKK VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
201 GCAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GCGGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAA CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASAAQGDTSSTGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSTGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			
g576-1.pep	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

893

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCGGCC TGGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GCGGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	DIGRSLQMKEQGAEIDLKVFTTEAMQAVYDQKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLQMKEQGAEIDLKVFTTEAMQAVYDQKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	DIGRSLQMKEQGAEIDLKVFTTEAMQAVYDQKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLQMKEQGAEIDLKVFTTEAMQAVYDQKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

g577.seq..

```

1  atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcataactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaaaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggtt
151 tttatttacg gagcaaacat gaaacttata tataccgtca tcaaaatcat
201 tatectgctg ctcttcctgc tgcttgccgt cattaatatg gatgccgtta
251 ccttttcccta tcttcggggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgtcgt cggcatcgtg ttcggaatgt ttgcctgtt
351 cgggcggctg ctgtccttgc gcggcgaaaa cagccgcctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaatgtctg ccgaatctgc caaacgcct taa

```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

g577.pep

```

1  MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLTQSW FRVRSCPCGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINM DAVTFSYLPQ QSVNPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAAESAKQP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

m577.seq..

```

1  ATGGAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAGTACG GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAAATAC GATGCCGTTA
251 CCTTTTCTA CCTGCCGGGG CAAAATTCG ATTTGCCGCT GATTGTCTGA
301 TTGTTCCGCG CATTTGTAGT CCGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTAC CAAACAGCCT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

m577.pep..

```

1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGCV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKNARL TGKELTAPPA
151 QNAPESTKQP *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577.pep	MERNGVFGKIVGNRILRMSSEHAAASYPKPKCSFKLAQSWFRVRSCLGGVFIYGANMKLI					
g577	MERSGVFGKIVGNRILRMPSEHAAAFYPKPCKSFKLTQSWFRVRSCPCGVFIYGANMKLI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m577.pep	YTVIKIIILLLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFAGFVVGIIIFGMFALFGRL					

895

```

|||||
g577  YTVIKIIILLFLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130      140      150      160
m577.ppep  LSLRGENGLRAEVKKNARLTGKELTAPPAQNAPESTKQFX
|||||
g577  LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAESAQKFX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAGGA ACGGTGTATT TGGTAAATTT GTCGGAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAACCTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
151 TTTATTACG GAGCAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCTGT CATTAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAATTCG ATTTGCCGCT GATTGTCGTA
301 TTGTCGGCG CGTTTGTCTG CCGCATCGTG TTCGGAATGT TTGCCTTGT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TCGCGGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTGC CAAACAGCCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.ppep
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSEKLAQSW FRVRSCPGGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENGL RAEVKKNARL TGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.ppep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCPGGVFIYGANMKLI
a577  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100     110     120
m577.ppep  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFFVVGIIFGMFALFGRL
a577  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130      140      150      160
m577.ppep  LSLRGENGLRAEVKKNARLTGKELTAPPAQNAPESTKQFX
a577  LSLRGENGLRAEVKKNARLTGKELTAPPAQNAPESTKQFX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1  atgggaaagc tcgacatcgg gatattgttt gccgatttct tcaaagattt
51  cgcgccacag ttcggtggtt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg ggcggattgg aaggccacgt gggcgatcgc
151 ggcgatttgc ctttcgctgt atttcattgt gttgtagcct tcgtgttcgc
201 cgttttccaa aacacggatg ccgcgcggtt cgccgaaata aatatcgccg
251 gtaagttcgc gcacaatcaa aatatccaaa ccggcaacga tttcaggctt
301 gagcgtggag gcgttggtta a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.ppep
1  MGKLDIGILF ADFFKDPAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGD
51  ADFAFAVFGH VVAFVFAVFO NTDAARFAEI NIAGKFAHNQ NIQTGNDPRL

```


101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTTTC TCGGTTTTTG GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTCGCTGT ATTTTCATGG GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACGCGGATG CCGCGCGGTT CGCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT

```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDPRL
101 QRGGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDAAADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQNDAAARFAEIDVAGEFAHNQNIQTGNDPRLQRGGVGX					
g578	VVAFFVAVFQNTDAARFAEINIAGKFAHNQNIQTGNDPRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTTTC TCGGTTTTTG GCGGATTGG AAGCGACGT GGGCAATACG
151 GCGGATTTCG CTTCGCTGT ATTTTCATGG GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACACGGATG CCGCGCGGTT CGCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQNDAAARFAEIDVAGEFAHNQNIQTGNDPRLQRGGVGX					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```


897

```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGCGC GCGCTGATTA TCCTGTTCG CCCGTTCAAA GTCGCGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TGGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTG GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCGCGC CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSLRITDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGCGC GCGCTGATTA TCCTGTTCG CCCGTTCAAA GTCGCGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTG GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSLRITDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRITDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRITDNEEVVLPNSVVM					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVNDYCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
g579	GNSIVNRSSLPLCRAQVIVGVNDYCDLKVAKEAVLKAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
g579	DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```

a579.seq
1   ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCTTGT AAAGACCAGC TGTCCAATTT
201 TGCCGCGCGC GCGCTGATTA TCCTGTTCCG CCCGTTCAAA GTCGCGGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TCGCGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCCTTCAAAA
501 CGAAGAGCGG CAGGCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```

a579.pep
1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

m579/a579 100.0% identity in 231 aa overlap

      10      20      30      40      50      60
m579.pep MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
a579      MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
      10      20      30      40      50      60

      70      80      90      100     110     120
m579.pep KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM
a579      KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM
      70      80      90      100     110     120

      130     140     150     160     170     180
m579.pep GNSIVNRSTLPLCRAQVIVGVNDYCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
a579      GNSIVNRSTLPLCRAQVIVGVNDYCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
      130     140     150     160     170     180

      190     200     210     220     230
m579.pep DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
a579      DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
      190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

899

```

1  ATGGACTTCA AACAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG ACAGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGT GCGGTGTGCC TTAAGAGACC AGCTGTCCAA
351 TTTTCCGCCG GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTCGGCGGT TTTGAAGGAT ATGTCCGGGA AATCAAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCAGC CTGCGCTTT
551 GCGCGGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGCC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CCGCAGCCCG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH LISVSGWHL AEKAWAFGLN LAAALLIFLV GKWAARKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVVLPSNVV MGNSIVNRSS LPLCRAQVIV GVDYNDCLKV
201 AKEAVLKAAA EHPLSVQNEE RQPAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA AACAATTGA TTTTACAC CTGATCAGTG TTTCCGGTTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGGTC GGAATGGG CGGCGAAACG CATTGTCGCT
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGT GCGGTGTGCC CTGAAAGACC AGCTGTCCAA
351 TTTTCCGCCG GCGCACTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCGCTGT
551 GCGCGGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CCGCAGGCTG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAARKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVVLPSNVV MGNSIVNRST LPLCRAQVIV GVDYNDCLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
m579-1.pep  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAARKRIVAVMRAAMTRAQ
          |||
g579-1      MDFKQDFDLHLISVSGWHLAEKAWAFGLNLAAALLIFLVGKWAARKRIVAVMRAAMTRAQ
          10      20      30      40      50      60

          70      80      90     100     110     120
m579-1.pep  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||
g579-1      VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90     100     110     120

          130     140     150     160     170     180
m579-1.pep  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPSNVVMGNSIVNRST

```


900

```

|||||
g579-1  GALLILFRPFGVDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180

          190      200      210      220      230      240
m579-1.pep  LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
g579-1  LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240

          250      260      270      280
m579-1.pep  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
          |||||
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA AACAATTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGTGTC GGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CGCATTTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GGCGGCGCGG GTTGGCGGTT GCGGTTGTCC TTGAAAGACC AGCTGTCCAA
351 TTTTGGCCGC GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGGTCGATT ACAACTGCGA TTGAAAGTG
601 GCGAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CCGCTTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACCGGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.pep
1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VVIAALGRIG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALLILFRFP KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSNVV MGNSIVNRST LPLCRAQVIV GVDYNDLKV
201 AKEAVLKA AV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRW
251 LQCDLNEQVV ENLRKVNINI PFPQORDIHI NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep  MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          |||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          10      20      30      40      50      60

          70      80      90      100     110     120
a579-1.pep  VDATLISFLCNVANIGLLILVIAALGRIGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||
m579-1  VDATLISFLCNVANIGLLILVIAALGRIGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120

          130     140     150     160     170     180
a579-1.pep  GALLILFRPFGVDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          |||||
m579-1  GALLILFRPFGVDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          130     140     150     160     170     180

          190     200     210     220     230     240
a579-1.pep  LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
m579-1  LPLCRAQVIVGVVDYNDLKVAKAEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240

          250     260     270     280
a579-1.pep  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX

```


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m579-1
 |||||
 AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

g580.seq
 1 atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
 51 cgcgtcgcag cccatttcga tggcaaggca gacttcgccc atcatgtcgc
 101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
 151 tcgaaaatca gcttggtaaa gccgttgctg caaccgttgg caatcgcacg
 201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
 251 ctttggcaga caattcggtt tcaccgacct atgccacttc gggggaagtg
 301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

g580.pep..
 1 MDSPKVGCOW MVLPMASASQ PISMARTSP IMSPPFGPTM PPPMMPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
 101 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

m580.seq..
 1 ATGGATTTCG CCAAGGTCCG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
 101 CACCGTTCCG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCGGCA
 151 TCAAAAATCA GCTTGGTAAA GCGGTGTCG CAACCGTTGG CAATCGCACG
 201 GCCGGAAGCC GCCCAGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
 251 CTTTGGCGGA CAGTTCCGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
 301 TAG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

m580.pep..
 1 MDSPKVGCOW MVLPMASASQ PISMARTSP IISPPFGPTM PPPMMPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
 101 *

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCOWMVLPMASASQPISMARTSPIISPPFGPTMPPPMMPVSASKISLVKPLS					
g580	MDSPKVGCOWMVLPMASASQPISMARTSPIMSPPFGPTMPPPMMPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPTHATSGEVX					
g580	QPLAIARPEAAHGKLALVILRPDALADNSVSPTHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

a580.seq
 1 ATGGATTTCG CCAAGGTCCG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCCG
 101 CACCGTTCCG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCAGCA
 151 TCAAAAATCA GCTTGGTGAA ACCATTGTGC CAACCGTTGG CAATCGCACG
 201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
 251 CTTTGGCAGA CAATTCGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
 301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep
 1 MDSPKVGCOW MVLPMASASQ PISMARTSP IMSPPFGPTM PPPMMPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

902

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASQPISMARQTSPIISPPFGTMTPPPMRPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMASQPISMARQTSPIISPPFGTMTPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLLVILRPEALADSSVSPTHTSAGEVX					
a580	QPLAIARPEAAHGKLLVILRPEALADNSVSPTHTSAGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1 atgcacttcg cccagcttgt gggtaaacc ggtatagaac aaaatacgtt
51 ctgtcgctgt ggttttacc gcacgatgat gggcggaat accgatgttg
101 cggtaacagg tgatcggggg cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagttagaga atgctttgtt ggcttcagcc atacgggtga
201 cttcttcacg ttttttcaac gcaccgccac ggccttcgga cgcataatc
251 aactcgctg ccaaacgcag atccatggat ttctcaccac gtttgcgggc
301 cgcgtcgca acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAPG RINQLACQTQ IHGFLTTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51 CTGTCGCTGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACCG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTCACG GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAPG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAPGRINQFACQTQVHGFLLTFAGRANPAHCQSQTAX					
g581	GFSHTVYFFTFFQRTATAPGRINQLACQTQIHGFLTTFAGRVANPTHQCSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

903

```

a581.seq
  1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51 CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTACGAGCC ATTTTATTAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGN TDVTVOADRG LTSHFISLSK
 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGLTTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVOADRGLTSHFISLSKLETEVRECFV					
	:::					
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTVOADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFG RINQFACQTQVHGLTTFAGRIANPAHCQSQTAX					
a581	GFSHTVYFFTFFQRTATAFG RINQFACQTQVHGLTTFAGRIANPAHCQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51 agagaccgcg ctgcaatgcg ccgctttgac ggacaatgtt acgcgtttgg
101 cgtgttaacga caggattttt gcggcacagc ttccgtcttc ggccagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggat aaggggcagg cggtcattgt tgttgaaaaa ggcggggatg
251 cgcttctgc cgacagtgcg ggcgaaaccg ccgatatacta tacgccttg
301 agcctgatgt acgacttggc caaaaacgat ttgcgcgggc tgttgggct
351 acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttccggacagc agaaacgtgc ggaaccacaa ttgcagggtt cgttcaaaag
501 caaaattgcc gaaaatttgt ttaaaaccgc cgcggtatctg tggttcggct
551 acaccacaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttccgca atacggatta caaacctgaa attttcctga cccagcctgt
651 gaagggcggat ttgcggttcg gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgct ccgaatcgcg ttctggaac
751 aggatattat ccatggcagg catggaatgg ggcaaatgga cggtgattcc
801 gcgcgtgtgg gtgcgtgctg tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatatggc acgtgaagct gcagtaaccg
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgtaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aaggggcaac
1001 tcaaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
  1 MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
 51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPPWY NNSPNYAPSS PTRGTTVQEK
151 FGQOKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFQSGDK NDNPDADYM GYGDKVLQYR
301 LNDKQNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKVVGR PHGYGESLID
351 YNHKQNGIGI GLMFNDWDGI *

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCCTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATTGT TGTGAAAAA GGCAGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGCAAAACG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGCGGCGT
351 ACCGGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACCAATTCGC
401 CCAACTATGC CCCGGGTTCT CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTGCGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGTG TTAACAACCG CCGGATCTCG TGGTTCCGGT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTCT GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CCACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTCGAACGCA GGCAGAAATG GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAGGCGT GGTACGCGGA TTCCACGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGRAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDRONVYSV LRYNPKTGYG AIEAAYTFPI KGKLGVVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

m582.pep	10	20	30	40	50	60
m582.pep	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
m582.pep	70	80	90	100	110	120
m582.pep	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH					
m582.pep	130	140	150	160	170	180
m582.pep	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNSPNYAPSSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL					
m582.pep	190	200	210	220	230	240
m582.pep	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
m582.pep	250	260	270	280	290	300
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVPVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVPVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
m582.pep	310	320	330	340	350	360
m582.pep						
g582						

905

```

m582.pep  LNDQRNVYSVLRYPNPKTYGAIEAAYTFPIKGKLGKGVVRGPHGYGESLIDYNHKQNGIGI
          |||
g582      LNDQRNVYSVLRYPNPKTYGAIEAAYTFPIKGKLGKGVVRGPHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||
g582      GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1   ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTGT
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTTC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAA TTGCAGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TTAACCCG CCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCGA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGCGCGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CGGCGATAAA AACGACAATC
851 CCGATATTGC CACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAAATG GTATTCCGTA TTGCGCTACA ATCCCAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1   MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQOKRAETK LQVSEKSKIA EDLFKTRADL WFGYTORSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTYG AIEAAYTFPI KGKLGKGVVRG PHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMSAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||
a582      MRYILLTGLLPMSAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          |||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          70      80      90      100     110     120

          130     140     150     160     170     180

```


906

```

m582.pep  NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
          |||
a582      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
          130      140      150      160      170      180

          190      200      210      220      230      240
m582.pep  WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
          |||
a582      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
          190      200      210      220      230      240

          250      260      270      280      290      300
m582.pep  QSRPESRSWNRIYAMAGMEWGKLTVI PRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
          |||
a582      QSRPESRSWNRIYAMAGMEWGKLTVI PRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
          250      260      270      280      290      300

          310      320      330      340      350      360
m582.pep  LNDRQNVYSVLRYNPKTG YGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          |||
a582      LNDRQNVYSVLRYNPKTG YGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||
a582      GLMFNDLDGIX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccagcggtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaacggcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaaacgca ctcaacgcat cgctcatcgc cgcgcccggt ttgtcggcgg
351 ttacgcgggt tactgcgacc aaccgcagcg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcgcca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcc
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAA GIGRGNSSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIAGR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLDP VGYGQCQNGQ AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTTCGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTGGGCGG
351 TTACGCCGGT TACTGCGACC AACCAGACGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCTGC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAGGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```


907

551 CCCAATTTC A TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VGYGQCQNOG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQFGKSETVTD					
g583	MIIDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQFGKSETVTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m583.pep	AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQNQRIGERTQRIahRRARFVGGYAG					
g583	AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQNQRIGERTQRIahRRARFVGGYAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m583.pep	YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLLDPVGYGQCQNOGAQYCGNGEGY					
g583	YCDQPDGNNRQRAQRHGLADNGGNHTDKHSGQRPSLRLLDPVGYGQCQNOGAQYCGNGEGY					
	130	140	150	160	170	180
	190	200				
m583.pep	RFETQFHHIDLRKKDRPEKSEKX					
g583	RFETQFHHIDLRKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCCGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGCGCAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACGCGCGC AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCCGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
401 AACGCGATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTTC A TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VGYGQCQNOG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQFGKSETVTD					

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```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQQFGKSETVTD
           10      20      30      40      50      60
           70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
           |||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRTRFVGGYAG
           70      80      90      100     110     120
           130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNGAQYCGNGEGY
           |||||:|||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNGAQYCGNGEGY
           130     140     150     160     170     180
           190     200
m583.pep  RFETQFHHIDLRRKKDRPEKSEKX
           |||||
a583      RFETQFHHIDLRRKKDRPEKSEKX
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1   atgctgcgtt ctattttggc ggcttccctg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcggcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgtaa aaaaattcaa
201 caatttcacc agaaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggagggca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtacgcaagg atgccgtttt gcgtttcaag gcgcgtgccc aaaaactggc
501 gggcggttcg ggtgcgtccg gttataaaat cgtcaaattg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggtg cggattcagc
651 cgaccgggtg gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:..

```

1   MLRSILAASL LAVSFPAABE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  BGRDKNVANA EFKKFNFT RKSKNGSPKT BLVRSAMPR YQYNGRRIO
101 TGWEERAEFK AGRDFDALN RFIADVQTD SLEDTFVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEBISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1   ATGTGCGTC TTGTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTTCATC AGAAAAATCGA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCCGGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGMAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC CCAACGAGGT CATCATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTCCG AAAAGTTGGC
501 GGGCGTTTGG GTGCGTCCG GTTATAAAAT CGTCAAATG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

m584.pep..

```

1 MLRLVLAASL SAVSFPAABE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51 EGRDKNAVNA EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VERISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAABEALNYNIVEFS ESAGVEVAQD TMSARFQVTA EGRDKNAVNA
              ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           MLRSILAASLLAVSFPAABEALNYNIVEFS ESAGIEVAQD TMSARFQVAAEGRDKNAVNA
              10      20      30      40      50      60

              70      80      90     100     110     120
m584.pep      EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ TGWEERAEFK VEGRDFDELN
              ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
g584           EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ TGWEERAEFK AEGRDFDALN
              70      80      90     100     110     120

              130     140     150     160     170     180
m584.pep      RFIADIQADA ALXYTDFHVS RERRNEVIXQ VSKDAVLRFK ARAEKLAVL GASGYKIVKL
              ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           RFIADVQDASLED TDFS RERRNEVIDQ VSKDAVLRFK ARAEKLAVL GASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep      NLGHIGSHIAGGGAAQAKML RAMPMAASVN MEGADSAAPG VEEISISVNG TVQFX
              || : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           NFGQIGSHIAGDGAVRAKML RAMPMAASVN MEGADSAAPG VEEISISING TVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1 ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51 .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGATTCAA
301 ACAGGTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGTA GGAATTTTGA
351 TGCGTTGAAC CGTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTGG GGTGCGTCCG GTTATAAAAT CGTCAAATG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCCTGGT GTGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

a584.pep

```

1 MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51 EGRDKNAVNA EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAABEALNYNIVEFS ESAGVEVAQD TMSARFQVTA EGRDKNAVNA
              ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584           MLRSILAASL----- IVEFS ESAGVEAVQD TMSARFQVTA EGRDKNAVNA
              10      20      30      40

```


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	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNGRRITQTGWEERAEFKVEGRDFDELN					
a584	EFVKKFNFTRKSKNGSFKTELVSRSAMPYQYTNGRRITQTGWEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  ttctgccaca  ttttgccgag  ttatcgctctg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattattt  ccgcattcaa  gacacggggc  gacaacggcg  cgccgcgaaat
201  cctgaccgaa  tggaaaaaca  gccccgtctc  atccgcgctt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaacc  gctatatcga  caattacacc
301  atagaaacgc  cccggctgtt  tgccgcacaac  aacccccatt  ccaaccttgt
351  ccgcacgaa  tacgaccgtt  tcggcgaaga  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggccgtgcgc  ttgccccgat  ttggcacgaa  ttcacatcc  tctccttcac
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aaccatcag  aatcttaggc  aacggcatgg  acaggggtgg  agaacgagaa
601  cttgaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLPQRIFAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETTLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQGEKKD  IINRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGEEYLE  PIKGDWNHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCCQVR  DRDDELADVA  MQPDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTCGCCACA  TTTTGCGCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCAG  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCCG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCTGACGGAA  TGGAAAGACA  GCCCCGTCTC  ATCCGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCCGGCTTTT  CGCCGCGGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTC  TTCACCAAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCTGTC  CCAGCCCCCT  GTTGATCCCC
451  GGCCCTGCCG  TCGCCCCGAT  TTGGCACGAA  CTCATCATAT  TGTCTTTCAT
501  CATCATCGTC  GGAATGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGTGGC  AAAACGAGAA
601  CTTGAAACCC  GTATCTCCA  ACAGGTGAC  GACCCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTGG  ACAAAATGGT  GGAAAACTC  GAAAACTCG
701  TTGCGAAGA  ACGCCACCTG  CTCCATCAG  TCTCCCATGA  AATGCGTTCT
751  CCCCCTGCGC  GCATGCAGGC  AATTGTGCGA  CTGATTCAGG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAACTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAACTG  TTAACCCTGT  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAGAAAG  CCTGAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAGAAGAC  AATCAAAGCA  TTGCCAGAA  AAACGGACAA  ACGTTACCC
1001  TGTCTGCCGA  CGGAAAAATC  CCCGAAAAA  CAACCATCCT  TGCCAACGAA

```


m585.pap..

1	1	MKLQRIFAI	FCAVIVCAIF	VASFQFWLVQ	NTLAENQPNQ	RRTIETITLMG
51	1	SIISAFPRAG	DAGAREILTE	WKDQSPVSSG	YVIQDQDKDD	ILNRYIDISYT
101	1	IERARLPAAG	HPHNSNLVHE	YDRGEYGLF	PTKDWKQLQA	LRPLSPILQS
151	1	GLPLAPITWHE	LILSFIIIV	GLLMAYILAG	NIAKPIRILQ	NGMDRVANGE
201	1	LETRISQOVD	DRDDELSHLA	IQDFDKMVEKL	EKLVAKEHRL	LHHVSHMERS
251	1	PLARMQOAVG	LIQAQPOKQE	QYKRLREGEL	TRMDTLRAGL	LTLRSLETNS
301	1	MALEKESLKL	LPFLGNLVED	NQSLQAQKNGQ	TVTLSDAGKI	PENTILITANE
351	1	SYLYRAFDNV	IRNAVNYSPE	GSTILLINTGQ	DHKHWIIDVT	DNGPGVDQM
401	1	LPHIPTAFYR	ADKANPKPT	GLGLALTQHI	IEQHCCKIIA	ENIKPNGLRM
451	1	RFLIPKKTKG	SKTESSAN*			

	10	20	30	40	50	60
m585.pep	MKLFQRIFATFC	CAIVCAIFVASF	SWLVQNTLAENQ	FNQRRTIETTL	MGSIISAFRARG	
						:
g585	MKLFQRIFATFC	CAIVCAIFVASF	SWLVQNTLAENQ	FNQRRTIETTL	MGSIISAFKTRG	
						:
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWK	DSVPVSSGVYVI	QGDEKKDILNRY	IDSYTIERARLP	PAAGHPHNSLVH	IE
		:	:	:	:	:
g585	DNGAREILTEWK	NSFPVSSAVYVI	QGDEKKDILNRY	IDNYTIERARLP	PAANNPHNSLVRI	E
		:	:	:	:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGGEYLFP	TKDWDKIQARRL	PSPLLIPLGLPL	APIWHELIILSF	IIIVGLLMAYILA	G
		:	:	:	:	:
g585	YDRFGGEYLFP	IKGWDNHQAQRL	PSPLFIPLGLPL	APIWHEFIILSF	IIIVGLLMAYILA	G
		:	:	:	:	:
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILNGM	DRVANGELETRIS	QVDDRDEL	SHLAIQFDMVEK	LEKLVAKEHRL	
		:	:	:	:	:
g585	NIAKPIRILNGM	DRVAKRELEDRV	CCQVDRDELAD	VAMQFDTMVEK	LEX	
		:	:	:	:	:
	190	200	210	220	230	
	250	260	270	280	290	300
m585.pep	LHHVSHEMRSP	LARMQAIVGLIQ	APQKQEQYKRL	REGELTRMDTLAG	ELLTSLRLET	SN
		:	:	:	:	:

a585.seq

1	ATGAAACTGT	TCCAACGCAT	CTTCGCCACA	TTTTGCGCGG	TTATCGTCTG
51	TGCAATCTTT	GTGGCGAGTT	TTTCTTTCTG	GCTGGTGAG	AACACCTTTG
101	CCGAAAAACCA	GTTCAACCA	CGCCGCACCA	TCGAAACCA	TTTGATGGGC
151	AGCATATCTT	CCGCATTCCG	GGCAGCGCGG	GACGCGGTG	CGCGCGAAT
201	CCTGACGGAA	TGGAAGACA	GCCCCGTCTC	ATCGGGCGTG	TACGTTATAC
251	AGGGCGACGA	GA AAAAAGAT	ATCCTGCACC	GGTATATCGA	CAGCTACACC
301	ATCGAACCGG	CCCGGCTTTT	CGCGCGCGCA	CACCCGCATT	CCAACCTCGT
351	CCATATCGAA	TACGACCGCT	TCGGCGAGA	ATACCTGTTT	TTCAACCAAG
401	ATCTGGGACA	ACTCCAAGCC	CGCGCGCTGC	CCAGCCCCCT	GTTGATCCCC
451	GGCCTGCCGC	TCGCCCCGAT	TTGGCACGAA	CTCATCATAT	TGTCCTTCAT
501	CATCATGCTG	GGATGCTGA	TGGCGTACAT	CCTCGCCCGC	AACATTTGCCA
551	AACCCATCAG	GAATTTAGGC	AACGGCATGG	ACAGGGTGGC	AACCGGAGAA
601	CTTGAACACC	GTATCTCCCA	ACAGGTCGAC	GACCGCGACG	ACGAATTGTC

912

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651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTGCGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAATG ACCCGCATGG
851 ATACGCTGGC CGGGGAATG TTAACCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGCGTGA CGAATGCAG
1201 CTCCCGCACA TCTTACCAGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAATGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCAGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

a585.pep

```

1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGEKKD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLA RRLPSLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELHLA IQFDKMVEKL EKLVAKEHL LHHVSHMRS
251 PLARMQAIVG LIQAQPKQEQ QYLRLEGELE TRMDTLAGE LTLRSLETNS
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIQ DHKHIIIDVT DNGPGVDEM
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG					
a585	MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGEKKDILNRYIDSYTTIERARLFAAGHPHNSNLVHIE					
a585	DAGAREILTEWKDSPVSSGVYVIQGEKKDILHRYIDSYTTIERARLFAAGHPHNSNLVHIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF FTKDWDKLA RRLPSLLIPGLPLAPIWHELIIILSFIIIVGLLMAYILAG					
a585	YDRFGEEYLF FTKDWDKLA RRLPSLLIPGLPLAPIWHELIIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNMGMDRVANGELETRISQQVDDRDDELHLAIQFDKMVEKLEKLVAKERHL					
a585	NIAKPIRILGNMGMDRVANGELETRISQQVDDRDDELHLAIQFDKMVEKLEKLVAKERHL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m585.pep	LHHVSHMRSPLARMQAIVGLIQAQPKQEQYLRLEGELETRMDTLAGE LTLRSLETNS					
a585	LHHVSHMRSPLARMQAIVGLIQAQPKQEQYLRLEGELETRMDTLAGE LTLRSLETNS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m585.pep	MALEKESLKLPLFLGNLVEDNQSIAQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV					
a585	MALEKESLKLPLFLGNLVEDNQSIAQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV					

913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1  atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51  ttggaaaacc acgggcaaag ggctgtttgc cctgctgatt ttggcggcac
101  tcggctactt gggatacacg gttaccacaa accgtgcggc tccccaaat
151  caggaagcgg cggcgggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201  agccccgcaa agcgaaatca atgccgaact gtccaaactc caacaaagct
251  accccatttc catttcgcgc gcccaagcca cgtgatggc ggcggaacc
301  gaatttgacg cgcagcgtta cgtgttgcc gaaggtcatt tgaatgggt
351  gttgtccaac caaaaagaca gcctgattca ggcgttgccg gcgcagcgtc
401  tggcgcttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451  ctgcacacgc cggttgaggg ggacttcgcc cccctgctga tggaaactaa
501  aggcgatggt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551  acggacaggg ttggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601  cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1  MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAELSKL QSYPHSISA AQATLMAAAT
101  EFDAQRYDVA EGHKRWLSN QKDSLIQALA AQLGVVLLQ QKKYDAALAA
151  LDTPVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201  LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1  ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATTT
51  TTGGAAGAAC ACGGGCAAAT GGCTGTTTGC CTTGCTGATT TTGGCGGCAC
101  TCGGCTACTT GGGATACACG GTTACCACAA ACCGTAAAGT TTCCCAAAAT
151  CAGGAAGCGG CGCGGTGCT GGCAAAACATC GTAGAAAAGG CGCAAGGCAA
201  AGCCCCGCAA AGCGAAATCA ATGCCGAATT GACCAAACTC CAACAAAGCT
251  ACCCGCATTC CATTTCCGCC GCCCAAGCCA CACTGATGGC GGC GGCAACC
301  GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351  GTTGTCACAC CAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401  TGGCGTGTGT GTTGTGCAA CAAAAAAAT ACATGCGCG GCTTGCCGCG
451  CTCGATACGC CGGTTGAAGC GACTTCGCC CCCCTGCTGA TGGAAACCAA
501  AGGCGATGTC TATGCCGCAC AGGAAAAAAG CCAGGAAGCC TTAATAAACT
551  ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTGG TCGCGAATTG
601  GTTCAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1  MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN
51  QEAAAVLANI VEKAQSKAPQ SEINAEITKL QSYPHSISA AQATLMAAAT
101  EFDAQRYDVA EGHKRWLSN QKDSLIQALA AQLGVVLLQ QKKYDAALAA
151  LDTPVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201  VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

```

10 20 30 40 50 60
m586.pep MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN QEAAAVLANI
|||||

```


914

```

g586      MAAHLEEQQEELDNFKYFWKTTGKWLFAALLILAAALGYLGYTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

m586.pep  70      80      90      100     110     120
VEKAQSKAPQSEINAEITKLQOSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      70      80      90      100     110     120
VEKAQNKAPQSEINAEITKLQOSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN

m586.pep  130     140     150     160     170     180
QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQKKSQEA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      130     140     150     160     170     180
QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQKKSQEA

m586.pep  190     200     210
LKNYGQALEKMPQDSVGRELQMKLDSLKX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      190     200     210
LKNYGQALEKMPQDSVGRELQMKLDSLKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1   ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51  TTGGAAGAAC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTACCAAAA ACCGTGCGGC TTCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 ATTGTCCAAC CAAAAAGACA GCCTGATCCA GGCCTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGAATTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAGAAC CCAGGAAGCC TTAAAAAAT
551 ACGGACAGGC TTAGAAAAAA ATGCCTCAAG ATTCTGTCCG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1   MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAEITKL QOSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKWLNSN QKDSLIIQALA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQKKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

m586/a586 97.6% identity in 209 aa overlap

m586.pep  10      20      30      40      50      60
MAAHLEEQQEELDNFKYFWKTTGKWLFAVLI LAALGYLGYT VYQNRAASQNQEAAAVLANI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      10      20      30      40      50      60
MAAHLEEQQEELDNFKYFWKTTGKWLFAVLI LAALGYLGYT VYQNRAASQNQEAAAVLANI

m586.pep  70      80      90      100     110     120
VEKAQSKAPQSEINAEITKLQOSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      70      80      90      100     110     120
VEKAQNKAPQSEINAEITKLQOSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN

m586.pep  130     140     150     160     170     180
QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQKKSQEA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      130     140     150     160     170     180
QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQKKSQEA

```


915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRELVQMKLDSLKX
                |||||
a586          LKNYGQALEKMPQDSVGRELVQMKLDSLKX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 cgcgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201 ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgcg tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgcaaactcg acggcaacgg
351 caaaaccgcg aacaaacgga tgtccgacat atccgccggc atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaagggg
501 gctttgcccc ttttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENSR
51  AALAAPVYIQ TGATSFIPIP TEIQENGST DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351 CAAAACCGGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCGCCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAATCTCT CATTGCTGCTG
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACACGCG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGAA CTGAAATTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQLW GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

m587.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
	: :
g587	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENSRAALAAPVYIQ
	10 20 30 40 50 60
	70 80 90 100 110 120
m587.pep	TGATSFIPIPTEIQENGSNITDMLVGLTGLRYGLTGNTDIYSGGSYLWHEERKLDGNSKTR
	: :
g587	TGATSFIPIPTEIQENGSNITDMLAGTGLRYGLTGNTDIYSGGSYLWHEERKLDGNGKTR
	70 80 90 100 110 120
	130 140 150 160 170 180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTTYKAIDPIV
	: :
g587	NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKKRGLCPFYNLRYNEY
	130 140 150 160 170 180
	190 200 210 220 230 240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587	X

```
a587.seq
1  ATGAAGCGCA TCTTTTGCC GCCTTGCCC GCCATCTGCG CTTTATCCGC
51  TTATGCCGAC TGCCTTGA CATATTGAAGA GACAAGGGCA GACAACCGCG
101 AATGGAAACT GGAAACTTCC CTATTCTACC TGAACACGCA AAACAACCGC
151 CCGCAACTTG CCGCACTGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCGT CGGTTTGCGT TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGT GCACGAAGAA CGCAACTCG ACGGCAACGG
351 CAAAACCGA AACAAACGGA TGTCCGAGT ATCCTCGCG ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCTCGCC TAATCAGCTT TCTTGAAGAC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTTGA
551 CCGCTGCCTA CGGTATCAAC GAGCAGCAAAA CCCTTTCAAG CAACACAAA
601 TACAAGACGAG CCAATTACTG GTGCTGAAT CCCAATTAT CTCTCGCGCG
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCT GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA
```

```

-a587.pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51  AELAAPVYIQ TGATSFPIPI TEIQENGSTN DMLVGTGLGR YLGTGNTDIY
101 GSGSYLWHEE RKLDCNGKTR NKRMSDVSIG ISHTFLKDDK NPALISFLES
151 TVYEKSNRKA SSGKSWLIGA TTYKAIDPVV LSLTAYAIRN GSKTLSNNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPAARDLGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGOSSSE LKFGVOHTF*

```

m587/a587 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m587.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	:					
a587	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m587.pep	TGATSFIPIPTEIQENGSSNTDMLVGTGLGLRYGLTGNTDIYSGSYLWHEERKLDGNSKTR					
	:					
a587	TGATSFIPIPTEIQENGSSNTDMLVGTGLGLRYGLTGNTDIYSGSYLWHEERKLDGNKTR					
	70	80	90	100	110	120

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

g588.seq

```

1  atgcttaaac atctcgcat cctactgcc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gccctatca ggaaccggc tgcacctacg
101 aaggcgggat cggaaaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaaacaaag gcttggcaca cggcagggtc gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

g588.pep..

```

1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

m588.seq..

```

1  ATGCTTAAAC ATCTCGCATT CCTACTGCCG GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCGTCTCTGA CTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAAACCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGTTTCG TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

m588.pep..

```

1  MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAKGKTWR
51  QDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPHKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
g588        MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGKPSGKGIWRCRDGRGYTGS
              10      20      30      40      50      60

              70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
g588        FKNGKFDGQGVYTVAAAGREVLEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
              70      80      90      100     110     120

              130     139
m588.pep    IMKCENGMKEVKLPKNKX
g588        YYEMRTRHDX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CGCCGCGTCC GCCGTTCTGA CTTCCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATCCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAGC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1   MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENMIK EVKLPKNK*

```

m588/a588 96.4% identity in 138 aa overlap

```

              10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
a588        MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGKPKAGKGTWRCQDGRNYTGS
              10      20      30      40      50      60

              70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
a588        FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
              70      80      90      100     110     120

              130     139
m588.pep    IMKCENGMKEVKLPKNKX
a588        IMKCENGMKEVKLPKNKX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1   atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgcgc attgaaaaag tgttgaacaa aaaagatttt gtcgaatcgg
101 cgggagtgaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcgaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcggtcg gcggttggtg cttttgctga ccatcaatat cccgttcctt

```


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```

301 atcgggatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt cgcctgtat ggagtttgt actggcaagc atagtgcac
401 tttggctggc aatccggtt tacaaaagcg cgtgggcaag cattaaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggcgtga tggatgacgg ttttgtgtcg
601 ctgggtaagt ttttggaaaca ccgcaccaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgcgcaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaaac catcgctgcc gacggcatta tcgaaagcgg
801 cagcggttgg gcggacgaaa gccaccttac cggcgaaatc aatcccgaag
851 agaaaaaggg gggcggaaca gtgttgccg gcgcgctgat gaccgaaggg
901 agcgtggtgt accgcgccgc gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgcttggtcg attaaggcg attggacggt
1101 cgcactgatg cagcgcttg ccgttttgtt gattgcctgc ccgtgcgcgc
1151 tcggtctggc gacccctgcc gcgattatgg tccggcatggg caaagcggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtattgg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc gcgcgtttat tacgttccc acagcggtt tgacgaagac
1351 gctttgtacc gcatcgccgc gcgctcagc caaaacgcgg cccaccgct
1401 cgcccgccgc atcgtctccg ccgcacaagc gcgcggttt gagattccc
1451 ctgcacaaaa tgcgcaaac gttgtcggag caggcattac cgccgaagt
1501 gaaggcgtgg gtttggtaaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgc atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccaagc catagggcgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgcgaag tgcagaaact caaagccgcc ggcaaaacgc tggcgatggt
1851 cggcgacggc atcaacgacg cgcgcgcgt tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcgggtgc gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatattggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcagggcggc caatggcggc aagctcggtt tcggtatttg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIARI IEKTYGAKKE KTEDTLPOPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMLKLG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPF YKSAWASIKG
151 GLANMDVLVT IGTYSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESLTGES NPEEKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIKR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CCGGGGTAAA CTTCCGCCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTACCGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTC AATCAACGT CCCGTTCTTT

```


920

```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATTA AGGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGCTTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTGG TGCACTGGG TAAATTTTGG
601 GAACACCGTA CCAAAAAATC CAGCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGCGC AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTT GCGGGGCGCG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GCGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TCGCGCGGTA GCCGATAAAG
1001 CCGCTGCGGT ATTCTGTCCT GCCGTGCTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGTCGGT ATGGGCAAAG CGGTTAAACA CGGTATTGTTG
1201 TTTAAGACG CGGCAGCAAT GGAGGAAGCC GCCACGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGTACGCG TGACCGAAGG CAGCCGCGAG GTTGCCGCGC
1301 TTTATTGCGT TCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCGCGCG TCGAACAAAA CGCCGCCCAT CCGCTGCCCC GTGCCATCGT
1401 CTCCGCGCGC CAAGCGCGCG GTTTGGACAT TCCGCGCGCA CAAAACGCAC
1451 AAACGTTGT CGGCGCAGGC ATTACGCGCG AAGTGGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TCGGCTCTCA GTCGATAACA
1601 AACCATCGG CGCATTCGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CCGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCCT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAATCTAAAG CCGCGGCGAA AACCCTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCGGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCTG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTC
2051 CTCTCGCCGC GCTTGGCTTT TTAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGCAAGCT CGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

m589.pep..

```

1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIANKI IEKTGYGAKE KTEDTLPOPE AEHHIGWRLW LLFTINVPFL
101 IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANM
151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVYFEVGMV IGFVSLGKFL
201 EHRTKKSSLN SLGLLLKLTP TQVNVQRNGE WKQLPIDQVQ IGDILIRANHG
251 ERIAADGIEE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSVVYR
301 ATQLGSQTQL GDMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLT
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEA AHVDAVVLDK TGTLTGSPQ VAAVYCVFDS GFDEDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVVAG ITAEVEGVGL
501 VKAGKAFAE LALPKFLDGV WDIASIVAVS VDNKPIGAF A LADALKADTA
551 EAIGRLKKHN IDVYIMSGDN OGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601 KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFAS EEAQVVFDDSKTSVADIANKI
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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921

g589 MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADI AKI
10 20 30 40 50 60

m589.pep 70 80 90 100 1 110
IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVFPFLIGMAGMMIG-----RHDWMI
|||||:|||||:|||||:|||||:|||||:|||||

g589 IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMLKGLNWTNRHDWMI
70 80 90 100 110 120

m589.pep 120 130 140 150 160 170
PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
||:|||||:|||||:|||||:|||||:|||||:|||||

g589 PPVWQFVLASIVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
130 140 150 160 170 180

m589.pep 180 190 200 210 220 230
AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
||:|||||:|||||:|||||:|||||:|||||:|||||

g589 AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
190 200 210 220 230 240

m589.pep 240 250 260 270 280 290
IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLAGALMTEG
|||||:|||||:|||||:|||||:|||||:|||||

g589 IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLAGALMTEG
250 260 270 280 290 300

m589.pep 300 310 320 330 340 350
SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFFIVTWL
|||||:|||||:|||||:|||||:|||||:|||||

g589 SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVGIALLTFFIVAWL
310 320 330 340 350 360

922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKGTGLTEGSPQVAAYVCVPDPSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKGTGLTEGSPQVAAYVVPDPSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEVEGVGLVKSGKAEFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAIGRLLKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAIGRLLKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589.seq
1  ATGCAACAAA AAGTCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCTC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTACCGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCTTT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGGCGA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCTGTATTCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGAACA CCGCACCAAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAACCTA CGCCAACCCA AGTCAACGTG CAACCGCATG
701 CGGAATGGCG GCAGCTACCC ATCGACCAAG TGCAATCCGG CGACCTAATC
751 CGCGCCAATC ACGGCGAACG CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG GCGGACGAAA GCCATCTTAC CGGCGAATCC AATCCCGAAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGGCGG GCGCGCTGAT GACTGAAGGC
901 AGCGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCGA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAAGCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTTC TGCCTGCCGT TGTGGGCATC
1051 GCACTTTTGA CTTTATATCG TACTTGGCTG ATTAAGGGCG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCCTGC CCGTGTGCAC

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923

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1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCCAGGC GCGCGGTTTG GAGATTCCCA
1451 CGGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTGGTAAA AGCAGGCAAA GCCGAATTTG CCGAACTGAC
1551 CTTGCCGAAG TTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAA CGGCAAACT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGCTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCGCCGAAG TGCAAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CCGCGACGGC ATCAACGACG CGCCCGCGCT CGCCGCGGCC AACGTCAGCT
1901 TCGCCATGAA AGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCGCTC GCCGCGCTCG GCTTTTAAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGTAATAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

a589.pep

```

1  MQQKVRFAQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDDS
51  KTSVADIARI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMLKG LNWTRHDWML SPLIQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSWG ADESHLTGES NPEKKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKPQVAAYV CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAHSVNGKP IGAFALADAL
551 KADTAEAIGR LKKNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVVDG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQLFEA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

```

m589/a589 94.9% identity in 725 aa overlap

```

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIARI
          10      20      30      40      50      60
a589      MQQKVRFAQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIARI

          70      80      90      100     110
m589.pep  IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
          70      80      90      100     110
a589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMVGMLKGLNWTRHDWML

          120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          130     140     150     160     170     180
a589      SPLIQFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA

          180     190     200     210     220     230
m589.pep  AYGMHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
          190     200     210     220     230     240
a589      AYGMHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP

```


924

	240	250	260	270	280	290
m589.pep	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
a589	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
	250	260	270	280	290	300
	300	310	320	330	340	350
m589.pep	SVVYRATQLGSQTQLGDMN	NALSEAQGSKAPIARVADKAA	AVFVPAVVGIALLT	FFIVTWL		
a589	SVVYRAAQLGSQTLLGDMN	NALSEAQGSKAPIARVADKAA	AVFVPAVVGIALLT	FFIATWL		
	310	320	330	340	350	360
	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIA	CPALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEEAA	HVDA		
a589	IKGDWTVALMHAVAVLVIA	CPALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEEAA	HVDA		
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTGSGPQVAA	VYCVDPDSGFDEDALYRIA	AAVEQNAAHPLARAIV	SAAQARGL		
a589	VVLDKTGTLTGSGPQVAA	VYCVDPDSGFDEDALYRIA	AAVEQNAAHPLARAIV	SAAQARGL		
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTIVVGAGIT	AEEVGVLVKGAKAEFAEL	ALPKFLDGVWDIASIV	AVSVDNKP		
a589	EIPTAQNAQTIVVGAGIT	AEEVGVLVKGAKAEFAEL	TLPKFSDGVWEIASV	VAVSVNGKP		
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEA	IGRLKKHNIDVYIMSGDN	QGTVEYVAKQLGIAHA	FGNMSPRDK		
a589	IGAFALADALKADTAEA	IGRLKKHNIDVYIMSGDN	QGTVEYVAKQLGIAHA	FGNMSPRDK		
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMV	GDGINDAPALAAANVS	FAMKGGADVAEHTASAT	IMQHSVNQLA		
a589	AAEVQKLKAAGKTVAMV	GDGINDAPALAAANVS	FAMKGGADVAEHTASAT	IMQHSVNQLA		
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLF	FAFFYNILGIPLAALGFL	NPVIAGAMAASSSVLS	NAIRLK		
a589	DALSVSRATLKNIKQNLF	FAFFYNILGIPLAALGFL	NPVIAGAMAASSSVLS	NAIRLK		
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
a589	RVKIDX					

The following partial-DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacggta tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtggttga acagccggtt acgctggtaa accatatcac gcacggccct
301 ttgcgcggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaag ttttggaacg ctttttggg aaacaagtcc
401 cggtttcctt tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc ccgcttttca ttatgaagaa ctgtcgggca tcaggctgca

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501 ctgggaagggc ctgacggggg aaacggttta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggtca aaatcaagct ggcagacaaa
601 ggcatgcccg cggttgaaaa agcgcatctt gattcggaag cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggg gtgcattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcgggcgcg tttatcgaca gcgaagggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaaaaatac ggcccgctgg acatccatat
951 cgctgcccga cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattggcg cagtcгааagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tectcaaaaa atgttggaag atttggcggt aagtcaggct ggaaatattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcccct gatggtggac agtacggctc aaagtatggc
1401 aaggggaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgcctg aagttaaacg ggaaaaagct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttcggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVKARES LTQQQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKPRL LHNQKYLEPD NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGRME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSRYNSYDA PLFKIKLADK
201 GDAAFKKAHF DSETSDGINP LALGSSNLT L EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG APINPNGSIA PSKIEVGLA FSTRKTGESSA FIDSEGRFRF
301 DTLVYGDKEY GPLDIHIAAE HLDASALTVL KRKFAQISAK RMTEBQIRND
351 LIAAVKGDAS GLPHTDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMKKEDLN
401 QLGLMLKKTE ANIRMSIPQK MLEDLAVSQA GNIPSVNAED RAEARASIAD
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 ..TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAATAACC TGCCGGATAA CCTGAAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCACGC AGGCGTACAT TGAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAA GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG.CTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAAGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTGTGTTTAA ATCAAGCTGG CAGACAAAGG CGATGCCCGG
451 TTTGAAAAAG TGCATTTTCA TTCGGAACCT TCAGACGGCA TCAATCCGCT
501 TGTCTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGT
601 ACCGATTTCG AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGCGAGT TCCGTTTCA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCAAC AACATCCCG TATTGACAT
951 TAAAACTTTT CGATTCACGC TGCCATCGGG AAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAT
1101 CCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTT AGCGTCAATG
1151 CGCAAGATGA GCGGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGTT TFCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590.pep..(partial)

1 ..WFTSMETT VI RLKPELLNNA RKYLPDNLKT VLEQPVTLVN HITHGPFAGG
51 FGTQAYIETE FKYAPETEKV LERFPKGQVP ASLANTVYFN GSGKMEVSV
101 AFDYEELSGI XLHWEKLTGE TVYQKGPKSY RNGYDAPL FK IKLADKGDAA
151 FEKVHFDSET SDGINPLALC SSNLTLEKFS LEWKEGVDYN VKLNLVNLV
201 TDLQIGAFIN PNGSIAPSKI EVGKLAPSTK TGESGAFINS EGQFRFDTLV
251 YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMT E QIRNDLIAA
301 VKGEASGLFT NNPVLDIKTF RFTLPQSKID VGGKIMPKDM KKEDLNQLGL
351 MLKKT EADIR MSIPQKMLED LAVSQAGNIF SVNAEDEAEG RASLDDINET
401 LRLMVDSTVQ SMAREKYLT L NGDQIDTAIS LKNNQLKLG KTLQNEPEPD
451 FDEGGMVSEP QQ*

m590 / g590 93.1% identity in 462 aa overlap

m590.pep	10	20	30
	WFTSMETT VI RLKPELLNNA RKYLPDNLKT		
g590	VKAESLTQQQKILQKTGFLT VESHQYDRGWFTSTETTVIRLKPPELLHNAQKYL PDNLKI		
	30	40	50
m590.pep	40	50	60
	VLEQPVTLVNHITHGPFAGGPGTQAYIETEFKYAPETEKVLERFPKGQVPASLANTVYFN		
g590	VLEQPVTLVNHITHGPFAGGPGTQAHIEEFKYAPETEKVLERFPKGQVPVSLANTVYFN		
	90	100	110
m590.pep	100	110	120
	GSGKMEVSVPAFDYEELSGIXLHWEKLTGETVYQKGPKSYRNGYDAPL FK IKLADKGDAA		
g590	GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGPKSYRNSYDAPL FK IKLADKGDAA		
	150	160	170
m590.pep	160	170	180
	FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNLVNLVTDLQIGAFIN		
g590	FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNLVNLVTDLQIGAFIN		
	210	220	230
m590.pep	220	230	240
	PNGSIAPSKIEVGKLAPSTKTGESGAFINSEGGQFRFDTLVYGDEKYGPLDIHIAAEHLDA		
g590	PNGSIAPSKIEVGKLAPSTKTGESGAFIDSEGRFRFDTLVYGDEKYGPLDIHIAAEHLDA		
	270	280	290
m590.pep	280	290	300
	SALTVLKRKFAQISAKKMT E QIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPQSKID		
g590	SALTVLKRKFAQISAKKMT E QIRNDLIAAVKGDASGLFTHD PVLN IKI FRFTLPQSKID		
	330	340	350
m590.pep	340	350	360
	VGGKIMPKDMKKEDLNQLGLMLKKT EADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG		
g590	VGGKIMPKDMKKEDLNQLGLMLKKT EADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG		
	390	400	410
m590.pep	400	410	420
	RASLDDINETLRLMVDSTVQSMAREKYLT L NGDQIDTAIS LKNNQLKLG KTLQNEPEPD		
g590	RASLADINETLRLMVDSTVQSMAREKYLT L DGNQIDTVIS LKNNALKLG KTLQNEPD PD		
	450	460	470
m590.pep	460	470	480
	FDEGGMVSV-EPQQX		
g590	FDEGDMVSGQPHX		
	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCAGCCTT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTGCGCGCG GATTGCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTTGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTATTTTAA ACGGCAGCGG TAAATGGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGGATGCCG CGTTTGAAAA AGTGCATTTT GATTGCGAAA CTTCAGACGG
651 CATCAACCCG CTGCTTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 CTGAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAATAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCCTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAATAACT TCCGATTACG GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTGAAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCSCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE AGFLTVESHQ
51  YERGWFTSTE TVVIRLKP EL LHNAQKYL PD NLKT VLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLT L EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSGIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNQKL KLNKTLQNE
501 PEPDFDEGGM VSEPPQ*

m590/a590 97.8% identity in 462 aa overlap

m590.pep
10 20 30
WFTSMETTIVIRLKPPELLNNARKYLPDNLKT
|||||

a590 VKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTETTIVIRLKPPELLHNAQKYLDPNLKT
30 40 50 60 70 80

m590.pep
40 50 60 70 80 90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
|||||

a590 VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
90 100 110 120 130 140

m590.pep
100 110 120 130 140 150
GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
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928

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|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAFTSTKTGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAFTSTKTGESGAFIDSEGQFRFGLTVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSGKID
          |||||
a590      SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLPSGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQKLNGKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQKLNGKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEFQQX
          |||||
a590      FDEGGMVSEFQQX
          510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCCA ATCGCACCAG
151 TATGAGCGCG GCTGCTTTAC CTCTATGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGGCG GATTCCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAATGGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCAGATGCCG CGTTTGAAAA AGTGCATTTC GATTCCGAAA CTTACAGCGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGGCGA TGAATAATAC GGCCCGCTGG ACATCCATAT
951 CGTGCCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGAAGTTTCA CCAACAATCC
1101 CGTATTGGAC ATTAAAACTT TCCGATTACG GCTGCCATCG GGAATAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGTAAT
1201 CAATTGGGTT TGATGCTGAA GAAACCCGAA GCCGACATCA GAATGAGTAT

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929

1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
 1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
 1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
 1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
 1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
 1501 CCGGAGCCGG ATTTTGATGA AGCGGGTATG GTTTCAGAGC CGCAGCAGTA
 1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE TGFLTVESHQ
 51 YERGWFSTME TTVIRLKP EL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
 101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
 151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
 201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL
 251 VNLVTDLQIG AFINPNNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
 301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KKKFAQISAK KMTTEEQIRND
 351 LIAAVKGEAS GLFTNNPVL D IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
 401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
 451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNQL KLNGKTLQNE
 501 PEPDFDEGGM VSEPQQ*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHQYERGWFSTME					
g590	MKKPLISVAAVLLGVALGTPYYLGVKAESLTQQQKILQKTGFLTVESHQYDRGWFTSTE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTVIRLKPPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE					
g590	TTVIRLKPPELLHNAQKYLDPNLKIVLEQPVTLVNHITHGPFAGGFGTQAHIETEFKYAPE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
g590	TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
g590	FKSYRNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNELVNLVTDLQIGAFINPNNGSIAPSKIEVGKLAFTSTKTGESGAFINSEGQFRF					
g590	VDYNVKLNELVNLVTDLQIGAFINPNNGSIAPSKIEVGKLAFTSTKTGESGAFIDSEGRFRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKYGPLDIHIAAEHLDASALTVLKRRKFAQISAKKMTTEEQIRNDLIAAVKGEAS					
g590	DTLVYGDEKYGPLDIHIAAEHLDASALTVLKRRKFAQISAKKMTTEEQIRNDLIAAVKGDAS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVL D IKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK					
g590	GLFTHDPVLN I K IKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEANIRMSIPQK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTLNGDQID					
g590	MLEDLAVSQAGNIFSVNAEDEAEARASLADINETLRLMVDSTVQSMAREKYLTLNGDQID					
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQLKLNGKTLQNEPEPFDDEGGMVS-EPQQX					

930

```

g590      |:||||| |||||:||||| ||| |:|
          TVISLKNNAKLNKLTQNEPDPDFDEGDMVSGQPHX
          490      500      510

a590/m590-1  98.3% identity in 516 aa overlap

a590.pep      10      20      30      40      50      60
MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQEAGFLTVESHQYERGWFTSTE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1      10      20      30      40      50      60
MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHQYERGWFTSME

a590.pep      70      80      90      100     110     120
TTVIRLKPPELLHNAOKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1      70      80      90      100     110     120
TTVIRLKPPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE

a590.pep      130     140     150     160     170     180
TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1      130     140     150     160     170     180
TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG

a590.pep      190     200     210     220     230     240
FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1      190     200     210     220     230     240
FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG

a590.pep      250     260     270     280     290     300
VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTKTGESGAFIDSEGQFRF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1      250     260     270     280     290     300
VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTKTGESGAFINSEGQFRF

a590.pep      310     320     330     340     350     360
GTLVYGDEKYGPLDIHIAAEHLASALTVLKRRFARISAKKMTTEEQIRNDLIAAVKGEAS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1      310     320     330     340     350     360
DTLVYGDEKYGPLDIHIAAEHLASALTVLKRRFAQISAKKMTTEEQIRNDLIAAVKGEAS

a590.pep      370     380     390     400     410     420
GLFTHNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1      370     380     390     400     410     420
GLFTNNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK

a590.pep      430     440     450     460     470     480
MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTINGDQID
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1      430     440     450     460     470     480
MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTINGDQID

a590.pep      490     500     510
TAISLKNNAKLNKLTQNEPEPDPDFDEGDMVSEPQOX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1      490     500     510
TAISLKNNAKLNKLTQNEPEPDPDFDEGDMVSEPQOX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

```

g591.seq
1   TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG GTTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGCT ACGTCAAAAT
201 GGTTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGTCCG
301 CTGACCAACC TCGCActggc ggTTTGTCTG TACGGACTGa gctTttcctt
351 cggcgtaaCC GAACTGCGGC CCTatgtcgg cacagtccaA cccgacaccg

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931

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401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaatcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATcgAT GCCGAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGc ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCGg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAacagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AACTAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTGCAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1  LQTLIAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG
51  DTEWCLAPIP LGGYVRMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNOGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR AFGMWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGLVNLN FVPVLDGGHL
401 VFYTVIEWIR KPLGERVQNI GLRFGIALMM LMMAAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCAACCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCGGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTGGC CACCATCGAT GCCGAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAA TCACCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACACACC CTGATCGGGC GCGTCGGCCT CCGTCGCGAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AACTAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACCGGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..


```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRK
51 DTEWCLAPIP LGGYVKMVD REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIAARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GKAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMAVAFFND VTRLIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGVGKPPFFTRKRGDTEWCLAPIP					
	:					
g591	LQTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGVGKPPFFTRKRGDTEWCLAPIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m591.pep	LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
g591	LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m591.pep	ELRPYVGTVEPDTIAARAGFQSGDKIQSVNGTPVADWGSQAQTEIVLNLEAGKVAVGVQTA					
	: : : : : : :					
g591	ELRPYVGTVEPDTVAARTGFQSGDKIQSVNGVSVQDWSSQAQTEIVLNLEAGKVAVGVQTA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m591.pep	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLPGDRLTA					
g591	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLPGDRLTA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
	: : : : : :					
g591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
g591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	+++++ + + + + + +					
g591	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTVIEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFLALMMLMMAVAFFNDVTRLIGX					
	: : :					
g591	GLRFLALMMLMMAAAFFNDVTRLIGX					
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:

a591.seq

933

```

1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGGCTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACAG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTGTCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCTG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCTCTAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGGCGGCGGC GTGAAAAAG GCAGCCCGCG CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTATCG CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCG GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTGCGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCCTCAA ATTTTTCGGC AAATAATCA CGCGCAACGC CTCCGTCAGC
1051 CATATTTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT GGCCTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG CGGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

a591.pep

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIAARAGF QSGDKIQSVN
151 GTPVADWGSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMAVAFFND VTRLLG*

```

m591/a591 99.6% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGVFGKPFTRKRGDTEWCLAPIP					
a591	LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGVFGKPFTRKRGDTEWCLAPIP					
	10	20	30	40	50	60
m591.pep	LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
a591	LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
	70	80	90	100	110	120
m591.pep	ELRPYVGTVEPDTIAARAGFQSGDKIQSVNGTPVADWGSQAQTEIVLNLEAGKVAVGVQTA					
a591	ELRPYVGTVEPDTIAARAGFQSGDKIQSVNGTPVADWGSQAQTEIVLNLEAGKVAVGVQTA					
	130	140	150	160	170	180
m591.pep	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGDRLTA					
a591	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGDRLTA					
	190	200	210	220	230	240
m591.pep	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGDRLTA					
a591	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGDRLTA					

934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQTHADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQTHADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLPLVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVSISLGVNLPLVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51  cgcggcagca ggcggcttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 cogaacgcgc cgcgcgcgc cgaagtgaac caccctgttt cgcaaggat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 cgccttcat catcttgatt taccaacagc cttatggcga tttagcgggt
301 gcggcgctga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 gggtttcttc gccgtcatcc tgtttatggt tgccctttcc accgttatcg
401 gcaactatgc ctatgcgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattacgc cgttttccg tatgctggtt ttggcggtgg tctatttcgg
501 cgcgggttgc aatgtgcctt tggctgggga tatggcggtt atggcgatgg
551 gcatcatgca gtggatcaac ctgctcgcca tcctgctgct ctgccattg
601 gcgtttatgc tgctgcgcga ttacacggcc aagctgaaaa tgggcaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccatgttttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRG LYSNEAGM GSA
51  PNAAAAAEVK HPVSQGMQM LGVFVDIIIV CSCTAFILI YQPYGDL SG
101 AALTQAAIVS QVGQWAGPL AVILFMFAFS TVIGNYAYAR SNVQFIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCgcgt TCAAATTCCA
51  CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACCGATGATGA
101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGGCGGTAT GGGTTCCGCG
151 CCGAACGCCG CCGCGCGCG CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGCGGTGT TTGTCGATAC CATCATCGTT TGTCTCTGCA
251 CGCCTTCAT CATCTTGATT TACCAACAGC CTTACGCGCA TTTGAGCGGT
301 CGCGCGCTGA CGCAGGCGGC GATTGTGAGC CAAGTGGGGC AATGGGGCGC
351 GGGCTTCCTC GCGTCATCC TGTATTATGT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTATCAA AAGCCATTGG
451 CTGATTACCG CGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCGG
501 CGCGGTTCGA AATGTGCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGCG GTGGATCAAC CTTGTGCGCA TCCTGCTGCT CTGCGCCTTG

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935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGATTG AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGS
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDLG
 101 AALTQAAIVS QVGQWAGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSAPNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWAGAGFL					
g592	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWAGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVW*					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVW*					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGCGGGTAT GGGTCCGCG
 151 CCGAACGCGG CCGCCGCCG CGAAGTAAA CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGCGGC GATTGTCAGC CAAGTGGGCG AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTCCG TATGCTGGT TTGGCGTGGG TCTATTTCCG
 501 CCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGATTG AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGS
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDLG
 101 AALTQAAIVS QVGQWAGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQMLGVFVDTIIVCSCFAFIILIYQOPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMQMLGVFVDTIIVCSCFAFIILIYQOPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1  atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcatc
151 gtccggccgg acggcggcga aattcggctg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaagccga agccgaacgc ctgccttgt cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gagggcgagaa gcaacggttg gcaactggcg gcgctttggt tgtccgccct
451 tccctgctgt tgctggatga atcgttttcc agtttgaca cgcatttgcg
501 cgaccggctg cgccgatga ccgccgaacg catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac ggcggcggac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcy gtacgcccgga
651 aaccttgatt caaacgcctg ccggcgtgca ggtcgcccggt ctgatggggc
701 tgcccaatgc cgacgatgac cgccatattc cgcaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgtcc gcctgcccga
801 ctgcgtccgg cttccgcgg tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccggaaa cggtagcggtc
901 cgcacccgcg tcgatgaagg gcgtatcgtc cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1  MLEINGLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDR LRRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNGTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGCGTCCGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCG

```


937

```

201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCG CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AACTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTTCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GCGGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTCGCCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
1 MLELNLCKR FGKNTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
51 VRPDGGEIWL NGENITRMP EKRRI SLMFQ DYALFPHMSA LENA AFGGLK
101 QKMPKAEAE LAMAALAEVG LENE AHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGR I LOYGPETLV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWLNLMRHA GAVSGKDTVR
301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

```

m593.pep      10      20      30      40      50      60
MLELNLCKRFGKNTVADNICLT VGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGEIWL
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g593          10      20      30      40      50      60
MLELNLCKCFGGKTVADNICLT VGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGEIRL

m593.pep      70      80      90     100     110     120
NGENITRMPPEKRRISLMFQDYALFPHMSALENA AFGGLKMQKMPKAEAE RLAMAALAEVG
||||| :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g593          70      80      90     100     110     120
NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMQKMPKAEAE RLALSALAEVG

m593.pep     130     140     150     160     170     180
LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN
||||| :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g593          130     140     150     160     170     180
LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK

m593.pep     190     200     210     220     230     240
GGIPAVLVTHSPEEACTTADEI AVMHKGRILQYGPETLVKTPSCVQVARLMGLPNTDDN
||||| :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g593          190     200     210     220     230     240
GGIPAVLVTHSPEEACTTADEI AVMHEGKILQCGTPETLIQTPAGVQVARLMGLPNTDDD

```


938

	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDLDM-RHAGAVSGKDTV					
	: : : : : : : : : : : :					
g593	RHIPQNAVCLDNHGTCECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	: : :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```
a593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAAACGC TTCGCGGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTTGG
101 GCGCGTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TGCGGGCATC
151 GTCCGGCCCG ACGGCGGGGA AATATGGCTG AATGGGAAA ACATTACCCG
201 TATGCCGCCC GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCA CTGGAAAATG CGGCATTGCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAGACG AGGCGCACCG CAAGCCTGAN AAACTTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCTTGCTGC TGTGGACGA ATCGTTTTCC AGTTTGACA CGCATTGCGG
501 CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GCGGCGATCC
551 CTGCCGTTT GGTAACGCAT TCGCCCGAAG AGGCCTGCAC GCGGCGAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAAATC CTTCAATGCG GTACGCCCGA
651 AACCTTGTT CAAACGCCCTG CCGCGGTGCA GGTGCGCCAT CTGATGGGGC
701 TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTTACG CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAAACGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```
a593.pep
1  MLELNLCKR FGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAES LAMAALAEVG LENEHRKPX KLSGGEKQRL ALARALVVRP
151 SLILLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDD RHIPQHAVRF
251 DQDGMCECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*
```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
	: : : : : : : : : : : :					
a593	MLELNLCKRFGGKTVDNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEERLAMAALAEVG					
	: : : : : : : : : : : :					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
	: : : : : : : : : : : :					
a593	LENEAHRKPXKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRILQYGTPELTKVTPSCVQVARLMGLPNTDDN					

g594.seq..

1	atgggtgcag	ataccgatgg	cgacaaggat	gttcggctta	atcgaacggg
51	tctcgtttt	agcatactcc	ggctgctgtt	ccgcacgga	attgggatcg
101	gtaagtctgc	cgttcaggcc	tttcaggctc	ttaagctgct	gattctgtacg
151	cttgagcacc	caaatcggtt	tgccttgcca	ctcggcggtc	agcagctgac
201	cgcgtctgat	tttactgaca	tccacctcga	cggcagcacc	ggaagccttg
251	gctttttccg	aagggaaaaa	actggccaca	aacggcggtg	ccacacccaa
301	tgctgccact	ccgcccgcg	cgcaggtcgc	aagtgtcagg	aaacggcggc
351	ggccgttgtt	gatttcttga	ttatccatta	ttcagtcgtc	ctaataTTTT
401	gggaatgcg	agccattaaa	cattgcaatt	ttaccagtt	tgcaagtata
451	ctcaaacgat	tatttaaaat	aaggtaa		

g594.pcp

1 MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51 VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIHYSVV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

m594.seq

1	ATGGGTGCAG	ATACCGATGG	CGACAAGGAT	GTTCGGCTTA	ATCGAACGGG
51	TCTCGTTTT	AGCATACTCC	GGCTGCTGTT	CCGCATCGGA	ATTGGGATCG
101	GTAAGTTCGC	CGATTCAGGCC	TTTCAGGTCT	TTAAGCTGCT	GATCTGTACG
151	GTTGAGCACA	CAATTCCGTT	TGCCTTGCCA	CTCGGCGGTC	AGCAGCTGAC
201	CCGCTTCGAT	TTTACTGACA	TCCACCTCGA	CGCGAGCACC	GGCGGCTTGG
251	GCTTTTTCCG	AAGGGA AAAA	ACTGGCCACA	AACGGCGTTG	CCACACCCAA
301	TGCTGCCACT	CCGCCCGCGC	CGCAGGTCGC	GAGTGTCAGG	AAACGGCGGC
351	GGCCGTTGTT	GATTTCTTGA	TTATCCATTA	TTCACTCGTC	CTAATATTTT
401	GGGAATACCG	AGCCATAATA	CGTTGCAATT	TTACCCAGTT	TGCAGTGATA
451	CTCAAAGCAT	TATTTAAAAAT	AAGGTAA		

m594 . pep

```

1  MGADTDGDKD VRLNRTGLVF SILRLLEFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIHYHSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRKQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```

a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTTAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGCGCCTTG
251 GCTTTTTCG AAGGGA AAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGT CAGG AAACGCGCGC
351 GGCCGTTGTT GATTTCCTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```

a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```

g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggtttt
51  gaccgctgac cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcggtt cggtcggtat cgccgtcaac

```



```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgatgat ggtgggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaat tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttggaat aactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacgca accgattgcc
601 gagcttttca gcgaactcga ccccgatcgc gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttcac cgtatcgaa
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaatggg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaa tcgtcgattt
951 gttccgtecg ttgattgagg ccaaaaacaa agccttggtg gaaaaaacg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcaccaa
```


942

1051 gacgggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttecgcgca
 1151 tactcggtt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGI AVN
 51 DNACEPMNLT VPSGQVVFNI KNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRKLVVAD SGFKDTANEA DLEKLPQPLA
 151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPVI DATEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAATAT CGCCGTCAAC
 151 GACAAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
 551 CCTGTGTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTCAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAGAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
 751 AAACCTGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATGGC
 801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 GTTCCGTCCG CTGATCGAGG CAAAAACAA AGCCTTGTG GAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQ TAN EGGSVSI AVN
 51 DNACEPMELT VPSGQVVFNI KNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQ TAN	EGGSVSI AVN	DNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGI AVN	DNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

943

m595.pep	VPSGQVVFN	IKNN	SGRKLEWE	ILKGM	VVDERENI	APGLSDKMT	VTLLPGEYEMTCGLLT
g595	VPSGQVVFN	IKNN	SGRKLEWE	ILKGM	VVDERENI	APGLSDKMNRNLLPGEYEMTCGLLT	
	70	80	90	100	110	120	
m595.pep	130	140	150	160	170	180	
	NPRGKLVV	TD SGFKDT	ANEADLEKLS	QPLADYKAYV	QGEVKELVAKT	KTFTTEAVKAGDIE	
g595	NPRGKLVV	ADSGFKDT	ANEADLEKLP	QPLADYKAYV	QGEVKELAAKT	KTFTTEAVKAGDIE	
	130	140	150	160	170	180	
m595.pep	190	200	210	220	230	240	
	KAKSLFAD	TRVHYERIE	PIAELFSELD	PVIDAREDD	FDGAKDAGFT	GFHRIEYALWVEK	
g595	KAKSLFAA	TRVHYERIE	PIAELFSELD	PVIDACEDD	FDGAKDAGFT	GFHRIEHALWVEK	
	190	200	210	220	230	240	
m595.pep	250	260	270	280	290	300	
	DVSGVKEI	AAKLMTDVE	ALQKEIDAL	AFPPGKVVG	GASELIEE	VAGSKISGEED	DRYSHTD
g595	DVSGVKET	AAKLMTDVE	ALQKEIDAL	AFPPGKVVG	GASELIEEA	AGSKISGEED	DRYSHTD
	250	260	270	280	290	300	
m595.pep	310	320	330	340	350	360	
	LSDFQANV	DGSKKIVDL	FRPLIEAKN	KALLEKTD	TNFKQVNEI	LAKYRTKDG	FETYDKLG
g595	LSDFQANA	DGSKKIVDL	FRPLIEAKN	KALLEKTD	TNFKQVNEI	LAKYRTKDG	FETYDKLS
	310	320	330	340	350	360	
m595.pep	370	380	389				
	EADRKALQ	ASINALAE	DLAQLRGIL	GLKX			
g595	EADRKALQ	APINALAE	DLAQLRGIL	GLKX			
	370	380					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

a595.seq

1	ATGAGAAAT	TCAATTGAC	CGCATTGTC	GTGATGCTT	G	CCTTAGGTTT
51	GACCCGCTG	CAGCCGCCG	AGGCCGAGAA	AGCTGCCCG	G	CAGCCGTCG
101	GTGAGCGCA	AACCGCCAAC	GAGGGCGGT	CGGTCAGTAT	C	GCCGTCACAC
151	GACAATGCT	GCGAACC	GAT	GGAAGTACC	G	TGCCGAGCG
201	GTTCAATAT	AAAAACAACA	GCGGCCGCA	GCTCGAATG	G	AAATCCTGA
251	AAGGCGTG	AT	GGTGGTGGAC	GAGCGCGAAA	A	CATCGCCCC
301	GATAAAATG	CCGTCAACCT	GTGCGCGGC	GAATACGAAA	T	GAATTCGCG
351	TCTTTTGAC	CAATCGCGCG	GCAAGCTGGT	GGTAACCGAC	A	GCGGCTTTA
401	AAGACACCG	CAACGAAGCG	GATTTGGAAA	AACTGTCCCA	A	CCGCTCGCC
451	GACTATAAG	CCTATGTTCA	AGGCGAAGTC	AAAGAGCTGG	T	GCGGAAAAC
501	CAAAACCTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	A	AGGCGAAAT
551	CCCTGTTTG	CGACACCCGC	GTCCATTACG	AACGCATCGA	A	CCGATTGCC
601	GAGCTTTTC	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	A	AGACGACTT
651	CAAAGACGG	GCGAAAGATG	CCGGATTAC	CGGCTTCCAC	C	GATCGAAT
701	ACGCCCTTT	GGTGAAAAA	GACGTGTCCG	GCGTGAAGGA	A	ATTGCAGCG
751	AAACTGATG	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	A	CGCATGGC
801	GTTTCCTCC	GGCAAGGTGG	TGGCGGCGC	GTCCGAAGT	A	TTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAAG	ACCGGTACAG	C	CACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAA	T	CGTCGATTT
951	GTTCCGTCG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTG	G	AAAAAACCG
1001	ATACCAACT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	C	CGGACTAAA
1051	GACGGTTTT	AAACCTACGA	CAAGCTGGGC	GAAGCGGACC	G	CAAAGCGTT
1101	ACAGGCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	C	TTCCGCGCA
1151	TACTCGGCT	GAAATAA				

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

a595.pep

1	MRKENLTALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSI	AVN
51	DNACEPMELT	VPSGQVVFN	IKNN	SGRKLEW	EILKGM	VVD ERENIA

944

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101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTA LSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSI AVNDNACEPMELT					
a595	MRKFNLTA LSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSI AVNDNACEPMELT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m595.pep	VPSGQVVFNIKNN SGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
a595	VPSGQVVFNIKNN SGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m595.pep	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
a595	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m595.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
a595	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m595.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
a595	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m595.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG					
a595	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG					
	310	320	330	340	350	360
	370	380	389			
m595.pep	EADRKALQASINALAEDLAQLRGILGLKX					
a595	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial-DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

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1 ..atgctgctct tggacgagcc gaccaaccac ttggatgcgg aatcggtgga
51 atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggttaa
101 cgcacgaccg ctacttcctc gacaacgccg ccgaatggat ttggaactc
151 gaccgcgac acggcattcc gtggaaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaagcgcat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

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945

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451   ttcggcgata aagtgtgat tgacggtttg agcttcaaa tgccggcggg
501   cgcgattgtc ggcacatcgc gcccgaaacg cgcggtata tcgacgtgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcga agtgaaaatc
601   gggcaaacg tgaaaatgag cttgattgac caaagccgcg aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaatc cccgcccgc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaa gcaaaatcgc aggcagcttt ccggcgcgca
801   acggcgccgt ctgcacttgg caaaaacctt gttggcgggc ggcaatgtgt
851   tgctgtgga cgaaccgtcc aacgatctcg acgtggaac cctgcgcgcg
901   ttggaagacg cattgttga atttgccggc agcgtgatgg tgatttcgca
951   cgaccgtctg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaac gccgactcgg caaagaaggc gcgaaaccga aacgcacaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMQKE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLNE VIEFVNVSXS
151 FGDQVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLLEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTC CCTTCTTTC TTCCCCGGCG
101 CGAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTGGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTGGAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GATTTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTT GTCCACGGGC GCGGTGCGG AACACGAATT GGAATCGCC
451 GCCGACGCGC TGCGCTGCC GGAATGGGAT GCCAAATCG ATAATTGTC
501 CGGCGGTGAA AAACGCCGCG TTGCCTTGT CAAACTCTG TTGAGCAAGC
551 CCGATATGCT TTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGA CAGTCGTTGC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAAAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1001 AATCGTTCCG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCTC
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCCG GCAAAGAGCA GCCTGATTCC GCGAGGTGA
1151 AAATCGGACA AACCCTGAAA ATGAGCTTGA TTGACCAAG CCGCAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAA ATTGCCGAAG GCCGCGACAT
1251 TTGTCAGGTT GGTCAAGTTG AAATCCCGC CCGCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCGCGAC CAAAGCAATA TTGAGGTCAT ATTGTCTGGC
1351 GCGCAACGCG GTCGTCTGCA CTGGCAAAA ACCTTGTGTA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTCCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTCTTCTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAATACA AACCAGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

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1  MSQQYVYSML RVSKVVPPOK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEP E LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADFD ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILEDRGHG IPWKGNYSSW
251 LEQKEKRLN EAKSEAAVRK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPD S GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV QQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGRHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGN Y QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

	160	170	180	190	200	210
m596.pep	LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTV					
g596	 MLLLDEPTNHLDAESVEWLEQFLVRFPGTV					
				10	20	30
	220	230	240	250	260	270
m596.pep	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSSWLEQKEKRLNEAKSEAAVRKAMKQE					
g596	 VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSSWLEQKEKRLNEAKSEAAVRKAMKQE					
	40	50	60	70	80	90
	280	290	300	310	320	330
m596.pep	LEWVRQNAKGRQAKSKARLARFEEMSNEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS					
g596	 LEWVRQNAKGRQAKPKARLARFEEMSNEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS					
	100	110	120	130	140	150
	340	350	360	370	380	390
m596.pep	FGDKVLIDDLSEFKVPAGAIVGIIIPNGAGKSTLFKMISGKEQPDSEVKIGQTVKMSLID					
g596	 FGDKVLIDGLSEFKVPAGAIVGIIIPNGAGKSTLFKMIAGKEQPDSEVKIGQTVKMSLID					
	160	170	180	190	200	210
	400	410	420	430	440	450
m596.pep	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR					
g596	 QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR					
	220	230	240	250	260	270

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	:					
g596	LHLAKTLLGGGNVLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGNVQEYEADKKRRLGEGAKPKRIKYKPVTRX				
	:				
g596	ACEGDSKWVFFDGNVQEYEADKKRRLGEGAKPKRIKYKPVTRX				
	340	350	360	370	

a596.seq

1	ATGTCCCAAC	AATACGTCTA	TCTATGCTG	CGCGTGAGCA	AGGTTGTGCC
51	GCCGCAGAAA	ACCATCATT	AAGATATTTC	CCTTTCTTTC	TTCCCCGGCG
101	CGAAAAATGG	TTTGCTCGGT	TTGAACGGCG	CGGGCAAGTC	CACCGTCTGT
151	CGGATTATGG	CGGGCGTGGA	TAAAGAATT	GAGGCGGAAG	CCGTGCCGAT
201	GGGCGGTATT	AAAAATCGGT	ACCTGCCGCA	AGAGCCTGAG	CTTGATCCGG
251	AAAAAACCGT	GCGTGAGGAA	GTGAAAGCG	GTTTGGGCGA	AGTGGCTGCC
301	GCGCAGAAAC	GTTTGGGAGA	AGTGATATGCC	GAGTACGCCA	ATCCCGATGC
351	GGATTTTGAC	GCGTTGGCGG	AAGACGAGGG	GCGTTTGGAA	GCGATTATTG
401	CGGCGGGTTC	GTCACGGGCG	GGCGGTGCGG	AACACGAATT	GGAATTCGCT
451	GCCGACGCGC	TGCGCCTGCC	GGAAATGGGAT	GCCAAAATCG	ATAATTTGTC
501	CGGCGGTGAA	AAACGCCGCG	TGCGTTTGTG	CAAACTCTTG	TTGAGCAAGC
551	CCGATATGCT	TTTGCTGGAC	GAGCCGACCA	ACCACCTTGA	TGCGGAATCG
601	GTCGAGTGCG	TGGAGCAATT	TCTCGTGCGC	TTCCCGGGTA	CAGCTCTTGC
651	CGTAACACAC	GACCGCTACT	TCCTCGACAA	CGCCGCCGAA	TGGATTTTGG
701	AACTCGACCG	CGGGCAGCGT	ATTCCGTGGA	AAGGAAATTA	CTCGTCTTGG
751	TTGGAGACCA	AGAAAAACG	TTTGAAAAAC	GAGGCGAAAT	CCGAAGCCGC
801	GCGCGTGAAA	GCGATGAAGC	AGGAATTGGA	ATTGGGTGCGC	CAAAAATGCCA
851	AAGGCCGTCA	AGCCAAGTCC	AAAGCGCGTT	TGGCGCGTTT	TGAAGAAATG
901	AGCAACCTAG	AATACCAAAA	ACGCAATGAA	ACGCAGGAAA	TCTTCATTCC
951	CGTCGCCGAG	CGTTTGGGTA	ACGAATGAT	TGAATTTTGT	AATGTTTCCA
1001	AATCGTTCGG	GCAAAAAGTG	CTGATTGACG	ATTTAGCTT	CAAAAGTGCT
1051	GCGGGCGCGA	TTGTCCGCAT	CATCGGTCCG	AACGGCGCGG	GTAAATCGAC
1101	ACTGTTTAAA	ATGATTCCGG	GCAAAAGTGA	GCCCGATTCC	GGTGAAGTGA
1151	AAATCTGGGCA	AACCGTGAAA	ATGAGCTTGA	TTGACCAAAG	CCGCGAAGGT
1201	TTGCAAAACG	ACAAAACCGT	TTGCAACAAC	ATTGCCGAAG	GTCCGCATAT
1251	TTTACAGGTC	GGGCAGTTTG	AAATCCCCGC	CCGCCAATAT	TTGGGACGCT
1301	TCAATTTCAA	AGGCAGCGAC	CAAAGCAAAA	TCACGGGGCA	GCTTTCGGGC
1351	GGCACAACGG	GACGTTTGCA	CTTGGCAAAA	ACCTTGTGTT	GCGGTTGGCA
1401	TGTGTTGCTG	CTGACGAAC	CGTCCAACGA	CCTCGACGTG	GAAACCTGAT
1451	GCGCGTTGGA	AGACGCAATT	CTGGAATTGT	CCGGCAGCGT	GATGTTGTTC
1501	TCGCACGACC	GCTGGTTCTT	CGACCGTATT	GCTACGCATA	TCTTGGCTTG
1551	CGAAGCGCAC	TCCAAATGGG	TGTTCTTTGA	CGGCAACTAT	CAGGAATACG
1601	AAGCCGACAA	GAAACGCCGA	CTCGGCGAAG	AAGGCACGAA	ACCGAAACGC
1651	ATCAAAATACA	AAACCGTAAC	GCGTTTAA		

a596.pep

1	MSQQYVYSML	RVSKVPPQK	TIIKDISLSF	FPGAKIGLLG	LNGAGKSTVL
51	RIMAGVDKEF	EGEAVPMGGI	KIGYLPQEPF	LDPEKTVREE	VESGLGEVAA
101	AQKRLEEVYA	EYANPDADF	ALAEQQRLE	AIIAAGSSTG	GGAHEHELEIA
151	ADALRLPEWD	AKTDNLSGGE	KRRVALCKLL	LSKPDMLLLD	EPTNHLDAES
201	VEWLEQFLVR	FFGTVVAVTH	DRYFLDNAAE	WILELDRHG	IPWKGNYSWW
251	LEQKEKRLFN	EAKSEAAVRK	AMQEDLEWVR	QNAKGRQAQS	KARLARFEEM
301	SNYEYQKRNE	TQEIFIPVAE	RLGNEVIEFV	NVSKSFGDKV	LIDDLSEKVP
351	AGAIVGIIGP	NGAGKSTLFE	MIAGKEQFDS	GEVKIGQTVK	MSLIDQSREG
401	LQNDKTVFDN	IAEGRDILQV	GQFEIPARQY	LGRFNFKGSD	QSKITGQLSG
451	GERGRHLHAK	TLLGGGNVLL	LDEPSNDLDV	ETLRALEDAL	LEFAGSVMVI
501	SHDRWFLDRI	ATHILACEGD	SKWVFFDGNV	QEYEAADKKR	LGEEGTKPKR
551	IKYKPVTR*				

m596/a596 99.3% identity in 558 aa overlap

948

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVPPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVPPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFP GTTVAVTHDRYFLDNAAEWILEDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFP GTTVAVTHDRYFLDNAAEWILEDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAA RVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAA RVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVS KSFGDKVLIDDL SFKVPAGAI VGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVS KSFGDKVLIDDL SFKVPAGAI VGIIGP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTLFKMI SGKEQPDSEVKGIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFKMIAGKEQPDSEVKGIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR LHLAKTLLSGGNVLLDDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGR LHLAKTLLSGGNVLLDDEPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGN YQEY EADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGN YQEY EADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGTPKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

```



```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTCGTAT CGGGGAACCTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGCGCGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGGGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaaaaagcc
601 gaacaccgCA TtcaggAtgc ggAagcaaaa agaAAATTGG CTGAagcCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCCGCGACG TCGCGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcggC GATGTTTGA AAGGCGTgTT CTATTCCACT
901 GCGCCTGCAA CGGTTGAAAG CATTGCGCcg gGAACggtta GCTATCGGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGTCGT GATCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGTG TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 ACGGTCGCGG CAGGAAGCAA AATCGGCACG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCCGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

```

g597.pep
1  MLLHVSNSLK QLQEEIRQE RIRQERIQA RGNLASVNRK QREAWDKFQK
51  LNTELNRKLT EVAATKAQIS RFVSGNYKNS RPNVALEFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSL
151 KRQGVTDAAE QTESRRQNAK ISKDARKLLE QKNEQQLNK LLSNLEKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKRPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD YGKVVVIDH GENYISYIAG LSEISAGKGY
351 TVAAGSKIQT SGSLPDGEEG LYLIQIRYRG VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

```

m597.seq
1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAAACAGCG CGAGGCTTGG GACAAAGTTC AAAAACTCAA TACCGAGCTG
151 AACCGTTTGA AACCGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTC
251 TGAAAAACCG CGAACCAGGT CAGAAAAACC GCTTTTTCG TTATACGCT
301 TATGTAACG CCTCCAATCG GGAAGTTGTC AAGGATTGG AAAAAACGCA
351 GAAGGCTTTG CGGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAAT TCAGGCAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAAGCCGC AGACAGAATG CCAAAATCGC
501 CAAAGATGCC CGAAAACTGC TGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAA AGGCCGAACA CCGCATTGAG
601 GATGCGGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCAG AACCGGAGCG
851 GCGGCGATAT TTGAAAAGGC GTGTTCTATT CCACTGCACC GGCACCGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAGCTAT CGGGACGAGT TGGACGGCTA
951 CGGCAAAAGT GTCGTGGTGC ATCAGGCGGA GAACTACATC AGCATCTATG
1001 CCGGTTTGTG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGAAG AGGGGCTTTA
1101 CCTGCAATAA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

```

m597.pep
1  MLLHVSNSLK QLQEEIRQE RIRQARGNLA SVNRKQREAW DKFQKLNTEL
51  NRLKTEVAAT KAQISRFVSG NYKNSQPNVA ALFLKNAEPG QKNRFLRYTR
101 YVNASNREV V KDLEKQOKAL AVQEQKINNE LARLKKIQAN VQSLLEKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKNE QQLNKLNSL EKKKAEHRIQ
201 DAEARRKLA E ARLAAEKAR KEAAQQAEEA RRAEMSNLTA EDRNIQAPSV
251 MGIGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEGLYLQI RYQGVNLNPS SWIR*

```


950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRLKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRELYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNNAVALFLKNAEPGQKNRELYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLNSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLNSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISIIYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISIIYAGLSEISVKGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA GTTCCAAAAA
151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAAGTCGCC CTACGAAAGC
201 GCAGATTTCG CGTTTCGTAT CGGGGAACTA TAAAAACAGC CAGCCGAATG
251 CGGTGCGCCT GTTCCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA ...
351 TTTGGAAGAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTGAAG AAAATTGAG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TGCGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATGCCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA GCCGAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAAGGCTG
701 AAGCAGCAGC TGCGGAAATG TCCAACCTGA CCGCGGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGGTT TCAGCCGCAT
801 GCAAGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGAACCG GAGCGCGGC GATGTTTGA AAGGCGTGT CTATTCCACT
901 GCACCGGCAA CGGTTGAAAG CATTGCGCG GGAACGGTAA GCTATGCGGA

```


951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGCATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTCCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTCGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

a597.pep

```

1 MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51 LNTELNR LKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQNLK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ OKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGQ VLNPPSSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

a597.pep	10	20	30	40	50	60
m597	10	20	30	40	50	60
a597.pep	70	80	90	100	110	120
m597	70	80	90	100	110	120
a597.pep	130	140	150	160	170	180
m597	130	140	150	160	170	180
a597.pep	190	200	210	220	230	240
m597	190	200	210	220	230	240
a597.pep	250	260	270	280	290	300
m597	250	260	270	280	290	300
a597.pep	310	320	330	340	350	360
m597	310	320	330	340	350	360
a597.pep	370	380	390			
m597	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTTGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
351 GAGCATGGGC AAACGACACC ACGCTATGAT GGGCATCGCC TCGGTGCGCA
401 TCGCGCCGCG CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGGCTT CCGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGCGCGC aaagcgtca
551 tgaGCCGCG CCGACgctg attatgaaa gttgGGTGCg cgttcccgat
601 gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDQQTAA KAVMSRSARV IMESWVRVPD
201 DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AAACGACACC ACGCATGATG GGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTA CCCGTACGCG TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CCGTCATGAG CCGTAGCGCA CGCGTGATGA TGGAAAGGTT GGTGAGGGTG
601 CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFH HPSGTLRVGA AAECQDQQT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

|||||
g601      TIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNAADIDLVRALSMG
          70          80          90          100          110          120

          130          140          150          160          170          180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          |||||
g601      KLHHAMMGTA SVAI--AAAVLGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          130          140          150          160          170

          190          200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |||||
g601      AAKAVMSRSARVIMESWVRVPDDCFX
          180          190          200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGCAATT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCGCA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTGCTGG TACGCGCCTT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTGCCA
401 TTGCGACCGC CGCCGCGTG CCCGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCGG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTGAGGGTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVREF HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

          10          20          30          40          50          60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          |||||
a601      MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          10          20          30          40          50          60

          70          80          90          100          110          120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
          |||||
a601      KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
          70          80          90          100          110          120

          130          140          150          160          170          180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          |||||
a601      KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          130          140          150          160          170          180

          190          200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |||||
a601      ATKAVMSRSARVMMEGWVRVPEDCFX
          190          200

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTTCTGCT
51  CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTCG GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA Tgcgagatta TATCACTGTC TTTtggcgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGQ INRHQASNR GLCSFGGFQG NREAQVFNAD
51  LIDRQIAQIS AGLHVCNVH ALFVLNIQII IEMCVLYGRQ MPSEKTLCAA
101 LQMRDYITC FWRLLH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAACGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLSRQ VNRHGQTGNG GLDAFCSLOG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNIV VEMCAWYGVS AGEYTVNLQM
101 RDIYTRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNGGLDAFCSLOGNRKAQVFDTDLIDRQIAQIS					
g602	MLLHQCDKARHMRPFLGGQINRHQASNRGLCSFGGFQGNREAQVFNADLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNIVVEMCAWYGVSA-GEYTVN---LQMRDYITRFQXQLHX					
g602	AGLHVCNVHALFVLNIQIIEMCVLYGRQMPSEKTLAAQLQMRDYITCFWRLLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCGGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLLRQ VNRHGQTGNC GLDAFCSLOG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNIV VEMCAWYGVS TGEYTVNLQM
101 RDIYTRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNNGGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
a602	MLLHQCDKARHMRLLLLGRQVNRHGQTGNCGGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVVSAGEYTVNLQMRDYITRFQQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC  GCCTGCGTGG  GAATGACGCT  AGGAAATACG  GCATACGCTT
51  TGCCCAAAGA  GGCCGTCTGA  AACACACTCC  GCCCAACGCC  CATCCTTTTT
101  CAGACGGCCC  CGCACCAAAA  AAACAACCAC  AACTACAAG   GAGAAACATC
151  ATGTCCGACC  AACTCATTCT  TGTCTGAAC  TCGTCAGTT  CATCGCTCAA
201  AGGCGCCGTT  ATCGACCGCA  AAAGCGGCAG  CGTCGTCCTA  AGCTGCCTCG
251  GGGAACGCCT  GACTACGCCC  GAAGCCGTCA  TTACCTTCAA  CAAAGACGGC
301  AACAAACGCC  AAGTTCCCCT  GAGCGGCCGC  AACTGCCACG  CCGCGCGCGT
351  GGGTATGCTG  TTGAACGAAC  TGGAAAAACA  CGGACTGCAC  GACCGCATCA
401  AAGCCATCGG  CCGCCGCATC  GCCCAGGCG  GCGAAAAATA  TCACGAGTCC
451  GTCCTCATCG  ACCAAGACGT  CCTTGACGAA  CTGAAAGCCT  GCATCCCGTT
501  CGCCCGCTG  CACAACCCCG  CCAACATCAG  CGGCATCCTC  GCCGCGCAGG
551  AACACTTTCC  CGGCCTGCCC  AACGTCGGCG  TGATGGACAC  CTCGTTCCAC
601  CAAACCATGC  CGGAGCGGGC  CTACACTTAT  GCCGTGCCGC  GCGAATTGCG
651  CAAAAAATAC  GCCTTCCGCC  GCTACGGTTT  CCACGGTACC  GGTATGCGTT
701  ACGTCGCCCC  TGAAGCCGCA  CGCATCTTGG  GCAAACCTct  ggaaGACATC
751  CGCATGATTA  TTGCCCACTT  AGGCAACGGC  GCATCTATTA  CCGCCGTCAA
801  AAACGGCAAA  TCCGTCGATA  CCGGTATGGG  TTTACGCGG  ATCGAAGGTT
851  TGGTAATGGG  TACACGTTGC  GCGGACACCG  ATCCGGGCGT  ATACAGCTAT
901  CCGACTTTCC  ACGCAGGGAT  GGATGTTGCC  CAAATTGATG  AAATGCTGAA
951  CGAAAAATCA  GGTTCCTCCG  GTATTTCcga  actTCCCAAC  GACTGCCGCA
1001  CCCTCGAAAT  CGCCGCGGAC  GAAGGCCGCG  AAGGCGCGCG  CCTCGCCCTc
1051  gaAGTCATGA  CCTGCCGCT  CGCCAAATAC  ATCGCTTCGA  TGGCTGTGGC
1101  CTGCGGCAGT  GTTGACGCAC  TCGTGTTCAC  CGGCGGTATC  GGCGAAAAC
1151  CGCGTAATAT  CCGTGCCAAA  ACCGTTTCCT  ATCTTGATTT  CTGCGGTCTG
1201  CACATCGACA  CCAAAGCCAA  TATGGAAAAA  CGCTACGGCA  ATTCCGGCAT
1251  TATCAGCCCG  ACCGATTCTT  CTCGGCTGT  TTTGGTCGTG  CCGACCAATG
1301  AAGAACTGAT  GATTGCCTGC  GACACTGCCG  AACTTGCCGG  CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGNDA  RKYGIRFAQR  GRLKHTPPNA  HPFSDGPAPK  KQPQTTRRNI
51  MSDQLILVLN  CVSSSLKGAV  IDRKSGSVVL  SCLGERLTTP  EAVITFNKDG
101  NKRQVPLSGR  NCHAGAVGML  LNELEKHGLH  DRIKAIGRRI  AHGGEKYHES
151  VLIDQDVLDE  LKACIPFAPL  HNPANISGIL  AAQEHFPGLP  NVGVMDTSFH
201  QTMPERAYTY  AVPRELRKKY  AFRRYGFHGT  GMRYVAPEAA  RILGKPLEDI
251  RMIIAHLGNG  ASITAVKNGK  SVDTGMGFTP  IEGLVMGTRC  GDTDPGVYSY
301  PTFHAGMDVA  QVDEMLNEKS  GFPGISLPPN  DCRTLIAAD  EGREGARLAL
351  EVMTCLRAKY  IASMAVACGS  VDALVFTGGI  GENSRNIRAK  TVSYLDPLGL
401  HIDTKANMEK  RYGNSGIISP  TDSSPAVLVV  PTNEELMIAC  DTAEAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCTCGC  GTAGGCGGGG  ACGGAATAAC  GATAGAAAAT  GCGGCATACG
51  CTTTGCCCAA  AGAGGCCGTC  TGAAACACCT  TCGCCTGAT  GTCTGC.CTT
101  TTTCAGACGA  CCCCACACTA  AAAAAACAAC  CACAACTAC  AAGGAGAAAC
151  ATCATGTCCG  ACCAACTCAT  CCTCGTCTG  AACTGCGGCA  GTTCATCGCT
201  CAAAGGCGCC  GTTATCGACC  GamaAAGCGG  CAGCGTCGTC  CTAAGCTGCC
251  TCGGCGAACG  cCtGACCACG  CCCGAAGCCG  TCATTACGTT  CAACAAAGAC

```


m603.ppt

1	LSSRRRRGRNN	DRKCGIRFAQ	RGRCLKHLAPD	VCKFSDDPTL	KKQPQTTRRN
51	IMSDQLILVL	NCGSSSLKGA	VIDRXSGSVV	LSCLGERLTT	PEAVITPNKD
101	GNKRQVPLSG	RNCHACAVGM	LLNELEKHGL	HDRIKAIGHR	IAHGGEKYSE
151	SVLIDQAVMD	ELNACIPLAP	LHNPNANISGI	LAQAEHFPGI	PNVGVMDSF
201	HQTMPERAYT	YAVPRELRKK	YAFRRYGFHG	TSMRVYAEPA	ARILGKPLED
251	IRMIIAHLGN	GASITAIKNG	KSVDTSMGFT	PIEGLVMGTR	CGDIDPGVYS
301	YLTSHAGMDV	AQVDEMLNKK	SGLLGISELS	NDCRTL EIAA	DEGHEGARLA
351	LEVMTYRLAK	YIASMAVCGG	GVDALVFTGG	IGENSRNIRA	KTVSYDLFLG
401	LHIDTKANME	KRYGNSGIIS	PTDSSPAVLV	VPTNEELMIA	CDTAELAGIL
451	*				

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

	10	20	30	40	50	60
m603 .pep	LSSRRRGRNRNDRKCGIRFAQRGRLKHLAPDVCXFSDDPTLKKQPQOTTRRNIMSDQLILVL					
	:: : :: :					
g603	MDSRLRG-NDARKYGI RFAQRGRLKHTPPNAHPFSDGPAKKQPQOTTRRNIMSDQLILVL					
	10	20	30	40	50	
	70	80	90	100	110	120
m603 .pep	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNKRQVPLSGRNCHAGAVGM					
g603	NCVSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFNKDGNKRQVPLSGRNCHAGAVGM					
	60	70	80	90	100	110
	130	140	150	160	170	180
m603 .pep	LLNELEKHGLHDRIKAIGHRIAHGGEKYSESVLIDQAVMDELNACIPLAPLHPNPANISGI					
	: : : :					
g603	LLNELEKHGLHDRIKAIGRRIAHGGEKYHESVLIDQDVLDELKACIPFAPLHPNPANISGI					
	120	130	140	150	160	170
	190	200	210	220	230	240
m603 .pep	LAAQEHPGGLPNVGVMDSFHSQTMPERAYTYAVPRELRRKYAFRRYGFHGTSMRYVAPEA					

957

```

g603      LAAQEHFPGLPNVGVMDSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLNGASITAVKNGKSVDTSMGFTPIEGLVMGTRCGDTPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISLSNDCRTLEIAADEGHEGARLALEVMYTRLAK
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISLPNDCRTLEIAADEGREGARLALEVMTCRLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||:|||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAACACAC TCCGCCAAC GCCCATCCTT
101 TTTCAGACGA CCCACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAAGC CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTC CCTGAGCGGC CGGAACTGCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAA ACACGAACG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCCACG GCGGCGAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATT CCCCGGTCTG CCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAACCA TGCCGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCCGTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAAAC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTGGTAAT GGTACGCGC TCGGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGTTGACG CACTCGTGT CACCGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTT CCTATCTTGA TTTCTGGGT
1201 CTGCACATCG ACACCAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGCACACTG CCGAACTTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1  LSSRRRGRNN DRKCGIRFAQ RGRLKHTPPN AHPFSDPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCIGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHPNANISGI LAAQEHFPGL PNVGVMDSF

```


958

201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
 301 YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
 351 LEVMTYRLAK YIASMAVCGG GVDALVFTGG IGENS RNIRA KTVSYLDFLG
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL
 451 *

m603/a603 96.7% identity in 450 aa overlap

	10	20	30	40	50	60
m603.pep	LSSRRRGRNDRKCGIRFAQGRGLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL					
a603	LSSRRRGRNDRKCGIRFAQGRGLKHTPPNAHPFSDDPTXKKQPQTTRRNIMSDQLILVL					
	10	20	30	40	50	60
m603.pep	70	80	90	100	110	120
	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNGKRVPLSGRNCHAGAVGM					
a603	NCGSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFSKDGNGKRVPLSGRNCHAGAVGM					
	70	80	90	100	110	120
m603.pep	130	140	150	160	170	180
	LLNELEKHGLHDRIKAIGHRIAHHGGEKYESVLIDQAVMDELNACIPLAPLHNPANISGI					
a603	LLNELEKHELHDRIQAVGHRIAHHGGEKYESVLIDQAVMDELNACIPLAPLHNPANISGI					
	130	140	150	160	170	180
m603.pep	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSRMRYVAPEA					
a603	LAAQEHFPGLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSRMRYVAPEA					
	190	200	210	220	230	240
m603.pep	250	260	270	280	290	300
	ARILGKPLEDIRMIIAHLGNASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	ACILGKPLEDIRMIIAHLGNASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
	250	260	270	280	290	300
m603.pep	310	320	330	340	350	360
	YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
a603	YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
	310	320	330	340	350	360
m603.pep	370	380	390	400	410	420
	YIASMAVCGCGVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
a603	YIASMAVCGCGVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
	370	380	390	400	410	420
m603.pep	430	440	450			
	PTDSSPAVLVPTNEELMIACDTAELAGILX					
a603	PTDSSPAVLVPTNEELMIACDTAELVGILX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
 151 GTCGGCGGCG TTTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG
 201 GCGCGACGAA GCGGGGTTTC GGCGTGCGCG GCGGGGCGGC GGCTTCGGAT

g604 . pep

m604.seq

m604 . pep

m604/g604

a604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCGCCTGCG GCAAGGTTGA
51 CCAGCGTACC GGGCACGGCG GCGGCGGTGC CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCAA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTGC GCGGCATTCA CGGTTTGGCC ACTGGAGGCG GTGTAATCGG

960

```

201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GCGGCGAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTC AGCGCACCCT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTACAGGAA AACGGTCGGA
401 ATGCCCCGCT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTCG CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1 MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51 IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VDDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFVAGWIK KFDLYFGCRE RYAVELKIAC FQNCVHLHRY
201 MGNNGFADV FLPDFCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

	10	20	30	40	50	60
m604.pep	MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA					
a604	MPEAHFFTRSAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFFLEFFQSRGIVDDVVLQLFA					
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFFLEFFQSCGIVDDVVLQLFA					
	70	80	90	100	110	120
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWI					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWIKKFDLYFGCRE					
	130	140	150	160	170	180
a604	RYAVELKIACFQNCVHLHRYMGNNGFADVFLPDFCADAVX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTC TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201 CATCATCAGC CCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtaccC cgGCCAGCTT TTTTgcaata ttgccgccga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGaa atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTAcccgT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC caccAGcAGC cggCTcggCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCTT TAAAGGCGTG GCGGAACCTG ATTTCCGGCA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCcgCAAC GCAGGCAAAAT CCGCGCGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACGC
851 TGACCAACCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATc CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCGG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CcgtcgCcaa AATCGAACCG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQORAO LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQGKIG LFDDFDFTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLPGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGOEKVN KIYDPACGSG SLLLOAKKQF DEHIIEBGF
251 GQEIHNHTTYN LARMNMFHLN VNYNKFHIEL GDTLTNPCLK DSKPFDVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEBQKI ROYLVGNYV ETVIALAPNL FYGTCAIVNI
401 LVLKSKHDNT DIQFIDASGF FKKETNNNLV TEEHIAEIVK LFADKADVPH
451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCCTTTA TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CAGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCCGCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCAG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCGCTT CCGCGTCTCT CAAAGGCGTG GCGGAAGTCG ATTTGCGCAA
501 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAAC TA CGTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACACAC CACCTACAAC CTCGCGCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GCGGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCGG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCGG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGCGGAAA CCGTCGCCAA AATCGAACCG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQORAO LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```


101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
 151 KRLA AVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
 201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF
 251 GQEIHTTYN LARMNMF LHN VNYNQFHIEL GDTLTNP KLK DSKPFDIVS
 301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
 351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
 401 LVLSKHKDNT DIQFIDASGF FKKETNNNLV IEEHIAETVK LFADKADVP
 451 IAQNAAQQTV KDNGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
 501 LRREIDEVIA EIEA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

m605.pep	10	20	30	40	50	60
	MMTEMQQR AQLHRQIWKIADEVRGAVD GWD FKQYVLGTLFYRFISENFTDYM QAGDSSID					
g605	MMTEMQQR AQLHRQIWKIADEVRGAVD GWD FKQYVLGTLFYRFISENFTDYM QAGDSSID					
	10	20	30	40	50	60
m605.pep	70	80	90	100	110	120
	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
m605.pep	130	140	150	160	170	180
	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFENHHIDLFGDAY					
g605	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFEDHRIDLFGDAY					
	130	140	150	160	170	180
m605.pep	190	200	210	220	230	240
	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF					
	190	200	210	220	230	240
m605.pep	250	260	270	280	290	300
	DEHIEEGFFGQEIHTTYNLARMNMF LHN VNYNQFHIELGDTLTNP KLK DSKPFDIVS					
g605	DEHIEEGFFGQEIHTTYNLARMNMF LHN VNYNQFHIELGDTLTNP KLK DSKPFDIVS					
	250	260	270	280	290	300
m605.pep	310	320	330	340	350	360
	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
g605	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
m605.pep	370	380	390	400	410	420
	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
m605.pep	430	440	450	460	470	480
	FKKETNNNLVIEEHIAETVKLFADKADVP HIAQNAAQQT VKDNGYNLAVSSYVEAEDTRE					
g605	FKKETNNNLVIEEHIAETVKLFADKADVP HIAQNAAQQT VKDNGYNLAVSSYVEAEDTRE					

	430	440	450	460	470	480
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX : : : :	490	500	510		
g605	VIDIRQLNAEISETVAKIERLRREIDEVIAEIETX					
	490	500	510			

a605.seq

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

a605.pep

1	MMTEIQRAQ	LHRQIWKIAD	EVGRGAVDGDW	FKQYVLGTLF	YRFISENFTD
51	YMQAGDSSID	YAAMPDSIIT	PEIKDDAVKV	KGYFIYPGQL	FCNIAAEAHQ
101	NEELNTKLKE	IFTAIESSAS	GYPSEQDIKG	LFDDFDTTSS	RLGSTVADKN
151	KRLAAVLKGV	AELDFGSFED	HHIDLFGDJA	EYLISNYAAN	AGKSGGEFFT
201	PQSVSKLIAR	LAVHGQEKVN	KIYDPACGSG	SLLLQAKKQF	DEHIEEGFF
251	GQEINHTTYN	LARMNMFLHN	VYNYKFHIEL	GDPTLNPKLK	DSKPFDAVVS
301	NPPYSINWIG	SGDPTLINDD	RFAPAGVLAP	KSKADFAFIL	HALNYLSGRG
351	RAAIVSFPGI	FYRGAEQKI	RQYLVEGVNV	ETVIALAPNL	FYGTGIAVNI
401	LVLSKHKDNT	DIQFIDAGGF	FKKETNNNVL	TEEHIAEIVK	LFADKADVPH
451	IAQNAAQQTV	KNDGYNLAVS	SYVEPEDTRE	IIDIQQLNAE	ISETVAKIER
501	LRREIDEVIA	EIEA*			

m605/a605 98.1% identity in 514 aa overlap

```

      10      20      30      40      50      60
m605.pep  MMTEMQQR AQLHRQIWKIADEVRGAVD GWDGDFKQYVLGTLFYRFISENFTDYMQAGDSSID
          |||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a605      MMTEIQQR AQLHRQIWKIADEVRGAVD GWDGDFKQYVLGTLFYRFISENFTDYMQAGDSSID
          |||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
      10      20      30      40      50      60
m605.pep  YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSA
          |||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

```


964

```

|||||
a605      YAAMPDSIITPEIKDDAVKVGKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS
              70      80      90      100     110     120

              130     140     150     160     170     180
m605.pep  GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAELDFGNFENHHIDLFGDAY
|||||
a605      GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAELDFGSFEDHHIDLFGDAY
              130     140     150     160     170     180

              190     200     210     220     230     240
m605.pep  EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGOEKVNKIYDPACGSGSLLLQAKKQF
|||||
a605      EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGOEKVNKIYDPACGSGSLLLQAKKQF
              190     200     210     220     230     240

              250     260     270     280     290     300
m605.pep  DEHIIIEGFFGQEIINHHTYNLARMNMFLHNVNYNQFHIELGDTLTNPCLKDSDKPFDAIVS
|||||
a605      DEHIIIEGFFGQEIINHHTYNLARMNMFLHNVNYNKFHIELGDTLTNPCLKDSDKPFDAVVS
              250     260     270     280     290     300

              310     320     330     340     350     360
m605.pep  NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI
|||||
a605      NPPYSINWIGSGDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI
              310     320     330     340     350     360

              370     380     390     400     410     420
m605.pep  FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF
|||||
a605      FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDAGGF
              370     380     390     400     410     420

              430     440     450     460     470     480
m605.pep  FKKETNNNVLIEEHIAEIVKLFADKADVPHIAQNAAQTVKDNNGYNLAVSSYVEAEDTRE
|||||
a605      FKKETNNNVLTEEHIAEIVKLFADKADVPHIAQNAAQTVKDNNGYNLAVSSYVEPEDTRE
              430     440     450     460     470     480

              490     500     510
m605.pep  IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX
|||||
a605      IIDIKQLNAEISSETVAKIERLRREIDEVIAEIEAX
              490     500     510

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

g606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGTGCGGAAG TCATCGACAC
51  GCCGcgCACC GAAGAAGAAG CCTGGCTTCT GAACACTGTC GAAGCCCAAg
101 cgcGGCAATG GAATCTGAAA ACGCCAGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCaCc ggtttgctcg accaTatgaC GCGCGACgaa gtggaagccg
251 tgTTGGCGCA CGAAATGGCG CACGTCGGCA ACGGCGACAT GGTACGCTG
301 ACGCTGatTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCCT AGTCAGCATG GTATTCCAAA TCCTGTTCCG CTCCTTGCC
451 AGCCTGATTG TCATGTGGTT CAGCCGCCAA CGCGAATACC GCGCCGacgc
501 gggCGcggCA AAACCTGGTCG GCGCACCGAA AATGATTTC GCCCTGCAAA
551 GGCTFAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACCC CTTGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTGTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAATGGCA CACGTGGCA ACGCGATAT GGTACGCTG
301 ACGCTGATC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTATTTCCT GTTCAGCATG GTATTCCAAA TCCTGTTCCG CTTCTTGCC
451 AGCTTAATG TCATGTGGT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGCA AACTGGTGC GCGCGCGAA AATGATTTC GCCCTGCAA
551 GGCTCAAAG CAACCCGTC GATTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGAG ATACGCGCA CTCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGTATC GCCCGCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCCT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGGCA AACTGGTTCG GCGCGCCGAA AATGATTTCG GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNATFATGAS RNSSLIAVST GLLDHMTRE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTFLVSM VFQILFGLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPPEPNATFATGAS					
a606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPPEPNATFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSOGTYFLVSMVFQILFGLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1  ATGCTGCTCG accTgaCCG CTTTTCCTtt tccGTCTTCC TGAAAGAAAT
51  CCGCCTGCTG ACGCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGATTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGGCG GGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCATGATTT TGATGTGGGC
351 GGCATTTACG CCGTTCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAatggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCCGCG
501 CCGTATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGCG AAATTCGGTA TGCCCGCTTT GGGTGGCGCA

```



```

601 GGTTCGGCGG TGGCGACAAT GCGCGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGACTGACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGcgcgCCCA TCGGGCTGTC TTATTTTGTG GAAgccaGcg cGTTTTCGTT
801 TATCGTGTTT TTGATTGCGC CTtccggCGA GGATTATGTG GCGGCGCAGC
851 AGGTCCGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTCG GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTC GCCGCTGGCA
1051 AGCATGTACA ACGATGATCC GGCAGTTTAA AGCATCGCCT CCACCGTCCT
1101 GCTGTTTCGCC GGCCTGTtcc aACCGGCAGA CTTCACCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFLILGIF GMILMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPRILIM LVSPAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVE LIAPFGEDYV AAQQVGISLS GILYMIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFERSPLA
351 SMYNDPAVL SIASTVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
401 AAAPFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCTTTT CCCGCTTCC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACC GACGAAGTGG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GCGGATTACG CCGTTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGCGGGCA
451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCGCGG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGGTTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
751 GCGCACCCCA TCGGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCCGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTC GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCAGGCAGA CTTCACCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAAAT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSF PVFLKEVRLT TLLALPMLLA QVAQVGIGFV DTVMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLLITTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS :: : : : : : : : : : : : :					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS 10 20 30 40 50 60					
	70	80	90	100	110	120
m607.pep	SAFATVIYITFMGIMAALNPIMIAQLYGAGKTDEVGETGRQGIFGLFGLGVFGMVLMWAAIT : : : : : : : : : : : : :					
g607	SAFATVIYITFMGIMAALNPIMIAQLYGAGKTGEAGETGRQGIFGLILGIFGMILMWAAIT 70 80 90 100 110 120					
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAMVHRALHAYTTSSLNRPRLI MLVSFAAFVLN : : : : : : : : : : : : :					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAMVHRALHAYASSLNRPRLI MLVSFAAFVLN 130 140 150 160 170 180					
	190	200	210	220	230	240
m607.pep	VPLNYIFVYGKF GMPALGGACGLATMAVFWFSSALALWIYYIAKENFFRPFGLTAKFGKPD : : : : : : : : : : : : :					
g607	VPLNYIFVYGKF GMPALGGACCGVATMAVFWFSSALALWIYYIAKEKFFRPFGLTAKFGKPD 190 200 210 220 230 240					
	250	260	270	280	290	300
m607.pep	WAVFKIQWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV : : : : : : : : : : : : :					
g607	WAVFKIQWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV 250 260 270 280 290 300					
	310	320	330	340	350	360
m607.pep	GSAGTVRIGFSLGRREFRSARYISGVSLV LGWMLAVITVLSLV LFRSPLVSMYNNDPAVL : : : : : : : : : : : : :					
g607	GSAGTVRIGFSLGRREFRSARYISGVSLVSGWVLAVITVLSLV LFRSP LASMYNDDPAVL 310 320 330 340 350 360					
	370	380	390	400	410	420
m607.pep	SIAATVLLFAGLFQPADFTQC IASYALRGYKVTKVP MFIHAAAFWG CGLLPGYLLAYRFN :: : : : : : : : : : : : :					
g607	SIASTVLLFAGLFQPADFTQC IASYALRGYKVTKVP MFIHAAAFWG CGLLPGYLLAYRFD 370 380 390 400 410 420					
	430	440	450	460		
m607.pep	MGIIYGFWTALIASLTIAAIALVWCLELC SREMVRSHKAVX : : : : : : : : : : : : :					
g607	MGIIYGFWTALIASLTIAAIALVWCLEKYSELMELVKSHKAVX 430 440 450 460					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1   ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCGT CCGTCTTGTG GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCACG
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGCTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCATTACG CCGTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCC GCG
501 CCTGATTATG TTGGTCAGCT TTGCGCGGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCCCTTT GGGCGGCGCA
601 GGCTCGGCAC TGGCGACGAT GCGGCTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGAATGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGAAAATC
751 GGGCACCCCA TCGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTGTTCG GGGATCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGGTGC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGCTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTCCGC GGCTTGTTCC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGTCTGCTG CCGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1   MLLDLNRFSE SVFLKEVRL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWEGFLGLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRAHAYA SSLNRPRIM LVSFAAFVNL VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVEFKQIWKI
251 GAPIGLSYEL EASAFSEFVE LIAFPGEDYV AAQQVGISLS GILYMIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFERSPLV
351 SMYNNDPVAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFMIH
401 AAAPFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCRS
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSPVFLKEVRLTTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSPVFLKEVRLTTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGLGVFGMVLMWAAIT					
	70	80	90	100	110	120
m607.pep	130	140	150	160	170	180
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAAMVHRAHAYTSSLNRPRIMLVSFAAFVNL					
	130	140	150	160	170	180
	190	200	210	220	230	240

970

m607.pep	VPLNYIFVYKFGMPALGGAGCGLATMAVFWFSALALWIIYIAKENFFRPFGLTAKFGKPD
a607	VPLNYIFVYKFGMPALGGAGCGLATMAVFWFSALALWIIYIAKENFFRPFGLTAKFGKPD
	190 200 210 220 230 240
m607.pep	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPOSV
a607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPOSV
	250 260 270 280 290 300
m607.pep	GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFRSPLVSMYNNDPAVL
a607	GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFRSPLVSMYNNDPAVL
	310 320 330 340 350 360
m607.pep	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPFIIHAAAFWGCGLLPGYLLAYREN
a607	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPFIIHAAAFWGCGLLPGYLLAYRED
	370 380 390 400 410 420
m607.pep	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
a607	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
	430 440 450 460

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

g608.seq

```

1  ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACCTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGAT
201 ACGGAAATC CTCCAAGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATcGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCatCaaa cAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACCGC
551 ACATTTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

g608.pep

```

1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TINIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPEGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

m608.seq

```

1  ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACCTGCGG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAA cAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```


971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng)

from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAAPAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	::					
g608	MSALLPIINRLILQSPDSRSELTSEFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPGAGDIGLEGLILGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	::					
g608	TFRNSAIRKILQGGEPGAGDIRLEGLDILGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGTT GAACTTGCCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGCG GCGAACC CGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG
301 CGTTCGCCG CATCGGACGA ATTGGCACGG ATTTTCGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

g609.seq

1	ATGTTTGTGG	ATAGACTCGA	AATTCCTGCT	CTCAGCAGCG	AAACTCTTGA
51	TGCGTTTGTC	GGCAATCAGC	GAAGTAGCGA	CATCGCGCAC	CATATCTTCC
101	ACGAATTCG	GGTTTTCGTA	GGCCTTTTCG	GTAACGTATT	TTTCATCGGG
151	CGGTTTGAGC	AGGCCCGTAG	GTGGCGAGCT	CGCCTCGCTT	TCCACATAAT
201	CGATAACTCT	CTCGATACCG	ACTTCGCGAT	CGGAAGTCAG	GTCACGGTGA
251	ACGTGCGAAC	GCTGATTATG	CGGCCCATAT	TGGGAAATTT	CTTTGGAACA
301	CGGGCAAAGC	GAGGTTACGG	GAATCATGAC	CTTCATACTG	TGGCCGATAG
351	CCCCGTCCTT	CAGGTACACC	GTGAGGCTGA	CATCATAATC	CAGTaa

g609.pap

1	MVVDRLLEILA	LDEETLDLAFV	GNQRSSDIAH	HIFHEFRVFV	<u>GLFGNVFFIG</u>
51	<u>AEEQAVELAA</u>	RLRFHIIDNF	LTDDFGIGSQ	ADGNVRTLM	RAILGNFFGT
101	RAKRGYGNHD	LHTVAVCPVF	HTREADIII	O	

```
m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51  TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTTTCGTA GCGTTTTTCG GTAACGTATT TTTTCATCGG
151 CGGTTTGAAGC AGCCGATAGA GTTGGCAGCT CGCCTCGCCG TCCACATAAT
201 CGATGACTTC TCGCGTACCG ACTTCGCGAT CGGCAGTCAG GCGACGGTA
251 ACGTGCGAAG GCTGGTTGTG CGCGCCGTAT TGGGAAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGCTATG
351 CCCGCTCTTT GATTTGCGCC GTGAGACAGA CATCAATACT CAGTAA
```

```
m609.pep
1  MVVDRLEILA LDEETLDFAV GNQRSSDIAH HIFHEFRVFV GFFGNVFFIG
51  AFEQAVELAA RLRLHIIDFD LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAQCPVF DFARETDII Q*
```

m609.pep MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVVFVGGFNGVFFIGAFEQAVELAA
 g609 MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVVFGLFGNVFFIGAFEQAVELAA
 m609.pep RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFFGTRAKRGYGNHDLHTVAVCPVF


```

                                130
m609.pep    DFARETDTIIIXQ
              |:|:|:|:|:|:|
g609         HFTREADIIIXQ
                                130

```

```
a609.seq
1 ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51 TCGCGTTTGC GGCATACGCA GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTC GGTTTTCGTA GGCTTTTTCG GTAACGTATT TTTATCGGAA
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTCGCCG TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTCGGAAC GCTGGTTGTG CGCGCCATAT TGGGAAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CACCGTCTTT CATTTCGCCC GTGAGGCTGA CATCATAATC CAGTAA
```

a609.pep

1	MVVDRLLEILA	LDDETLDAFV	GNQRSSDIAH	HIFHEFRVFEV	GFFGNVFFIG
51	AFEQAVELAA	RLRLHIIDDF	LDTDFGIGSQ	ADGNVRTLVV	RAILGNFFGT
101	RAKRGYGNHD	LHTVAVCTVF	HFAREADIII	Q*	

		10	20	30	40	50	60
m609.pep		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFGFFGNVFFIGAFEQAVELAA					
a609		MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFGFFGNVFFIGAFEQAVELAA					
		10	20	30	40	50	60
		70	80	90	100	110	120
m609.pep		RLRLHIIDDFLDTFDGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF					
a609		RLRLHIIDDFLDTFDGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF					
		70	80	90	100	110	120
		130					
m609.pep		DFARETDIIIQX					
a609		HFAREADIIIQX					
		130					

g610.seq

```
1 ATGATGTGGAG GGCTTATGCA ATTTCTTTAC CGCAATGTTG CGGCTTCGCG
11 TATGCGCGGT ATGCGCAGGG ATGATTTTTC ACGCGCGCTG ATGCGCGAGC
101 ATATGCTGAC GCGCGATGAT TTGATTTATC CGGTGTTCTG ATTTGAGGGG
151 GCGGCGCGCG AGCGAGGTG GCCTCTCTAG CCGCGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGCGCGGAAG GCGCGTGGAAG CTCGGTATTTC
251 CGATGTGGCG ACTCTTTCCC GTGGTATACGG CAACAAACAA CCGCGGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG tccgagccTT
351 GCGCGAGAGG TttcCgaaac tggggattat gcggatgttc gcgctcAtc
401 cttatacpgt gcaacGGTACG GACGGCATGA cagcagaaaa cggttaCGTG
451 ATGAatgATg aaaCCGTAGA AGTCTTGGTG AAACAGGCTT TATGTCTATC
501 AGAGCGCGGC ACGCAGGTCG TTGCTPCTTC CGATATGATG GACGGCGGTA
551 TCGGCGCCAT CCGCGAGGCT TTGGAGGATG CCGGACATAT CCATACGCGG
601 ATTATGGCAT ATTCGCCCAA ATATGCTTCT GCATTTACAG GCGCTTTCGG
651 TGATGCGGTA GGCAGTTCGG GCAATTGGGG AAAGGCAGAT AAAAAGACCT
701 ATCAGATGGA TCCTGCAAAAT ACCGATGAGG CGCTGCATGA GTTGGCGCTC
751 GATATTCAGG AAGGTGCCGA TATGCTGATG GTGAAGCCCG GTTGCCGCTA
```


801 TTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
 851 CCTATCAGGT TTCGGCGGAA TATGCGATGT TGCAGGCGGC GGTTCGCAAC
 901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGG GAAAGCCTGC TGGCATTCAA
 951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
 1001 AGATGCTGAA GCGTTGA

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

g610.pep
 1 MIGGLMQFFY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
 51 AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
 101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHGQ DGLTDENGYV
 151 MNDETVEVLV KQALCHAEAG QVVAPSDMM DGRIGAIRES LEDAGHIHTR
 201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTQMDPAN TDEALHEVAL
 251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLOAAVAN
 301 GWLDGGKVVV ELLAFKRAE ADGILTYAI EAAKMLKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

m610.seq
 1 ATGATTGGAG GGCTTATGCA GTTCTCTTAC CGCAATGTC CCGCTTCGCG
 51 TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCGCCTG ATGCGCGAAC
 101 ACACGCTGAC CGCCGATGAT TTGATTATC CCGTGTTCGT ATTGGAGGGG
 151 TCGGGCGCGG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
 201 TTTGGACAGG CTGCTGTTTA CGCGGAAGA GCGCGTAAAG CTCGGTATTC
 251 CGATTGTGCG ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
 301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
 351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
 401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAA CGGTTATGTG
 451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC
 501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTTC CGATATGATG GACGGGCGTA
 551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
 601 ATTATGGCGT ATTCCGCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
 651 TGATCGCGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAGACCT
 701 ACCAGATGGA TCCGCGAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
 751 GACATTCAGG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTTGCCGTA
 801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
 851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCCAAC
 901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGG GAAAGCCTGC TGGCATTCAA
 951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
 1001 AGATGTTGAA GCGTTGA

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

m610.pep
 1 MIGGLMQFFY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
 51 SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
 101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHGQ DGLTDENGYV
 151 MNDETVEVLV KQALCHAEAG AOVVAPSDMM DGRIGAIRES LEDAGHIHTR
 201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTQMDPAN TDEALHEVAL
 251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLOAAIAN
 301 GWLDGGKVVV ELLAFKRAE ADGILTYAI EAAKMLKR*

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFFYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFFYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
m610.pep	70	80	90	100	110	120
	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
m610.pep	130	140	150	160	170	180
	FPGLGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGQVVAPSDMM					
g610	FPGLGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGQVVAPSDMM					
	130	140	150	160	170	180
m610.pep	190	200	210	220	230	240
	DGRIGAIRESLEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLKGADKKTQMDPAN					

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```

g610      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240
           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAIAN
           |||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300
           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRGADGILTYAIEAAKMLKRX
           |||||
g610      GWLDGGKVVLESLLAFKRGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTGGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTGCCAAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTC GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1  MIGGLMQFPY RNVSASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHQD DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KPTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSCE YAMLOAAVAN
301 GWLDGGKVVV ESLLAFKRAG ADGILTYYAI EAAKMLKR*

```

m610/a610 99.4% identity in 338 aa overlap

```

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||||
a610      MIGGLMQFPYRNVSASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
           130     140     150     160     170     180

```


976

```

m610.pep    FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
a610        FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep    DGRIGAIAREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
a610        DGRIGAIAREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep    TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTTYAYQVSGEYAMLQAAIAN
a610        TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTTYAYQVSGEYAMLQAAVAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep    GWLDGGKVVLESLLAFKRAGDGILTYAIEAAKMLKRX
a610        GWLDGGKVVLESLLAFKRAGDGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

g611.seq

```

1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGCTCG CCGGGGCAGG TGCTTCGGTT TTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCGCGCG CGTCCGCATT Ctcgcgcagg ttgtGGctgt
201 tatcctTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctgA
251 TcgcgGTCTa tggtttcCCa ttCcatcagg gctttgcaca TCGTTTCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTCTCGGAA
401 ATGTTTTCGG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTtc gCTCATgcCG TAGCGCGTTA
501 CCATTTCCGC TGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

g611.pep

```

1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAVYGFP FHQGFARHFH
101 LVAVFIEDFV GNLLLLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAPKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

m611.seq

```

1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTGCGAA
101 GCGGTGCTCG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCGCGCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTCGCGG CCATGATTC CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTGTGTCGCG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCGG AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTtc GCTCATGCCG TAGCGCGTTA
501 CCATTTCCGC CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

m611.pep

```

1  MPSENGMKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIAVDGFP FHQGFARHFH
101 LVAVFIEDFV GNLLLLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAPKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep  MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g611      MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
          10      20      30      40      50      60

          70      80      90      100     110     120
m611.pep  LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g611      LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
          70      80      90      100     110     120

          130     140     150     160     170     180
m611.pep  ADFRVDVLLGFLGNVLRRTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g611      ADFRVDVLLGFLGNVLRRTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
          130     140     150     160     170     180

m611.pep  X
          |
g611      X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGCTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCAG TCGGAGCGTG
151 CGGCGCGTTA TCTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCGA TGGTTCCCA TTCCATCAGG GCTTGCACA TCGTTCCAT
301 CTGTGCGCG TTTTCATCGA GGATTTGTG GGCAACCTGA TACTGCTCGT
351 CAAAATCCG GCGGATTTC GCATCGATGT CCTGCTGGGT TTTCTCGAA
401 ATGTTTTGCG AACGGGTAC GTCGCTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTG GTCATGCCG TAGCGGTTA
501 CCATTCGCG CGCATTGG GTTGC CGCTT CAAAGTCGT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRRTGY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

          10      20      30      40      50      60
m611.pep  MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a611      MPSENRMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
          10      20      30      40      50      60

          70      80      90      100     110     120
m611.pep  LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a611      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
          70      80      90      100     110     120

          130     140     150     160     170     180
m611.pep  ADFRVDVLLGFLGNVLRRTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a611      ADFRIDVLLGFLGNVLRRTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
          130     140     150     160     170     180

m611.pep  X

```


a611 |
 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

```
g612.seq
1  ATGGGcttcg gcggcaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51  AGCCTttgac ttgacggca TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCATTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

```
g612.pep
1  MGFGGNIARK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRRFFY GHSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

```
m612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCATTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

```
m612.pep
1  MGFGGNIARK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRRFFY GHSN*
```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIARKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIARKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY					
g612	KCAENVLFKVPPIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

```
a612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GTTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCATTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTT.TT.AC GGCATTCAA ATTAA
```


This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
 51  GKVFADKAVE KCAENVLFEEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep     .MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
a612          .MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep     .KCAENVLFKVPAlHRAAYFVGNFNLAVALGALLHFGHHRNPYXKLNSKSPDIFRRFFY
a612          .KCAENVLFEEVPAIHRAAYFVGNFNLAVALGALLYFGHHRNPYXKLNSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep     GHSNX
a612          GHSNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTtTGCGGA CTCGGGTTTCG CGGGAAAATC CGCCGATTTC TTCGGCGATG
151  TTCTGCGCGA TTTGtttGAt GCCGTGTCCG ATGTCGGTGG CACGgtgccc
201  gatgcCTGCC TGCCTGCCGA AAATCCGTGC CAATCgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCG
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCCGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGTCACTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFFAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201  ILQA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTtTGCGGA CTCGGATTTCG CGGGAAAATC CGCCGATTTC TTCGGCGATG
151  TTCCTGCCGA TTTGTTTtGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGTCTGCC TGCCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCCGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGTCACTGT TTTGCCTGCA AAGGCGGCCA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT

```


601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

m613.pep

```

1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLEMFADSDS RENPPICSAM
51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KFFPAESKPS SVMRPASFSP
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201 ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLEMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLSRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLEMSACVPEKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPWRIFCTA					
	:					
g613	MSVARLEMPACVPEKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSAPGSPWRIFRIA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAPKAASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAPKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1  ATGTCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTCTG  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101  TGTTCGCGGA  CTCGGGTTCTG  CGGGAAAATC  TGCCGATTTG  TTCGGCGATG
151  TTCCTGCCGA  TTTGTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201  GATGTCTGCC  TCGGTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251  AACGCAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCTG
301  CCTTCGAGCC  CGATGTGCGC  CGCCCAGGGT  TCGCCGCCTT  GGAGGATTTT
351  CTGTACCGCG  CTGTTGCGGA  AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401  CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451  GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGCGGCAA  GTTCCGAGCG
501  GCTGTCCGGG  CTTTCAGAA  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551  ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTTGCT  GTTGACGCTT
601  ATTTTACAGG  CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1  MSRSSRSRSL  LRRSTPSRSL  LISSRQSARA  SLPMFADSGS  RENLPICSAM
51  FLPICLMPCP  MSAARLPSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101  PSSPMSPAPG  SPPWRIFCTA  LLRKVISVSA  KPFPAESKPS  SVMRPASFPN
151  AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201  ILQA*

```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRSLRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRSLRSTPSRSLLISSRQSARASLPMFADSDSRENLPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPSACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPWRIFCTA					
a613	MSAARLPSACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPWRIFCTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAPKAASSERLSGLCRIRRLMMG					
a613	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAPKAASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

982

g614.seq

```

1   AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acgggcaaat
51  cgaaTATTCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCCTTGGATG ACAACCTGAT
201 TCAAACCTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGACTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCGCTa
501 tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCctgCtg gcgGgcagcc
551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC
601 GTGCCGTTCT TCAGCATTTT CCGTTCCGAT TTTGTGAAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG
701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
751 GGCGCAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGatn ttGAACGTCC ATTCTaaAAA AGTGCcttTG gacgaATCTg
1001 tggatTTATT GTCCCTCGCG CGCGGCACGC ccggtttTt cggcgccgat
1051 tTggcgaaac tggTcaacga agcccccctg tttgcccggc gccgcaacaa
1101 agtgaaagtc gatcaaagcg attTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep

```

1   MAAFNALDGK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFFTNA PLDDNLIQTL LNKNVVRVKVT PEEKPSALTA LFYSLLPVLL
101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDROVVVP LPDIRGREQX LNVHSHKVPL DESVDLLSLA RGTGPGFSGAD
351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq

```

1   ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACTTTCTT CACCAACGCG CCTTGGACG ACAACCTAAT
201 TAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCCGAC TTTGTGAAA TGTTCTGTCG
651 TGTCGGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTGTCCCC CTGCCGGACA TCCGAGGGCG
951 CGAACAGATT TTGAACGTCC ATTCTAAAAA AGTGCCTTTG GACGAATCTG
1001 TGGATTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

983

m614.pep
 1 MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
 51 TDKSTFFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
 101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
 151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAAGEAG
 201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
 251 GAGLGGGND EREQLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
 301 GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD
 351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

	10	20	30	40	50	60
m614.pep	MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER TDKSTFFFTNA					
g614	MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER TDKSTFFFTNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m614.pep	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG					
g614	PLDDNLIKTL LDKNVRVKVT PEEKPSALTA LFYSLLPVLL LIGAWFYFMR MQAGGGKGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m614.pep	AFSFGKSRAR LLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
g614	AFSFGKSRAR LLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m614.pep	AGSPGTGKTL LAKAIAAGEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAAGEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m614.pep	DEIDAVGRQR GAGLGGGND EREQLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQR GAGLGGGND EREQLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m614.pep	GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD LANLVNEAAL					
g614	GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD LAKLVNEAAL					
	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W					
g614	FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

a614.seq
 1 ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51 CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCAGCGC
 151 ACCGACAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
 201 TAAACACTG CTCGACAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
 251 AACCAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCTGCTG

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301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAAG TGCAAGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGCGGCGG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CCGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTC AGGTTCCGAC TTTGTCGAAA TGTTCGTCCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCAACGC
751 GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATGTGTTGTT GAAATGGACG GTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTGTGCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGVS VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MOTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND EQLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

          10      20      30      40      50      60
m614.pep  MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGVS VSGYLIKERTDKSTFFTNA
          |||
a614      MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGVS VSGYLIKERTDKSTFFTNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m614.pep  PLDDNLIKTL LDKNVRVKVTP EEEKPSALAA LFYSLLPVLL LIGAWFYFMR MOTGGGKGG
          |||
a614      PLDDNLIKTL LDKNVRVKVTP EEEKPSALAA LFYSLLPVLL LIGAWFYFMR MOTGGGKGG
          70      80      90      100     110     120

          130     140     150     160     170     180
m614.pep  AFSFGKSRAR LLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL
          |||
a614      AFSFGKSRAR LLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL
          130     140     150     160     170     180

          190     200     210     220     230     240
m614.pep  AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
          |||
a614      AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
          190     200     210     220     230     240

          250     260     270     280     290     300
m614.pep  DEIDAVGRQR GAGLGGGNDEREQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          |||
a614      DEIDAVGRQR GAGLGGGNDEREQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          250     260     270     280     290     300

          310     320     330     340     350     360
m614.pep  GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLA RGTGPGFSGAD LANLVNEAAL
          |||
a614      GRFDRQVVVP LPDIRGREQI LNVHKKVPL DKSVDLLSLA RGTGPGFSGAD LANLVNEAAL

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	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1   ATGTGGA AAC GCGCGCGCG CCGTGtcggc AGCTTtgaag agcagcGaAT
51  agatgCCGCC GGCAAACAC AATGCGGAAa gcaggCtgaa gcGGTtgcgC
101 GGCagcTTca tGCCGCCTCC TcGTCCaGCC ACGtttGgca gattttggac
151 aggcgcAGga ATTTGcgcCc gcgtgcggCA agtatgtcgc gcCAttgtgc
201 cacttcttcg gcggacggTG cttcgtcgaT gctgCATTcG TACagcagga
251 aatcgagggt ttcttcgatg acggGgatgg AttccgTTTG GataAgCTgc
301 ttgagttcgt tcatgactGt TCgGATAcgg aaatcgggaa aatgccgtct
351 gAaagggcct CAGACGGCat tggATTATTT GCTGTGCAGG AAgcgcgttg
401 cctcttccca ttgCGGAA AtgATGTCGg gtacggcctg cAGGGATttg
451 gCGACGGcat cgtcgatttg ccgGcgggtgc ttCcgcgctc ggtttGTtca
501 agacgtagcc gaCGACGagg ttgcggtcGC CGGGGtgggc GATGCCGAGG
551 CGCAGGCGGt aatagtctgC CGTGCCGAGT TTTGCctgAA TGTCTTCAA
601 GCCGTTGTGT CcgCGttgc cgcCGCCGAG TTTGAATTTg ATCCGTCCGC
651 AAGGGATGTC GAGTTCGTcG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTGTAGAACT GTGCAAGCGC GGCAACCGCC TGTCCGGAAC GGTTCATGAA
751 CGTGCCCGGT TTGAGCAGCC AAACATCGCC GTCGGGCAGG GCGGCGCGGG
801 CAACTTCGCC GAAGAATTTT TTTTCTTCTT TAAACGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CAAAAGCCC GCATTGTGGC GGGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGttcg
951 acatgataTT TtccgtgTTT CTgTCgaatg cggTctgaAG GCTTCAGacg
1001 gcatggTtaT TCTTCTTgaT TttgaACgcg tgtgcggCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACACTTCGA TGCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1   MWKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSEMTVRIR KSGKRLKGL QTALDYLLCR KRVASSHLPE MMSGTACRDL
151 ATASSICRRC FRARFVDVA DDEVAVAGVA DAEAQAVIVC RAEFCLNVFO
201 AVVSAVAABE FEFDPsARDV EFVVDEDEFF GFDFVELCKR GNRLSGTVHE
251 RGRFEQPNIA VGQGAGNFA EEEFFFFKRS LPFPRQFVEE PKARIVAGLF
301 VFFARVAQAD NHFDCVRHDI FRVSVECGLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq Length: 1116
1   ATGCGGAAAA GCGGTTGGCG CCGTTTCGCC AGCTTTGAAA AGCAGTGAGT
51  AAATGCTGCC TGCAAACAC AATGCCGAGA GCAGGATAAA GCGGTTGCGT
101 GGCAGATTCA TGCTTGTTCC TCTTCAAGCC ATGTCTGGCA TAGTTTGAT
151 AGGCGCAGGA ATTTCCGCC GCGTGCGGCC AGCATATCGC GCCAAACGGC
201 AATTTCTTCG GCGGAGGGGG CATCGTCTAT GCTGCATTcG TAGAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGATGG ATTcGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CCGGTCATT TCTGTGCAGG AAGCGGGTTG
401 CTCTTCCCA TTGCGCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTtG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTGT .TCGGTACTG GGTtTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTcGC CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCGCCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTcG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTGTAGAACT GTGCAAGCGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGCAGGT TTGAGCAGCC AAACGTCGCC GTCGGGCAGG GCGGCACGGG

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986

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801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGCGG TACACTTCGA TGCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SF EKQXVNA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFPPRAA SISQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFO
201 AVVSAAAAE FEFDPSAGNV EFVVDDEDFG GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTG DFA EEEFFFKXS LPFPQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVX HDI FRVSVECLK ASDGMVILL DFERVCGALLW
351 GRSTAGGTLR CGRRRAACRLX L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS LDRRRNFPPRAA					
g615	10	20	30	40	50	60
	MWKRRRRGVGSFEEQRIDAAGKPQCGKQAEAVARQLHAASSSSHVWQILDRRRNLPPRAA					
m615.pep	70	80	90	100	110	120
	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
g615	70	80	90	100	110	120
	SMSRHCA TSSADGASSMLHSYSRKS RVSSMTGMDSVWISCLSSFM TVRIRKSGKCR LKGL					
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIADDEVAVARVA					
g615	130	140	150	160	170	180
	QTALDYLLCRKRVASSHLPEMSGTACRDLATASSICRRCFRARFVQDVADDEVAVAGVA					
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQAVVSAAAAE FEFDPSAGNV EFVVDDEDFG GFDFVELCKR					
g615	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQAVVSAAAAE FEFDPSARDVEFVVDDEDFG GFDFVELCKR					
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPNVAVGQGGTG DFAEEFFFKXS LPFPQFVEE PKTRIVACLF					
g615	250	260	270	280	290	300
	GNRLSGTVHERGRFEQPNIAVGQGGAGNFAEEFFFKRSLPFPQFVEE PKARIVAGLF					
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHFD CVXHDIFRVSV ECLKASDGMVILLDFERVCGALLWGRSTAGGTLR					
g615	310	320	330	340	350	360
	VFFARVAQADNHFD CVRHDI FRVSVECLKASDGMVILLDFERVCGALLWGRSTAGGTLR					
m615.pep	370					
	CGRRRAACRLX					
g615	370					
	CGRRRAACRLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC GGC GCGCGGCG CCGTGTCTGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGGCGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCTGAT GCTGCATTTC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CCGGTCATT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTTG
451 GCGACGGCAT CGTCAATCTG TCGCGGGT. TTCCGTACTG GGTTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGCTTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCGCG
651 AGGGAATGTC GAGTTCGTCTG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGTCCGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 CCACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CAGGCCAGTT CGTCGAGGAA CAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCGGGTTGTC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACACTTCGA TCGGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCAATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLEA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPSAGNV EFVVDDEDF GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTGDFE EEEFFFFK*S LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS	SLDRRRNFP	PRAA			
a615	MRKRRRRGVGSFEEQRIDAA	GKPQCGKQAEAVARQLHAAS	SSSHVWQILD	RRRNLPPRAA		
	10	20	30	40	50	60
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIW	KSGTCRLKGL				
a615	SMSRHCAATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIW	KSGTCRLKGL				
	70	80	90	100	110	120
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIAD	DEVAVARVA				
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIAD	DEVAVARVA				
	130	140	150	160	170	180
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPSAGNVEFVVDDEDF	GFDFIKLRKG				
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPSAGNVEFVVDDEDF	GFDFIKLRKG				
	190	200	210	220	230	240
m615.pep	GFDFIKLRKG					
a615	GFDFIKLRKG					
	250	260	270	280	290	300

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFFFFFKXSLPFPQFVEEPKTRIVACLF
a615      GNCLSGTVHERGRLEQPDIAVGQGGTGDFAEFFFFFFFKXSLPFPQFVEEPKTRIVACLF
           250      260      270      280      290      300

           310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDCVXHDFRVSVECCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
a615      VFFARVAQADNHFDCVXHDFRVSAECLKASDGMVILLDFERVCGALLWGRSTAGGTLR
           310      320      330      340      350      360

           370
m615.pep  CGRRRAAACRLX
a615      CGRRRAAACRLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCCT GACGAACTGG
101 CGTGGAAATG GAAGGCTTCG TTTAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTTGGCTGC TCAAACCGGC
201 CACGTTTATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGAC GGATCAAATT CAAACTCGGC GcgggcaacG gcgGACACAA
351 CGGCTTGAAG GACATTcagG CAAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCTCGG CATCGgccaC CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAAcA aaccgagcgc gGaagcaccg Ccgggcaatc gacgatgCCG
501 TCGccaaATC CCTGcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gCTTCTTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCaccgt ccgccaaga
751 agtggcacia TGgcgcgaca tactTGccgc acgcgGcgGC AAATtcCTgc
801 gcctgtccaa aatctgcCaa aCGTGGCTGG ACgAGGAGGC GGCatgAAgc
851 tGCGCgcaA CCgcttcaGc ctgctTTCG CATTTGgTT TGCCGGCGGc
901 atctAttCgc tgetcttcaA AGCTGccgaC ACCGCGCCGC CGCCGTTTCC
951 ACATTTcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGGCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTGCGcACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCGC CGCGTTCTGC CTGCCGCCg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWEL DELAWKWKAS FKEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSGQAVAAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151 VLNKPSAEAP PANRRCRROI PAGRTRHHER QMGRGNALPA QQIIQCRLKP
201 FQTAFSREPY PNSHRTQAA YPNGIHPRHR RNPRFPVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPNRFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAHLALFFA QILFLAKAFK TGKLPPIPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGSGLDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCCT GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTTAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CCGCCCTGCC CGACGGCGAC GTTTGGCTGC TCAAACCTGC
201 CACGTTTATG AACCGTTCCG GACAGGCGAT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGGCGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAG GACATTcagG CAAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCTGAACA AACCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA

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989

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551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTCTCTG TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCGGTT TGGCGCGATA TGCTGGCCGC ACGCGCGCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGTGC CTGCCGCCCC
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLGTD YRLRLGIGH PGDRNLVVGY
151 VLNKPSTEXP PTDXRRCRRI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFFP PNSHRTQAA YPNRIHPRHR RNPRFPALRM QHRRCPILRR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAEE TAPPPFPHFD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGLGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLG	NPNPGKEYEQ	TRHNAGFWFL	DELAWKWKAS	FKEEKKFFGE	VARAALPDGD
g616	MSNTIKMVVGLG	NPNPGKEYEQ	TRHNAGFWFL	DELAWKWKAS	FKEEKKFFGE	VARAALPDGD
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMN	RSGQAVALAQ	FYKIKPEEIL	VVHDELDI	PCGRIKFKLG	GNGGGHNLK
g616	VWLLKPATFMN	RSGQAVALAQ	FYKIKPEEIL	VVHDELDI	PCGRIKFKLG	GNGGGHNLK
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTDY	YRLRLGIGH	PGDRNLVV	GYVLNKPST	EXPPTDXRC	RRIQIPASH
g616	DIQAKLGTDY	YRLRLGIGH	PGDRNLVV	GYVLNKPST	EXPPTDXRC	RRIQIPASH
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPA	QMTRCRLKPF	QTACSRFFP	PNSHRTQAA	YPNRIHPRH	RNRPRFPAL
g616	QMGRSNPLPA	QMTRCRLKPF	QTACSRFFP	PNSHRTQAA	YPNRIHPRH	RNRPRFPAL
	190	200	210	220	230	240
	250	260	270	280	290	300
m616.pep	QHRRCPILRR	RNCRLARYA	GRTRRKIP	APIQTMPDM	AXRGTSMNL	PRNRFILLS
g616	QHRRCPILRR	RNCRLARYA	GRTRRKIP	APIQTMPDM	AXRGTSMNL	PRNRFILLS
	250	260	270	280	290	300
	310	320	330	340	350	360
m616.pep	IYSLLFKAEE	TAPPPFPHF	DKVAHLAL	FFAQIWLTK	AFRTDNRPI	PYRSLMVFA
g616	IYSLLFKAEE	TAPPPFPHF	DKVAHLAL	FFAQIWLTK	AFRTDNRPI	PYRSLMVFA
	310	320	330	340	350	360
	370	380	390	400		
m616.pep	FSECAQAWFT	ATRTGLGDV	LADLTGAAL	ALFTARAAC	RPDX	
g616	FSECAQAWFT	ATRTGLGDV	LADLTGAAL	ALFTARAAC	RPDX	
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq

```

1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTGGCGGAA
151 GTCGCCCGTG CTACCCCTGCC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCCG GACAGGCAGT TGCCGCCCTT GCGCAGTTTT
251 ATAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCCTGCA CAGCAAATGA CCGATGCCG TCTGAAGCCC
601 TTTGAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTC
701 GATTTCTGCG TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGGCACA TGGCGCGACA TACTTGCCGC ACGCGCGGCG AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGCTGG ACGAGGAGGC GGCATGAAGC
851 TGC CGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGGT TGCCGGCGGC
901 ATCTATTCGC TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTGCGC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAAA ACCGGAACAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTATAC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
1151 TGGCAGGTAC GGTTCCTCGA CTCTTTGCCG CCCGCGCCGC CGACCGCCCG
1201 GACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep

```

1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARATLPDGD VWLLKPTTFM NRSGQAAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHHGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QOMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPVRM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPNRNFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QIWLTKAFK TGKLPPIYRS
351 LMVFALCFAL FSECAQA*FT ATRTGSGLDV LADMAGTVLA LFAARAADRP
401 D*

```

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
a616	VWLLKPATFMNRSGQAAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHHGLK					
	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
a616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
a616	QMGRSNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRNPRFPALRM					
	190	200	210	220	230	240
	250	260	270	280	290	300

q619.seq

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

g619.pap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

m619.seq

1	ATGCCGCTCTG	AAAAAATAT	CGGTTTTATG	GCAGGAAGCA	GCCGCCCGTT
51	CTGGGTCGCC	TTTGGCGTGT	TGCTTGGTTT	CTCGGCTCTG	TTTAGTACGC
101	TCACAGCTCAA	AGGCGATTGG	GATTTTCTCT	TGCAACTTCG	GCTGACCAA
151	CTTGCCGCGC	TGCTGATGGT	CGCCTATGCG	GTCGGCGTGT	CCACGCAACT
201	CTTGCCAAACG	CTGACCAATA	ATCCGATCTT	GACCCCTTCA	ATTTTGGGTT
251	TCGATTGCGT	GTATGTGTTT	TTGCAGACCT	TGCTGGTGTG	TACGTTCCGC
301	GGCGTGGGCT	ATGCTTCCCT	GCCGTTGACG	GGCAAATTCG	GCTTTGAACT
351	GGTCGTCTAG	ATGGGCGGGT	CGCTGCTGCT	GTATCTACAG	CTCATCAAC
401	AGGGCGGACG	CGATTTGTGC	CGCATGATT	TAAATCGGCT	GATTTTCCGG
451	ATTATTGTTC	CGACGCTGCG	GTCGCTGCTT	TCGCGCATGA	TCGATCCCGA
501	AGAATTATTACC	CGCGCGCAGG	GCGATCTGTT	TGCCGGATCT	AATACGCTCC
551	ACAGCGAGCT	TTTGGGCATA	GGCGCATGTA	TTCTGCTGTC	CAGCGGGCGC
601	GTGTTTGGTC	GCGAACGCTA	CCGCTTGGAC	GTTTACCTTT	TGGGGCGTGA
651	CCAAGTCCGC	AATTTGGGCA	TGAGCTACAC	CGCGCAACCC	TATCGGATAC
701	TGCTTTGGAT	TGCCGCATTG	TGCGCAGACG	CGACC CGCGT	GGTCCGGCCC
751	GTAAGCTTTT	TCGGGCTTCT	CGCGCGCTCG	CTTGCCAAC	ACTTTTCCCC
801	CTCCGCTCAA	CATTCCGTCG	GCCTGCCGAT	GACGGTTTGT	ATCGCGGCGA
851	TGCTCTTGGT	CGCGCGACAG	ACCGTGTTGC	AACACCTGGT	CGGATGACGA

901 GCAGTGTGA GCGTAGTAGT AGAATTGCG GCGGACTCG TTTCTCTCA
 951 TCTCGTTTTA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNKGDW DFVLQRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
 101 GVGYSASLPLT GKFGFELVVM MGGSLLLFYT LIQGGGRDLS RMILIGVIFG
 151 ILFRSLSSL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ
 301 AVLSVVVEFA GGLVFLYLVL KHKK*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNKGDWDFVLQRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNKGDWDFVLHLRLTKLAALLMVAYA					
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFQTLVFTFGGVGYASLPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVFQTLVFTFGGVGYTSLPLTGKFGFELVVM					
m619.pep	130	140	150	160	170	180
	MGGSLLLFYTLIQGGGRDLSRMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGGGRDLPHMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF					
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVRSSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
m619.pep	250	260	270	280	290	300
	VATATAVVGPFVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGPFVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKKX					
g619	AVLSVVVEFAGGLVFLYLVLKHKKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq
 1 ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
 51 GTGGGTTGCC TTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTC TGCACTGCG CCTGACCAAG
 151 CTGCGCGCGC TGCTGATGGT CGCCTATGCG GTCGCGGTTT CGACCCAGCT
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT
 251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTCGGC
 301 GCGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
 351 GGTCTGTATG ATGGCGGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
 401 AGGCGGGCGC CGATTTGCCG CGTATGATT TAATCGGCGT GATTTTCGGG
 451 ATTTTGTTC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA
 501 AGAATTTACG GCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
 551 ACAGCGAGCT TTTAGGCATA GCGCGCTGA TTCTGCTCGT CAGCGCGGCG
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTACACCTTT TGGGGCGCGA
 651 CCAAGCCATA AATTGCGCA TCAGCTACAC GCGCAACACC TTATGGATAC
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTGCGCCCG

993

751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
 801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
 851 TCCTCTTGGT CGGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
 901 GCGGTATTAA GCGTGGTGGT CGAATTGCG GCGGACTCG TTTTCCTCTA
 951 TCTCGTTTAA AGACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

a619.pep

1 MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFLVHLRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLLEVTFG
 101 GVGYSASLPLT GKFGFELVVM MGSLLLFYT LIKQGGRLDP RMILIGVIFG
 151 ILFRSLSSL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
 301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

	10	20	30	40	50	60
m619.pep	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA					
a619	MPSEKNIGFMAGSSRPLWVAFALLLVSCILEFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
m619.pep	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLEVTFGGVGYSASLPLTGKFGFELVVM					
a619	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLEVTFGGVGYSASLPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLEVTFGGVGYSASLPLTGKFGFELVVM					
a619	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLEVTFGGVGYSASLPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	MGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSL SRMIDPEEFTAAQANMFAGF					
a619	MGSLLLFYTLIKQGGRLPRMILIGVIFGILFRSLSSL SRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
m619.pep	MGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSL SRMIDPEEFTAAQANMFAGF					
a619	MGSLLLFYTLIKQGGRLPRMILIGVIFGILFRSLSSL SRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
m619.pep	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
a619	NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
a619	NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
a619	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
m619.pep	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
a619	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
m619.pep	AVLSVVVEFAGGLVFLYLVLKHKKX					
a619	AVLSVVVEFAGGLVFLYLVLRHKKX					
	310	320				
m619.pep	AVLSVVVEFAGGLVFLYLVLKHKKX					
a619	AVLSVVVEFAGGLVFLYLVLRHKKX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

g620.seq

1 ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gTTTCGCCT TAAGTGCCTG
 51 CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGCGAG AtTAGCGacc
 101 gttcgggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
 151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTGGTTCTC
 201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
 251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
 451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

g620.pep
 1 MKKTLLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDA YIFK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

m620.seq
 1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCCAGA TTTTCTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
 201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCGAA GAGCCTAAAG
 251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAG CCTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGCGGTAAG
 451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

m620.pep
 1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLLAIVAVFALSACRQAEEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMDGNVTDWTNPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMDGNVTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

a620.seq
 1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCCAGA TTTTCTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
 201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCGAA GAGCCTAAAG
 251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAG CCTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGCGGTAAG
 451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

a620.pep
 1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

995

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a620	MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFYTKLPEEPKIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
a620	DQPVWFSTIKQMFYTKLPEEPKIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGKVVGFDDMPDTYIFKX					
a620	GFIGGMGAEDALPFGNKEQAEKFAKDKGKVVGFDDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

```

g622.seq
1  ATGCAactta ccgctgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTTCGG CGTTGCCTGC
301 GGCTTGGATT CGATGGTTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGGT CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTITCCGTTG CTAAAGAAGT CCGTACCGAT
451 ACCGCTGTCT GCGAAAAATC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GCGCGAACAG ATTTTTCCTG ACATCGGCCG TTGAAACGTA TTGTTTATCG
551 GCGCAGGCCA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAAT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GGCAGGCCAG
751 CTTCGCGATG TCGGCAAAAG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GATTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTTGAAC GATGCGTATC TTTATACGGT GGACGATATG
901 GTCACATCGT TCCAAAGCGg caaggaggca aggcagaaag ccgcccgcCgc
951 gcgcgaaacg ctggtGTCCG AAAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGGAGGCA GagcgttcCG CTGATTAAGG CCTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AGCAGGTGTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaacCGGC GAAGaggttt TGgaacggct gtccgtcCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCAAT CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGatttGG TTCATGCCgt cGCGCAGAtt tatcatttGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

```

g622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEQESMG AKLNALFORT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAIHLHY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGLDN DAYLYTVDDM
301 VNIIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVF LKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

```

m622.seq
1  ATGCAACTTA CCGCTGTCCG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCCGCCGC CCTGCCATAA GCCGTCGCCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTTCGG CGTCGCGTGC

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301 GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCCTATG GCTTCCGCTT CCGTCAAATT
501 GGCAGAACAG ATTTTCCCG ACATCGGCGA TTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAGG CATGGTGGAG CGTGCAATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTGATTGGC AGTGCCCGGT GACATTGAAG
851 CGGAAGTCGG CGATTTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGCCAGGCA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGCGGAG
1051 AAAGCGCGCA AACAGGTGTT GGAAATGCC ATGAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGGT TTCATGCCGT CGCGCAGATT TATCATTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRMLTVANRT LARAQELCDK LGVNAEPCLL SLDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMPL FMLDLAVPR DIEAEVGLND DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

m622.pep	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
m622.pep	70	80	90	100	110	120
	SEEIIRWLADYHSLPIEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
m622.pep	130	140	150	160	170	180
	RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEESMGAKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
m622.pep	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRMLTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
m622.pep	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
m622.pep	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
m622.pep	370	380	390	400	410	
	MKQLAKGATAEEVLERLSVOLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVOLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

a622.seq

```

1  ATGCAACTTA CCGCTGTCCG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCGTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGT TGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCTGTG CTAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAACTC GGTTCATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCG ACATCGGCGA TTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTGCCA CTTATTTGC CGCCAAAAGT
601 CCGCGGCTGA TGACGGTTC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTTG TCGGCAAAGG TATGGTGGAG CGCGCATGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAGTTGC CGAATTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCTG TTAATCAGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGTCTT GGAAATGCG ATGAAACAGC TGCCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGCGGG GGAAGAAGAT
1201 AAAGATTGG TTCACGCCG CCGCAGATT TATCATTGG ACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

a622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGLN DAYLYTVDDM
301 VNIVQSKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/a622 98.1% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
a622	MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
a622	SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
a622	SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
a622	RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVILENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVILENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq
 1 ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
 51 GATAATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTACTAC
 101 TCTCCGCGCG CTGCTGGGCA AAGGCatccc cgcgcTTTca ccgCTGGCTG
 151 CACcggCacc gCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTCCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
 251 cctgcctcat gatctTTtgg CattTTCccc aacnctgggt ggctcGGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTGTGtacc ATacggatgt gGcacAGacc
 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep
 1 MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPOXWWVGA
 101 VSSVFCSLVT IRMWRPES*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq
 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCT TACTGTTGGG
 51 TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTACTGC
 101 TCTCCGCGCG CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
 151 CACCGGCACC GCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTCCCG CGCAAAGCCA AAATATTTCGC CATCAGTATG ATGACCGCAT
 251 CCTGCCTGAT AATGTTTTCG CAGTTTCCCC AACGCTGGTG GGTcGGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTGTGCGCC ATATGGATGT GCGCAGGCC
 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep
 1 MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLMIFW QFPQRWWVGA
 101 VSSVFCSLVA IWMWRPES*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m624 . pep	HNWEQNGAVPRKAKIFAISM	MTASCLIMFWQFPQRWWVGAVSSVFC	SLVAIWMWRRPESX			
g624	HNWEQNGAVPRKAKIFAISM	ITASCLIMFWHFPQXWVGAVSSVFC	SLVTIRMWHRPESX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624 . seq
1   ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTCCC TGCTGTTGGG
51  TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCCG CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCCG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTGCGGGCG
301 GTTTCATCGG TTTTGTGTC CCTTGTCGCC ATATGGATGT GCGCAGGCC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624 . pep
1   MIRYLLIACG CISLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624 . pep	MIRYLLIACGCISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
a624	MIRYLLIACGCISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m624 . pep	HNWEQNGAVPRKAKIFAISM	MTASCLIMFWQFPQRWWVGAVSSVFC	SLVAIWMWRRPESX			
a624	HNWEQNGAVPRKAKIFAISM	ITASCLIMFWQFPQRWWVGAVSSVFC	SLVAIWMWRRPESX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625 . seq
1   ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625 . seq
1   atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtctTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCGCGCG
101 CGGtcgttcc CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAGGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gTAA
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625 . pep
1   MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
```


1000

51 VLSLGVPFKS PQTKMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPME ASAVPTASRA
51 VLSLGVPFKS PQTKMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTKMPPEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNMRKSNVQKAVILPX					
g625	PQTKMPPEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPME ASAVPTASRA
51 VLSLGVPFKS PQTKMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTKMPPEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNMRKSNVQKAVILPX					
a625	PQTKMPPEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTCC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCCGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCTG TTTCAATcgc TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

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```

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CatcgTACAT
601 ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1 MSGWLKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSL LAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
201 TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1 ATGTCCGGCC TTTGGAACCG CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AACTCTTCC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGCATCTT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTACCCTG TTTCATTGCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGCGCT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1 MSGWLKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSL LAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

```

          10      20      30      40      50      60
m627.pep  MSGWLKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG
          |||||
g627      MSGWLKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG
          10      20      30      40      50      60

```


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	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVS	LVHDTAGHPINVMYFWMSGILSAFLDNAPT				
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVS	LVHDTAGHPINTMYFWMSGILSAFLDNAPT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMG	SVFMGALTYIGNAPNFMVKAIAEQRGVPMP				
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMG	SVFMGALTYIGNAPNFMVKAIAEQRGVPMP				
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGGCC TTTGGAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTGGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCCTG TTTCATTCGC TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVS	LVHDTAGHPINVMYFWMSGILSAFLDNAPT				
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVS	LVHDTAGHPINVMYFWMSGILSAFLDNAPT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMG	SVFMGALTYIGNAPNFMVKAIAEQRGVPMP				
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMG	SVFMGALTYIGNAPNFMVKAIAEQRGVPMP				
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

1003

a627 TFFGYMMWSVAFLTPVFIVHTLIFVFKLLX
 190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
 1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
 51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
 101 ACACATGGAT TTTACGTTTC GTACGGCGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
 301 GATTGAATCA GGTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
 351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
 1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRLNLTNRPR
 51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHVKP
 101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
 1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
 51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCCTTAC
 101 AAACATGGAT TTTGCGTTTC GTCAAACGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
 251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
 301 GATTGGATCA GGTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
 351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNLTNRPR
 51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHVKP
 101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQTWILRSVKRLNLTNRPR	LKSSAASLIM			
g628	MCVPLKPAGCGPPNSCVSILAAFS	DGTSAPAAALHTWILRSVRLNLTNRPR	LKSSAASIMM			
	10	20	30	40	50	60
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHVKPDWIRLRRTSSPLKFASASGA				
g628	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHVKPDWIRLRRTSSPLKFASASGT				
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

```

a628.seq
1  ATGTGCGTGC  CACTCAAACC  GGCCGGATGC  GGGCCGCCGA  ATTCATGTGT
51  TTCGATGTTG  GCAGCATTTT  CAGACGGCAC  GTCTGCGCCA  GCTGCCTTAC
101 ACACATGGAT  TTTACGCTCG  GTCAAACGGC  TCAATACCAG  CAAACCTCGT
151 CTGAAATCCT  CGGCGGCTTC  TTTGATCACA  ACCACAGGGT  CTGCCGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GGCGAACGGC  TCGGCATCGA
251 CGGCAGGGAT  TTTGCTGAAC  GGACGGGTAC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GATTGCGGCG  CACTTCTTCG  CCGCTTAAGT  TTGCCAACGC
351 TTCGGGCGCG  TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
1  MCVPLKPAGC  GPPNSCVSML  AAFSDGTSAP  AALHTWILRS  VKRLNTSKPR
51  LKSSAASLIT  TTGSAASGLV  SIALTKMANG  SASTAGILLN  GRVRSVAVHKP
101 DWIRLRTSS  PLKFANASGA  *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLA	AFSDGTSAPAALQTWILRSV	KRLNTNRPRLKSSAASLIM			
a628	MCVPLKPAGCGPPNSCVSMLA	AFSDGTSAPAALHTWILRSV	KRLNTSKPRLKSSAASLIT			
	10	20	30	40	50	60
m628.pep	TVGSAASGLVSIALT	KMANGSASTAGILLNGR	VRSAVHKPDWIRLRTSS	PLKFASASGA		
a628	TTGSAASGLVSIALT	KMANGSASTAGILLNGR	VRSAVHKPDWIRLRTSS	PLKFANASGA		
	70	80	90	100	110	120

```

m628.pep  X
           |
a628      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
1  ATGACTGCca  aacCTTTTTC  CCTCAACCTG  GCcaaCCTCC  TGCTGCCggc
51  ggtatTGTTT  GCCGTCAGcc  tGtcggTCGG  cattgccgaT  TTCCGCTGGT
101 CGGATGTGTT  TTCGCTGTCC  GACAGCCAGC  AAGTGATGTT  CATCAGCCGC
151 CTGCCGCGCA  CGTTTGcgaT  TGTGTTGACG  GGCgcgtcga  tagcgGtggc
201 gGGGatgatt  atgcagATTC  TGATGCGCAA  CcgtTTTGTC  GAGCCTtcta
251 tggcgGGTGC  GGGCCAAAGT  gcgGCTTTGG  GTttgcttct  gAtgtccctg
301 ctgtgcctg  CcgCgcccgt  gccggtcaAA  ATGTCGGtag  Cgcgccgttgc
351 CGCGCTGATC  GGGATGTTGG  tctTtatgct  gctaataccgC  Cgcctgccac
401 cgacggcgca  gctgatgGTg  ccgCTGGTGG  Gg.ttATTTT  CGGCGGCGTG
451 GttgaGGCGG  TGGCGACGTT  TGTCGCGTAT  GAGTTTGAGA  TGCTGCAAAT
501 GTTGGGCGTG  TGGCAGCAGG  GCGACTTTTC  AAGCGTGCTG  CTGGGGCGGT
551 ACGAGCTGCT  TTGGATTACG  GGCGGTTTGG  CGGTGTTTGC  CTACCTGATT
601 GCCGACCGGC  TGACGATTTT  GGGGCTGGGC  GAGACGGTGA  GCGTGAATTT
651 GGGTTTGAAC  CGGACGGCGG  TGTGTGTCG  GGGTTTGATT  ATTGTGGCAC
701 TGATTACATC  GCTGGTCATT  GTAACGGTCG  GCAATATTCC  GTTTATCGGG
751 CTGGTCGTGC  CGAATATCGT  CAGCCGCTG  ATGGGCGACA  GGCTGCGCCA
801 AAGCTGCCT  GCGTCGCCC  TCTTGGGCGC  GTCTTTGGTT  TTATTGTGCG
851 ACATTATCGG  ACGCATGATT  GTGTTTCCGT  TTGAAATTCC  GGTCTCCACG
901 GTTTTGGTG  TGTGGGTAC  GGCTTTGTTT  TTGTGGCTTT  TGTTAGGAA
951 ACCCGCTAT  GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
1  MTAKEPFSNL  ANLLPAVLV  AVSLSVGIAD  FRWSDVFSLS  DSQQVMFISR
51  LPRTEAIVLT  GASIAVAGMI  MQILMRNRFV  EPSMAGAGQS  AALGLLMSSL
101 LLPAAPLPVK  MSVAAVAALI  GMLVFMLLIR  RLPPTAQLMV  PLVGXIFGGV

```


m629.seq

m629.ppt

Homology with a predicted ORF from *N. gonorrhoeae*

		10	20	30	40	50	60
m629.pep		MTAKPFSLNLTNLLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
		:	:	:	:	:	:
g629		MTAKPFSLNLANLLLPVLFVAVSLSVGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
		10	20	30	40	50	60
		70	80	90	100	110	120
m629.pep		GASMAVAGMIMQILMRNRFVEPSVMVGASQSAALGLLLMTLLLPAPLPARKMSVAAVAALI					
		: : : : : : : : : :					
g629		GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLLMSLLLPAPLPVKMSVAAVAALI					
		70	80	90	100	110	120
		130	140	150	160	170	180
m629.pep		GMLVFMLLIRRLPPTAQLMVPLVGIIFFGGVIEAVATFIAZENEMQLMGVWQOGDFSSVL					
		: : : : : : : : :					
g629		GMLVFMLLIRRLPPTAQLMVPLVGXIFFGGVVEAVATFVAYEFEMQLMGVWQOGDFSSVL					
		130	140	150	160	170	180
		190	200	210	220	230	240
m629.pep		LGRYELWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSIVI					
		: : : : : : : : :					

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```
g629      LGRYELLWITGGLAVFAYLIADRILTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
          190      200      210      220      230      240
          250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVPNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFPEIPVST
          250      260      270      280      290      300
          310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
          310      320
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```
a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTGCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGGCAT TGTGTTGACG GGCGCGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTGTG GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTGCTTCTT GATGTCCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTATTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTTG CTCGGACGGT
551 ATGAAGTGTG GTGGGCAACG GGGATTTTGG CTTGTGTTGC CTATTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGTCG GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATAGCGGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GCGTTGTTT TTATGGCTTT TGTTAAGGAA
951 ACCTGCTCAT GCCGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```
a629.pep
1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLLMSL
101 LPPAAPLPVK MSVAAVAALI GMLVFMLLR RLPPTAQLMV PLVGIIFFGV
151 VEAVATFIAY ENEMQLMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVENIISRL IGDRLRQSLP AVALLGASLV LLCIDIIGRVI VFPFPEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*
```

m629/a629 95.7% identity in 322 aa overlap

```
          10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
          10      20      30      40      50      60
          70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLLPAAPLPKMSVAAVAALI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLLPAAPLPVKMSVAAVAALI
          70      80      90      100     110     120
          130     140     150     160     170     180
m629.pep  GMLVFMLLRRLPPTAQLMVPLVGIIFFGVIEAVATFIAYENEMQLMLGVWQQGDFSSVL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```


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```

a 629      GMLVFEMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAZENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep   LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           |||||  ||  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep   VTVGNIPFIGLVVFNIIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      VTVGNIPFIGLVVFNIIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEPVST
           250      260      270      280      290      300

           310      320
m629.pep   VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||
a 629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccattgt tttacggcat
51  gtacaacgtc GCGGCACAGG CATTTCGGTGC CTTAACGCC CATTtgcgtgc
101 aacaaagcat cgcccacgac ggcaattacg ccttcgccaa cgctttgggc
151 atcaatatgt ccccgaaGc ggcggtgtTg ggcaaatgc tgttcgGCGC
201 GATttacttc ctgccgattt acgcgaccgt attTATTGTG Gcggtcttct
251 ggGaagtCTT GTTCGCATCc gtACGCAAAc ACGAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCGCCCA CGCTGCCGCT
351 GTGGCAGCGC GCTTTGGGTA TTTCTTTCGG CGTTGTGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCGC
451 GCCTTCCTGT TCTTCGCTA CCCCGCCAaC TTGAGCGGCG ATCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGCGCAaC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAcGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCG GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGGTT TATCGTGTG GCCCGCATCG
701 CTtcttgGCG CATTATTGcC ggCGTGATGA TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 ctgggtacat ggcacttggT GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLQOSIAHD GNYALANALG
51  INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAS VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLEFFAYPAN LSGDAVNTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFFIV ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWWRDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GCGCGCAGG CATTTCGGTGC GTTAACGCCT GATTtgcgtgc
101 AACAAAACAT CGCCAACGAC TGGCATTACG CTTTGCCTAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GCGCGTGTG GACAAAATGC TGTtTGCGC
201 GATTTTACTT CTGCCGATT ACGCCACTGT ATTGTGTGTG GGCGGTTTCT
251 GGAAGTTTT GTTCGCCACC GTGCGCAaC ACGAAATCAa CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCGCCCA CGCTGCCGCT
351 GTGGCAGCGC GCTTTGGGTA TTTCTTTCGG CGTTGTGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCGC
451 GCTTTCTGT TCTTCGCTA CCGTCCAaC TTGAGCGGCG ATCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGCGCAaC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAcGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCG GGCTCCATTG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGGTT TATCGTGTG GCCCGCATCG
701 CTCTTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TCGGATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC

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801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
 851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
 901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
 951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
 1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep

1 MMILVWLALF PAMFYGMYNV GAQAFGALT PDLLQONIAND WHYAFANALG
 51 INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVL FAT VRKHEINEGF
 101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
 151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVTGQTIT
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
 251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMDPVS ASFTNVGKWW
 301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
 351 ARSNG*

m630/g630 93.5% identity in 275 aa overlap

m630.pep	10	20	30	40	50	60
	MMILVWLALFPAMFYGMYNVGAQAFGALT	PDLLQONIANDWHYAFANALGINMSSEAGVS				
g630	10	20	30	40	50	60
	MMILVWLALFPMPFYGMYNVGAQAFGALT	PDLLQQSIADHGNALANALGINMSPEAGVL				
m630.pep	70	80	90	100	110	120
	DKMLFGAIYFLPIYATVFVVGGFWEVL	FATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
g630	70	80	90	100	110	120
	GKMLFGAIYFLPIYATVFIVGGFWEVL	FASVRKHEINEGFFVTSILFALIVPPTLPLWQA				
m630.pep	130	140	150	160	170	180
	ALGISFGVVVAVEVFGGTGKNFMNPALAGRA	FLFFAYPANLSGDAVWTAVDGYSGATALA				
g630	130	140	150	160	170	180
	ALGISFGVVVAVEVFGGTGKNFMNPALAGRA	FLFFAYPANLSGDAVWTAVDGYSGATALA				
m630.pep	190	200	210	220	230	240
	QWAAHGADGLKNAVTGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
g630	190	200	210	220	230	240
	QWAAHGADGLKNAVTGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
m630.pep	250	260	270	280	290	300
	GVMIGMIAMSSLFNFIGSDTNAMFAMPWY	HLVVGGFAIGMLFMDPVSASFTNVGKWW				
g630	250	260	270	280	290	300
	GVMIGMIAMSSLINFIGSDTKAMFAM	----HLVHGTWTKDDYHSLYIK.				
m630.pep	310	320	330	340	350	
	YGALIGVMCVLIRVVNPAYPEGMMLAILFA	NLFAPIFDYFVAQANIKRRKARSNGX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq

1 ATGATGATT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GCGCACAGG CATTTCGGTG GTTAACGCCC GATTTCCTGC
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGCAAAATGC TGTTCGGCGC
 201 GATTTACTTC CTGCCGATT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
 251 GCGAAGTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGTGCCGCT
 351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
 401 TATTTCGGCG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
 451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
 501 GACGCGCGTT GACGGCTATT CCGCGCAAC CGCGCTGGCG CAATGGGCGG
 551 CACACGGTGC AGACGGCCTG AAAACGCCA TAACCGGTCA AACCATCACT
 601 TGGATGGATG CGTTATCGG CAACTGCCG GGCTCCATCG GCGAAGTCTC
 651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTT GCCCGCATCG

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701 CTTCTTGGCG CATTATTGCC GGC GTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTG
1001 CCCCATT TTT CGACTATTTC GTGCGACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQQSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMN PALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

m630/a630 98.3% identity in 355 aa overlap

      10      20      30      40      50      60
m630.pep MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQNIANDWHYAFANALGINMSSEAGVS
|||||
a630      MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQSIANDWHYALANALGINMSSEAGVL
      10      20      30      40      50      60

      70      80      90      100     110     120
m630.pep DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
|||||
a630      GKMLFGAIYFLPIYATVFIVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
      70      80      90      100     110     120

      130     140     150     160     170     180
m630.pep ALGISFGVVVAKEVFGGTGKNFMN PALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
|||||
a630      ALGISFGVVVAKEVFGGTGKNFMN PALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
      130     140     150     160     170     180

      190     200     210     220     230     240
m630.pep QWAAHGADGLKNAVTGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
|||||
a630      QWAAHGADGLKNAITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
      190     200     210     220     230     240

      250     260     270     280     290     300
m630.pep GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
|||||
a630      GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
      250     260     270     280     290     300

      310     320     330     340     350
m630.pep YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
|||||
a630      YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
      310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTGCGGT ATTTAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTCGAAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCTCA AACGACGCGC
201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAG

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301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
 351 TCTGCAATTT GATTTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
 401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

g635.pep

1 MTRRRVGKQN RIAIHSAYR KMVFAVFQI HDDGDFQLRE LFERQGIAPR
 51 LKTQIGHNAP HILKRRALHF LTQFFQHFFF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IPRFPTLQF DFSVNNRIIV KHRCSIQTIR QGSVPD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG
 201 GCATCTGCTC CTTATCCAGT TTTTAAACA CGTCCTCTTC CGTCAGCTTT
 251 TGCCCGTAAA AATTGTCAA AAGCGTCACC ACCGAAGCCG CCCCAGGGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep

1 MTQRRVGKQN RIAVYTAQYR EMIIIAVFQI HDDGDLQLCK LLERQGIAPR
 51 FKTQIRHNAP HILKRRGHLI LIQFF*HVLV RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIAPRFTQIRHNAP					
	: : : : : : : :					
g635	MTRRRVGKQNRIAIHSAYRKMVFAVFQIHDDGDFQLRELFERQGIAPRLKTQIGHNAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m635.pep	HILKRRGHLIQLFFXHVLFRLLPVKIVQKRRHRSRPAGKIQILLYNIEIAPFFPTLHF					
	: : : : : : : : :					
g635	HILKRRALHFLTQFFQHFFFRLLPVKIVQKRRHRSRPAGKIQILLYNIEIPRFPTLQF					
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRIIVDX					
	:					
g635	DFSVNNRIIVKHRCSIQTIRQGSVPDX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 CTCAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCCTCTTC CGTCAGCTTT
 251 TGCCCGTGAA AATTGTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep

1 MTQRRVGKQN RIAVYTAQYR EMIIIAVFQI HDDGDLQLCK LLERQGIAPR
 51 LKTQIRHDAP HILKRRALHL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

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m635.pep    MTQRRVVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIQIAFRFKTQIRHNAP
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a635        MTQRRVVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIQIAFRFKTQIRHDAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m635.pep    HILKRRGHLLLIQFFXHVLFQRLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
              |||||:|||||:| |||||||||||||||:|||||:|||||:|||||:|||||
a635        HILKRRGHLLLIQFFXHVLFQRLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
              70      80      90      100     110     120

              130
m635.pep    DFSISNRRIIVDX
              |||||||||||
a635        DFSISNRRIIVDX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc attGTAGGCA AAAACGCCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTAGCATGA TGCCTAATC GCGGCTGCCG ACGGCGATAT TGTGCAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGaattcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCT GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGGcgccgg CgcgtTCCAA ACGGTAACGC CATTCGCCG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTGTC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCC GCTCTTGTC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GGCGCGGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCACG
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCCGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCCTGTTT
951 TATAGCGAAA CCGCCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGNALARF VDNIVVNIGI VDIVHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVIH VDGETQVAEA VVFIGVVRAG
101 IGNNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAEIR IKNIVFNQG ARGFFEINT GIHCWQAHTG TGNGQVAERY
201 VRRVYGYGTP ALVFFDGCCT VGRPFNRNRF VDIKFGLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGVHSHVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTAGCATATA TGCCTGATC GCGGCTGCCG ACGGCGATAT TGTGCAATAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGC AAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCT GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACC GGG TGCCTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCC GCTCCTGTCG CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```


1012

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep

```

1  MIGKEFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFGVVRAG
101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151 RTMQIYADRI IQNIIVFNQG ARGSF FEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251 GAGKCGIPIS IIGS*

```

m638/g638 88.2% identity in 254 aa overlap

m638.pep	10	20	30	40	50	60
	MIGKEFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY FEPLGKHQHI					
g638	MIGGQFIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVEH FEPLGKHQHI					
m638.pep	70	80	90	100	110	120
	AHIVAHGNIA ADFAVVG VHI VDGETQIAE AVVFGVVRAG IGKNAVPPFG NVVADDLRTG					
g638	AHIVAHGNIA ADFAVVG VHI VDGETQVAE AVVFGVVRAG IGKNAVPPFG NVVADDLRTG					
m638.pep	130	140	150	160	170	180
	CVPNGNAVAA LVHAQSRVAD DFILAHHRIG RTMQIYADRI IQNIIVFNQG ARGSF FEINT					
g638	RVPNGNAIAA LIHAQGR IADDFILAHHRIG RTMKVYAE RI IQNIIVFNQG ARGSG FEINT					
m638.pep	190	200	210	220	230	240
	GIHCGQAHTG TGNGQVAERY VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA					
g638	GIHCGQAHTG TGNGQVAERY VRRVYGYGTP ALVPFDGCCT VGRPFNRNRF VDIKFGLIYA					
m638.pep	250	260				
	GSQFERIARP GAGKCGIPIS IIGSX					
g638	GSQFDRIARP GAGKCNFGKV LRGNVDDGCRCLKNAAGGKYQHGLQPYTERGCVHSVPLF					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq

```

1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTTAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151 TTTAGCCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCCACGG
201 AAATATTGCC GCTGATTTTCG CTGTCGTTGG TGACATATA GTGGACGCGG
251 AAACGCAAT CGCTGAAGCG GTTGTTTTAA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351 GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACC ATCGCATCGG
451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGTAACGC GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
651 TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
701 AGTTTGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCGCCCCG
751 GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep

```

1  MIGGQFIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NIVADDLRTG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151 RTMQIDADRI IQNIIVFNQG ARGSF FEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGLIYA GSQFERIARP

```


1013

251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGLIIGKYALCLVDNVVNVIGIVDIVEHNLIAAADGDIVEYFEPLGKHQHI					
a638	MIGGQFIVVGIVGKNALARFVDNVVNVIGIVDIVEHDALVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60
m638.pep	AHIVAHGNIAADFVAVGVHIVDGETQIAEAVVFVGVVRAGIGKNAVPPFGNVVADDLRTG					
a638	AHIVAHGNIAADFVAVGVHIVDGETQIAEAVVFIGVVRAGIGKNAVPPFGNIVADDLRAG					
	70	80	90	100	110	120
m638.pep	CVPNGNAVALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIIVFNQARGSFEEINT					
a638	RVPNGNAIALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQARGSFEEINT					
	130	140	150	160	170	180
m638.pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCCTVGRPFNNRNFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGCRTVGRPFNNRNFVDVKFGLIYA					
	190	200	210	220	230	240
m638.pep	GSQFERIARPGAGKCGIPISIIGSX					
a638	GSQFERIARPGAGKCGIPISIISWX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGCGGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTCCAAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAA CAATATAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTC GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCAGC ACAATATTAT
501 CAACAAAGCG GGCAAGTGGC TTTTGGCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTTCCGCGCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGCGCATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGCGAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAFG AOVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEVSGN ISVGNMNGYV LMFSERLKVF DNIAGVSRD*
151 GIMLNYYVNS DIHDNIINKA GKCVFAYNAN YDKLSANHEE NCQIGMHFTA
201 AIEGTSLEHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA FKIQTRYQAM KDELLKEAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

m639-1.seq

```

1  ATGAGCGCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AACTGCCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGAA
201 CGCACCCGGT GCGCAGGTCG TCGGCAACGA CATTTCCAAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACA CCTACAAAAA CAACCGCTTC
301 AGCGATTTCG GTTTCGCCGT CCACTATATG TACACCAACG ACACGGAAT
351 CAGCGGCAAT ATTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCG GATATTACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGGC TATTTGCCTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAA TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCCACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAG TTCCCGCCG TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
1001 AATGGGCGAG GCGGAAAAC GGTTCCTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNMGGYV LMFSERLKVF DNIAVGSRDQ
151 GIMLNIVNYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF PPAVLPGGVV
301 DSKPLMKPYA PRIQTRYQAM KDELLKEVET RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMGGYVLMFSERLKVF DNIAVGSRDQXGIMLNIVNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGGYVLMFSERLKVF DNIAVGSRDQXGIMLNIVNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTA AIEGTSLHDNSFINNGSQVKYVSTRFLDSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTSLHDNSFINNESQVKYVSTRFLDSEGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSDSAYRPGI IDQIIWRAPVSRLLMNSPAISIVKWAQAF PPAVLPGGVV					
m639-1	NSAFDLNGDGFSDSAYRPNGI IDQIIWRAPVSRLLMNSPAISIVKWAQAF PPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLKEAETRQSERGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

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```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGCCTCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CCGCGCCCGG GCGCAGGTCG TCGGCAACGA TATTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACACA CCTATAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAGCGGCT CAAAGTGTG GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCG GATATTCAGC ACAACATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCGCCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTACGCA CGCGCTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CCGGCGACGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 CCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAA TTTCCCGCCG TTTTGCCTGG CCGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAAA AGTCGAAACG CCGCAGTTGG
1001 AATGGGCGAG GCGGGAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVMNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSISGN ISVGNMGGYV LMFSEKLVF DNIAGVSRDQ
151 GIMLVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHF NCQIGIHFTA
201 AIEGTSIHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPN IIDIWRAPV SRLLMNSPA ISIVKWAQAQ FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a639-1.pep	NGVTVMNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVMNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a639-1.pep	ISVGNMGGYVLMFSEKLVFDNIAGVSRDQGIMLVNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGGYVLMFSEKLVFDNIAGVSRDQGIMLVNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a639-1.pep	YDKLSANHFENCQIGIHFTAIEGTSIHDNSFINNESQVKYVSTRFLDWESEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAIEGTSIHDNSFINNESQVKYVSTRFLDWESEGGHGNYSW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a639-1.pep	NSAFDLNGDGFGDSAYRPNIGIIDQIWRAPVSRLLMNSPAISIVKWAQAQFPAVLPGGVV					
m639-1	NSAFDLNGDGFGDSAYRPNIGIIDQIWRAPVSRLLMNSPAISIVKWAQAQFPAVLPGGVV					
	250	260	270	280	290	300
	310	320	330	340		
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

1016

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1   ATGATTTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCAGC
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTGCA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCAGCGT
501 GCGCGCGGGC GACATCATCA GcggTGCgAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCGGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCAGC CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTGTGA TGTGCTTGTG GTCAGCCAGC CTTCCATCGG TAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACC CGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCGCGGTT TTAAGAAGT TTCTTGGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTTGACGGT GCGGAGCCGT GCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1   MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VELTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNDSIQRS YKVIANQYRL
201 GSDKALQTAS ASDVREAAPA SETPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGD PD DTFIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGSYVRGGI FDRIEMIQGE
351 NSFRFTDAQH ERVVELSAAD APRFKEVSF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1   ATGATTTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCTTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCGTGATT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCAGC
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1   MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VELTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKS	IGISGIVMSC	FSIKRMSAFR	ARITAFFAAF	VELTAALPAY	AERLPDFLAK
g640	MIHIISILKS	IGISGIAMSC	FSIRMSAFR	ARITAFFTAF	VELTAALPAY	AERLPDFLAK
	10	20	30	40	50	60
	70	80	90	100	110	120

1017

```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAN
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||||||||||||||||
g640          DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIGLNFIKNPPTPSVAPGDIISGATVTL
                130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTT TGCCGCCTTT GTCTTTTGA CGCGGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGTTGCCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGAGC GAAATTGGT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

                10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
                10      20      30      40      50      60

                70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
                ||||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAK
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                ||||||||||| |||||
a640          DGTIAGAKLVDHHEPIMLIGIPH
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGGTTTTG CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTGCCCCG CTATCCGCAA
101 TATCGGAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG TGTTCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTCG AGGGCGCAGG CGTCGGTCAG GGTGTGTTC
251 TGCAGGAAGC TCGGATGTC TTCGGGCAA GCGTAgtCgc gGGCAACGGC
301 GGcaaagcgG ACatcggTtT Gcacggcgtc gagCAGGGtt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGGCGgc gTAAGTGTAT
551 TCCGTGGCGa ggGTTTTGac gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggCGGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCGG
651 AAACCTGATG GCGGCGTTGG ATTTCCGGCG GTTCGTAATC GACGAATCTG

```


1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTCAGGCA TTTCCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGCAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTCCGGCG
1051 GttgACGTAA ATGGTTTgtt cgtcggtata ttcgtagcag gactgcaTTT
1101 CCGGTGCAAT cgCcgcgccg gaggtTtcgg gttcggtaAc gcccaaacgg
1151 cggctttcgc ctTTGAAAT CATGTCCAAA CCTTGTGCGA CTTGCgcttc
1201 gccgccgaac tCTTGACAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

```

g642.pep
  1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADVQQEKG
 51 GVVFVLLYED KKSDDFADE DFLQAGVGVQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WVSFAFTLRA QEFLOHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFNH
251 AVRHADQLQA AADKDVLEA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRALPVFRG
351 VDVNGLFVG FVAGLHFACN RRAGGFGFGN AQTAFAFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

```

m642.seq (partial)
  1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
 51 CTTTGC GGAT GTCGTT CAGC AGGAAGGCTG CCGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GCGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTT CTGCAGGAAG CTGCGGATGT
201 CTTACGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGCGGCT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CCGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTTCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGCGGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCGGCGCGG
601 GATTTGCGGG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCAGGCG GGTTCGAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGAGC GGATGTATGT TTTGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGAATGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTTGAAAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTTGCAAT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

```

m642.pep (partial)
  1 ACRRICPLPA ISAVQYIFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
 51 QGAGIGQGVF LQEAADVFRQ SVVAGDGKKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFQIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVFSQI FKDVFNHNAV HADQLQAAAD KDVLERAQTG
251 SVALGEFHG GCRHFGIDAV DGVTGGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFVV GLHFACNRRR
351 GGFPGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP

```


1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VVQEGCGVFVFLRYED		
g642							
	10	20	30	40	50	60	
m642.pep	40	50	60	70	80	90	
	KESGDDFADKDFLQ	GAGIGQGVFLQEAADV	FRQSVVAGDGGKAGIGLQ	AVEQGLVFLVQLH			
g642							
	70	80	90	100	110	120	
m642.pep	100	110	120	130	140	150	
	ACFFFFGGGADKL	VVNFGIKHIVRAFKN	REGADVDS	DIAGGVS	AFKTLRTQ	EFLQHLRGG	
g642							
	130	140	150	160	170	180	
m642.pep	160	170	180	190	200	210	
	VSVFRGEGFDDVRL	HQLMGDGNRRNGMAD	VAVKNLGNLMAAPD	FAAFVIDE	FVVDVADVS		
g642							
	190	200	210	220	230	240	
m642.pep	220	230	240	250	260	270	
	FQIFKDVFN	NAVRHADQLQAAADK	DVLER	AQTGS	VALGEFHHGGCR	HFGIDA	VDGVT
g642							
	250	260	270	280	290	300	
m642.pep	280	290	300	310	320	330	
	QAFGCEGFAADV	CFGDEQQVDDFGE	FAVFALFGGNEE	EVALRVALP	VFRGVDV	NGLSVDI	
g642							
	310	320	330	340	350	360	
m642.pep	340	350	360	370	380	390	
	FVVG	LHFACNRRAGG	FGFGNTQTAA	LAFENHLQ	TLRDLRFIAE	LLQWLQHQ	RAFDAGTOR
g642							
	370	380	390	400	410	420	
m642.pep	400						
	NGHAVMPRNP						
g642							
	430						
	NGHAVMPRNPX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1  GCCTGCCGCC GTATTGCCG GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTCCGGAT GTCGTTGAGC AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTGG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCCGATGT
201 CTTCCGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAATTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGCGCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGC CGGGCGG CGTAAGTGT TCCGTGGCG AGGGTTTGA
501 CGATGTTGCG CTCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGC GCGGCCG
601 GATTTCGCGG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCATAA TGCCGTGCGT CATGCCGATC

```


1020

```
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTGCAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GCGGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCGCGG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCCGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G
```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```
a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVFSQV FKGVEHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVRGVDV NGLSVGIFVV RLHFSGNRRA
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP
```

m642/a642 95.8% identity in 407 aa overlap

```
10 20 30 40 50 60
m642.pep ACRRICPLSAISAVQYVFADVVQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
||||| :|||||
a642 ACRRICPLSAISAVQYVFADVVQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
10 20 30 40 50 60

70 80 90 100 110 120
m642.pep LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLNVNFGIKHIV
||||| :|||||
a642 LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLNVNFGIKHIV
70 80 90 100 110 120

130 140 150 160 170 180
m642.pep RAFKNREGADVDSDIAGGVSFAKTLRTOEFLQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
||||| :|||||
a642 RAFKNREGADVDSDIAGGVSFAKTLRAQEFQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
130 140 150 160 170 180

190 200 210 220 230 240
m642.pep RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVFSQIFKDVFNHNAVRHADQLQAAAD
||||| :|||||
a642 GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVFSQVFKGVFNHNAVRHADQLQAAAD
190 200 210 220 230 240

250 260 270 280 290 300
m642.pep KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
||||| :|||||
a642 KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
250 260 270 280 290 300

310 320 330 340 350 360
m642.pep GEFVAFALFGGNEEEVALRV ALPVRGVDV NGLSVGIFVVRHLHFSGNRRAGGFGFGNTQT
||||| :|||||
a642 GEFVAFALFGGNEEEVALRV ALPVRGVDV NGLSVGIFVVRHLHFSGNRRAGGFGFGNAXT
310 320 330 340 350 360

370 380 390 400
m642.pep AALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQRNGHAVMPRNP
||||| :|||||
a642 AALAFENHVQTLCDLRFIAELLQWLQHQRAFDAGTQRNGHAVMPRNP
```


1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

g643.seq

```

1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
51  gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTCCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagaTGgTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGat
351 GACCTGCGCg aGTGtTCCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTG a

```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

g643.pep

```

1   MVLPLMLLAT IRSATLTIXR LAMLNRVSPS TTRWMLAWSG EVSASPSAAL
51  ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGGMTCA SVAVWVSDGM AVCFSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

m643.seq

```

1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGgTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCCGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

m643.pep

```

1   MVLPLMLLAT IRSATLTIL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*.

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTIXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
g643	MVLPLMLLATIRSATLTIXRLAMLNRVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m643.pep	LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
	: :					
g643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFGGMTCA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMVAVCFVSX					
g643	SVAVWVSDGMVAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

a643.seq
 1 ATGGTGTTC CTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
 51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
 101 GGATGCTGGC ATGGAGCGGG GAGATTTTCG CTTGCGCCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
 201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
 351 GATCTGCGCG AGTGTGCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
 401 TTTCCGTTTG A

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

a643.pep
 1 MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
 51 ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFSV*

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGTICA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMVAVCFVSX					
a643	SVAVWVSDGMVAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

g644.seq
 1 ATGCCGCTCG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
 51 GTTTAGAAAA TTAACCTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCCGCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
 201 ATTcCCCCGc ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAC ACGGCGGGCG CAAGGCGAGT CAGTTTGAAA TCCAAGAAGT
 351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCTCTGC AAGagttcgg cggcgaaagcG
 451 CAAGTCGCAC AAGGTTTGGA CATGATTTTC AAaggcgaaa gccgcccgtt
 501 gggcgTtacc gaacccgaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
 551 agtcctgcta cgaatatacc gacgaacaAA CCATTTACGT caaCGCCGCG
 601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgcccgaA
 651 agagcgcaaa aacGGcaaac tcgcccgaagt CATCGACCTG CTGCTCGTCC
 701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CCTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCGTG CAACCGCCGT
 801 GATGAAACTC TCCCGGGCGG ACGCTGCGCG TTGCGCGCGG TTCCAAAAACA
 851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
 951 CGTCGATTAC GAACGCGCGG AAATCCAACG CCGCCATCAG GTTTCGAAA
 1001 TCCTTTACCG CTACGTCTGC CATTCCGTTT CGcccgtegc GCccgTCGCC
 1051 CATCAATTGA TGGAGCGGAA catcgTCAAA ACcctCGCCA CGGAATACAC
 1101 TTAcgcCGCC GCGCAAATGT TGCAAAAACT CTTGGCGCGG AAGGGTTTTG
 1151 AACGCGGACA CCCAGCGGCG AATATCGCCA TCGATATCCG CCCCTTCACG
 1201 ATTTTGAAGC GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAATT
 1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAA
 1301 accaaaCCCT Getcgagcc gtgCAAaccg atGTcgettt tgCCGCGTT
 1351 GCCcgcGacT ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACC GACGCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

1023

1451 TCGCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep

1 MPSEPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLDMIF KGESRRLGVT EPETSGAIA REMQSCYEYI DEQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHQQ VSEILYRYVC HSPVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEEAGIK LDKNQTLDDA VQTDVRFPAV
 451 ARDYALPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQEEHEDTTA
 501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq

1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG CGCGTTTGAC CGGCCGCCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAGCACA TCGAATCCGC
 201 ATTCCGCGCG ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGCGAGC CAGTTTGAAA TCCAAGAAGT
 351 CcTGCAGATT CGCGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
 451 CAACTCGCGC AAGGTTTGGA GATGATTTTC AAAGGCGAGG CGGCGGGTTT
 501 GGGTGTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCCGG
 601 AAATACTGGC AGGGCAACTC GCAAGCGAC TTCCTCCTCG TTGCCGCCAA
 651 AGAGCGCAAA AACGGCAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
 701 CCAAACATA CATCCGCTGC GAAACCCCTG CATCGAAGG CTTGCGCGCC
 751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCTG CAACCGCGCT
 801 GATGAACTC TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
 851 TCTTTATCCG CAGCGCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
 951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
 1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCTGTTGC CCCCGTCGCC
 1051 CATCAGCTGA TGGAGCGGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCCGCC CGGCAATGT TGCAAAAAC CTTGGGTGCG AAGGTTTGTG
 1151 AACCGGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACACACAGTT
 1251 TGTCCGCCGC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
 1301 ACCAACCCCT GCTCGACCGC CTGCAAAACG ATGCCCGCTT TGCCGCCGTC
 1351 GCCCGCGACT ACACTTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACC GATGCCGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
 1451 TCGCCCGACT CTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep

1 MPSEPADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAIA REMQSYEYI DGQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSRL QLIGMTHGIM
 301 EYILDNLNRY VRNDIKFVDY ERREIQRHQQ VSEILYRYVC HSPVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
 401 IFEGPNDMLY AEIYDQFVRA TAEKEEAGMK LDKNQTLDDR LQTDARFAAV
 451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAKHEDTAA
 501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSEPADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
g644	MPSEPADCCPVHFVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					

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	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
g644	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKHGGRKGSQFEIQEVLRI					
m644.pep	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLQPLQEPGDEAQAQGLEMI FKGE GGLGVTEPETS GAAIA					
g644	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLQPLQEPGGEAQAQGLDMI FKGE SRR LGVTEPETS GAAIA					
m644.pep	190	200	210	220	230	240
	REMOSYYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
g644	190	200	210	220	230	240
	REMOSCYEYTDQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
m644.pep	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
g644	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFQNI FIRSRLQLIGMTHGIM					
m644.pep	310	320	330	340	350	360
	EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
g644	310	320	330	340	350	360
	EYILDNLNRYVRNDIFVDYERREIQRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
m644.pep	370	380	390	400	410	420
	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
g644	370	380	390	400	410	420
	TLATEYTYAAAQMLQKLLGAKGFERGHPAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
m644.pep	430	440	450	460	470	480
	TAAEKEAGMKLDKNQTLDDRLQTDARFAAVARDYTLPE DIRSFLQEHTLT DACALQKVFI					
g644	430	440	450	460	470	480
	TAAEKEAGIKLDKNQTLDDAVQTDVRF AAVARDYALPE DIRSFLQEHTLT DACALQKVFI					
m644.pep	490	500	510			
	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
g644	490	500	510			
	GKIIARLFVVFQEEHEDTAAFLNDIRKDILDCRYCGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

a644.seq

```

1  ATGCCGTCGTG AAAGGTCGCGC GGATTGTTGC CCGCGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG CCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCGAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTGTGTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCGC CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CPTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GGCATTGCC CGAGAAATGC
551 AATCTTACTA CGAATATACC GACGGACAAA CCATTACGTT CAACGCCGCG
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCGCT
801 GATGAAACTC TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA

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1025

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851 TCTTTATCCG CAGCCGCTCG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACGACCAATT
1251 TGTCGCGGCC ACCGCGAAG AAAAAGAAG AGGCATGAAG TTGGACAAAA
1301 ACCAAACCT GCTCGACCG CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCGACT CTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPERSADCC PAHFVVKFRK STLNCGRREFD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKYGGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYET DGQTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIFFIRSL QLIGMTHGIM
301 EYTLNLERI VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGTAG NIAIDIRPFT
401 IFEGPNOMLY AEIYDQFVRA TAEKEEAGMK LDKNQTLLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644/a644 97.3% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPERSADCCPAHFVVKFRKSTLNCGRREFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
a644	MPERSADCCPAHFVVKFRKSTLNCGRREFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	10	20	30	40	50	60
m644.pep	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
a644	LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
a644	LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQAQGLEMI FKGGGGLGVTEPETSGAAIA					
a644	AGHYGVPVXXXXXEGALVLQPLQEFGDEAQAQGLDMVFKGGGGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQAQGLEMI FKGGGGLGVTEPETSGAAIA					
a644	AGHYGVPVXXXXXEGALVLQPLQEFGDEAQAQGLDMVFKGGGGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	REMQSYEYIDGQTIYVNAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
a644	REMQSYEYIDGQTIYVNAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	REMQSYEYIDGQTIYVNAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
a644	REMQSYEYIDGQTIYVNAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIFFIRSLQLIGMTHGIM					
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIFFIRSLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIFFIRSLQLIGMTHGIM					
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIFFIRSLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQMEANIVK					
a644	EYILENLERIVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQMEANIVK					
	310	320	330	340	350	360
m644.pep	EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQMEANIVK					
a644	EYILENLERIVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQMEANIVK					

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSFLOEHTLTDACALQKVFI					
a644	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSFLOEHTLTDACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
a644	GKIIARLFVQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATGTCG ATGCCGGTTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCAGCG AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata cCTGTCTCC GCGTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTCACG
301 GCGAGGCGCG GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TGGCGGAAT CCGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGTGCGCAG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATT
501 TATGTCTGTC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGCGGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGGGCG AGTACGGCGA
701 CCTGTTTGCC GCCATCACC GCCACAAACG CGGCGCGAAG GCGCACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTAATCA CGGcggcgat ggcggcggc TGGTCTTCGG
851 TTTCTCTGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645 . pep

```

1  MMVLALGMS MPVSMMEQVS NTLNLCKKKS RMTCSRSSR SCPCATPIRA
51  SGRSVSSRSR IFSIVSTSLC RNTCPPLRS SRNTASRTL SLNGLTKVFT
101 ARRLGAVVI SEKSRPSSA MLRVRGIVA VMVMSTLAR RRLSCSFCRT
151 PKRCSSSIIN KPKFLNFMSS CTNLCPVITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKFAA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA cCTGTCTCC GCGTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGCGCG GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACCGGAAT CCGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCGAG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATT
501 GATGTCGTCC TGACCAAGT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGCGGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAAAGCGT GGTGCGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCATCACC GCCACAAACG CGGCGCGCAG GCGCACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTAATCA CGGCGCGCAT GCGGCGGCC TGGTCTTCGG

```


1027

851 TTTCTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep

```

1  MMMVLALGIS IPVSMMEQNS NTLNRCCKKS RMTCSRSSRSR SCPCATPMRA
51  SGRSVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTLP SLKGLTKVLT
101 ARRRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
151 PKRCSSSIIT KPFELNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKFCFA CCSTKSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMMEQNS	NTLNRCCKKS	RMTCSRSSRSR	SCPCATPMRA	SGRSVSSRSR	
g645	MMMVLALGMSMPVSMMEQNS	NTLNRCCKKS	RMTCSRSSRSR	SCPCATPIRA	SGRSVSSRSR	
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPLRSS	RNTASRTLPSL	KLTKVLTARRRLGAV	VEKSRSPSNA		
g645	IFSIVSTSLCRKNTCPPLRSS	RNTASRTLPSL	KLTKVLTARRRLGAV	VEKSRSPSNA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLAR	RRLSCSF	XRTPKRCSSSIIT	KPFELNLMSS	CTSLCVPITI	
g645	MLRVRGIGVAVMVRISTLAR	RRLSCSF	CRTPKRCSSSIIT	KPFELNLMSS	CTSLCVPITI	
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLL	KRERLATFTGK	SAKRSKFCAC	CCSTKSVVGA	STATCLPPIT	
g645	STVPSAMPSSAALVALLLL	KRERLATFTGK	SAKRSKFCAC	CCSTRSVVGA	STATCLPPIT	
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPHT	RRSIGFACVK	SLITAAMAAA	WSSVSSX		
g645	ATNAARRATSVLPKPTSPHT	RRSIGFACVK	SLITAAMAAA	WSSVSSX		
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq

```

1  ATGATGATGG TGTGGCGTT GGGAAATGTCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
251 CCGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAG TCGGCGAAGC GGTGCGCAAA
651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGTGCG AGTACGGCAA
701 CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AACGACATC GCCGACACAG AGGCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCTGCC TGGTCTTCGC
851 TTTCTTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep

```

1  MMMVLALGMS IPVSMMEQNS NTLNRCCKKS RMTCSRSSRSR SCPCATPMRA

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1028

51 SGSRVSSRSR MFSMVSTSLC RKNTCPPLS SRNTASRTLPL SLNGLTKVLT
 101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
 151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
 201 RERLATFTGK SAKRSAKFA CCSTRSVVGA STATCLPPIT ATNAARRATS
 251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

m645/a645 96.9% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMVEQSNLTNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR					
a645	MMMVLALGMSIPVSMVEQSNLTNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPLSSRNATASRTLPSLKGTLKVLTAARRLGAVVISEKSRSPSNA					
a645	MFSMVSTSLCRKNTCPPLSSRNATASRTLPSLKGTLKVLTAARRLGAVVISEKSRSPSSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLARRLSCSFXTPKRCSSSIITKPKFLNLMSSCTSLCVPITI					
a645	ILKVRGIGVAVMVRMSTLARRLSCSFXTPKRCSSSIITKPTFLNFMSSCTSLCVPITI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT					
a645	STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT					
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX					
a645	ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

g647.seq
 1 ATGCAAAGGC TCGCCGAGA CGGCATCCAA ATCTTTTTTG TAGTGTCGA
 51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
 101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
 151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
 201 GGACACCGTT TTTGCCGAGA TAGTAGCGT AGTTGATGAC ACCGATGCCG
 251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
 301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

g647.pep
 1 MQRLAADGIQ IFFVGVGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
 51 GFKGTVGQTE RGTVAVADTV FRQIVGVVDD TDAERTAVHS RGRGIFYRIS
 101 LII*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

m647.seq
 1 ATGCAAAGGC TCGCCGAGA CGGCATCCAA ATCTTTTTTG TAAGTGTCGA
 51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
 101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
 151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
 201 GGACACCGTT TTTGCCGAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
 251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
 301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

m647.pep
 1 MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

1029

51 GFKGTVGQTE RGTVAADTV FRQIISIVNH ADAERTAHS RGRGFYRIS
101 LII*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQR	LAADGIQ	IFFVSDGQ	FALRINGLV	KERARTV	FFGKVCRCFEQVILYGFKGTVGQTE
g647	MQR	LAADGIQ	IFFVSDGQ	FALRINGLV	KERARSV	FFGKVCRCFEQVILYGFKGTVGQTE
	10	20	30	40	50	60

	70	80	90	100
m647.pep	RGTVAADTV	FRQIISIVNHADAERTAHS	RGRGFYRIS	LIIX
g647	RGTVAADTV	FRQIVGVDDTAERTAVHS	RGRGFYRIS	LIIX
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq
1 GTGCAAAGGC TC GTTACACA CAGCGTCCAA GTCTTTTGTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC
201 GGACACCGTT TTTGCCCAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep
1 VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS
101 LII*

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQR	LAADGIQ	IFFVSDGQ	FALRINGLV	KERARTV	FFGKVCRCFEQVILYGFKGTVGQTE
a647	VQRL	VTHSVQV	FFVGVDGQ	FALRINGLV	KERARTV	FFGKVCRCFEQVILYGFKGTVGQTE
	10	20	30	40	50	60

	70	80	90	100
m647.pep	RGTVAADTV	FRQIISIVNHADAERTAHS	RGRGFYRIS	LIIX
a647	RGAVAVADTV	FRQIIRIVDHADTERTAHS	GGTRGFYRIS	LIIX
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51 CGACGTTTGT AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC
101 GTGGAACAACA GGTCCGCGAGC CGGAATGATA CGCTTGCCTA TGTTCGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAA TTCGTCTTGG TCGGCAAAAA
201 ACCTTCGTA CAACCCCGAA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATT GCACGCCATA
301 ATCAAGCTGG CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCACC TTGCGAACA GATTGACCG CCGCCTGAAA
451 CATCTTAAAG AAGGGAATGC AGCCGGTATG CCGGGCTTCA CCGCCCGGA
501 TTTGCTGTC CAGCCCGCG ATACGTCCGG CATTGATGCC GATGCCCGCG
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGATTCAA TCAGCACACA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1030

```

1  MNRRNARIER AVRIIVIDVL NVDAPGPGTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVIDLHAI
101 IKLADTVVFH APVVFQHQQA FGFMPPQGV E QGCRAAAHAT LRTRFDRRLK
151 HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTGT AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCGCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCCGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCGGG CATGTAGGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIIVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
101 IKLTDTVVFH TAVVFQHQQA FGFMPPQGV E QGCRAAAHAA LRTRFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

m648.pep	10	20	30	40	50	60
	MNRRDARIERAVRIIVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
g648	: : : : : : : : : :					
	10	20	30	40	50	60
m648.pep	70	80	90	100	110	120
	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
g648	: : : : : : : : :					
	70	80	90	100	110	120
m648.pep	130	140	150	160	170	180
	FGFMPPQGV E QGCRAAAHAA LRTRFDRRLKHFKENAGM PRFAAPDFAV QTADTSGIDA					
g648	: : : : : : : : :					
	130	140	150	160	170	180
m648.pep	190	200	210			
	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
g648	: : : : : : : :					
	190	200	210			
	DARALGNVFHNRAGSGIDGIQTIVAFNQHTAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTGT AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGCTTCG CCGCCCCGGA

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1031

501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCCGA
 551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCT TCGCATTCTGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQVE QGCRAAAHAT LRTGFDCLRK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQORNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648	FVLVGKKRFVQSRNLVGRKQORNVAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPQVEQGCRAAAHAALRTGFDRLKHFEKGNAAGMPREFAAPDFAVQTADTSGIDA					
a648	FGFDMPQVEQGCRAAAHATLRTGFDCLRKHFKEGNAAGMPCFAAPDFAVQSADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
a648	DARTLGNVFHNRAGSGVDGIQAVVAFDQYAAAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACCTGC
 51 CGCTGCCCGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCAGCA
 101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC CGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECKRYLER
 51 RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCRAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTC GGACTGGTAT CGACAACCTGC
 51 CGCTGCCCGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
 101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC CGCGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

```

1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||
g649          MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||
g649          VQELRENKKARKAFRTLPHYAEQKIQCRAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGA CTGGTAT CGACA ACTGC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTGGAACGC
151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA
201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||
a649          MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||
a649          VQELRENKKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g650.seq
1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCGCGC CTATTTGCGC AGGCTCGTCA ACCGGAGCCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCGCTTCCCG TTATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGAAA AAACacgGT TTACGacgGC aggcacGacg TttacgcaGc
501 taccgatgcc gcactCAACT AtctGcAATA TCTCTAtggA CTGTTCCGGCG
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCGTC ACGCGGCCG CGACCAAGGG CTCGAACCGA CCTACGAAA
651 CCGCGGTATG CCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
701 TCGCAACAT TATTGCCACC CCCCATCTT TCGGCATGAA TATCAGCGAC

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1033

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751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTCAAC GTCCCCGCGt tcatCCCCAA AAACaaacgc
901 aaactGCTGC TTCCTGTCGC GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCGCA CCGGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacTa ccgttccaaT
1201 ATGCGggcag gcaCGGTGAA CGTCAGCATT gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggacatta ccgtcgaccc ttgcccgcga gaaaccgtcc
1301 gtacgggaac ccgatcccct tgtccgcaTt accgaacccg ccctTGGCAG
1351 AGCCGCAGCg CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

g650.pep

```

1 MSKLKTIALT ASGLSVCPGF LYAONTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGFMRGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHV GASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFOAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVSI ARIOPAAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

m650.seq

```

1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TC CGGTTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCCAAT CCGGACGCT GTGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCC CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TC GCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGFAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCGCG
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGCG
551 ACTGGCCGCT TGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CTGCGGTATG CCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
701 TCGGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAATGCTGTC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCGCA CCGGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG. AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAA CCGAAAAACA GACCGCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

m650.pep

```

1 MSKLKTIALT ASGLSVCPGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGFMRGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHV GASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFOAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGFRMGEVNPVLVRRHESKFIAHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
g650	LRQGFRMGEVNPVLVRRHESKFIAHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
g650	LFGDWPLAFAAYNWGEGNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFGMNIISIDINKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFGMNIISIDINKPYFQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIIDINTPDYRSNMPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIIDINTPDYRSNMPAGTVNVSIARIQAAAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
g650	ADITVAPLPQETVRTGTTRSPCPHYRTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

a650.seq

```

1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCGTCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCGAAT CCGGCAGCCT GTGGAGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTTCATCG
251 CAAGCCACAG CTATTTC AAC AGGGTCATCA ACCGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGCG AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACA TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAACT GGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTTCCCAAG CTGCTCGCCG
701 TGCGCAACAT CATTGCCGCC CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCGTATTT TCAGGCAGTC GAACCGGACC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCGCGGT TCATCCCCAA AAGCAAACGC

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1035

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901 AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CAAAACCAG CTGTGTCGAC ATCTCGACGG CAACGGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAA CCGAAAAACA GACCGCCATG CCGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```
a650.pep
 1 MSKLKTIALT ASGLSVC PGF LYAQNTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWSE LRQGRMGEV NPELVR RHES KFIASHSYFN RVINRSR PYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIAATDA ALNYLQYLYG LFGDWPLAFA AYNWGE GNVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPN TYRSN
401 MPAGTVNVGI ARIRPAAQ T ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

m650/a650 99.1% identity in 465 aa overlap

          10      20      30      40      50      60
m650.pep  MSKLKTIALTASGLSVC PGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
a650      MSKLKTIALTASGLSVC PGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE
          10      20      30      40      50      60

          70      80      90     100     110     120
m650.pep  LRQGRMGEVNP ELVRRHESKFIASHSYFN RVINRSR PYMYHIANEVKKRNMPAEAALLP
a650      LRQGRMGEVNP ELVRRHESKFIASHSYFN RVINRSR PYMYHIANEVKKRNMPAEAALLP
          70      80      90     100     110     120

          130     140     150     160     170     180
m650.pep  FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
a650      FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG
          130     140     150     160     170     180

          190     200     210     220     230     240
m650.pep  LFGDWPLAFAAYNWGE GNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
a650      LFGDWPLAFAAYNWGE GNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA
          190     200     210     220     230     240

          250     260     270     280     290     300
m650.pep  PQSFGMNISDIDNKPYFQAVEPDRPLDNEA IARLAGITQSELLALNPAFNVP AFIPKSKR
a650      PQSFGMNISDIDNKPYFQAVEPDRPLDNEA IARLAGITQSELLALNPAFNVP AFIPKSKR
          250     260     270     280     290     300

          310     320     330     340     350     360
m650.pep  KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
a650      KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          310     320     330     340     350     360

          370     380     390     400     410     420
m650.pep  NLVNAGRSILVAKNGKTLQTASESVVSIDI DNTPD TYRSNMPAGTVNVGIARIRPAAQ T
a650      NLVNAGRSILVAKNGKTLQTASESVVSIDI DNTPN TYRSNMPAGTVNVGIARIRPAAQ T
```


1036

	370	380	390	400	410	420
	430	440	450	460		
m650 . pep	ADITVAPLPQKTVRVTXTRSPCPYCRTCPCDSRSATSNRKTRDRHAVX					
a650	ADITVAPLPQKTVRVTXTRSPCPYCRTCPCDSRSATSNRKTRDRHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652 . seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCGG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGCGG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATACTTGGAA GGCTTGTTA
551 ACGAATTCCT GATTATTTCC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATTCTTGCC GAAGGCATCG
701 AAAAAGCGGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCTGAAAGc cgtcgatctg gCAAAATGCA accgctacGc
801 cagCTGTGAT AGCCAccgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTA AAAaccgG TTCTTTGAGc
901 cgTTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGcctACT ACCCCGGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652 . pep

```

1  MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANN SLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFP IIS IEDGMDENDW
201 EGWKKLLEKL GKKVQLVGGD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVN SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMARYNQ LLRIEELAE AAYYPGKA AF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652 . seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCGG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGCGGACCG
401 AAGCCGCCGG CTACAAAGCG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGTTAGAG TTCAATTGGT
651 TGGCGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGGCC GAAGGCATCG
701 AAAAAGCGGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAAACCG TTCTTTGAGC
901 CGTTCGACC GCATGGCGAA ATACAACCA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652 . pep

```

1  MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANN SLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

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1037

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
 151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
 201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/g652 98.2% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAAEEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
g652	MIELDGTENKGNLGNATLAVSMAVARAAAEEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
g652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
g652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFPIISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
g652	GLVNEFPIISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTILSETLKAVDLAKRNRYASVM SHRSGETEDSTIADLAVATN CMQIKTGSLS					
g652	LLVKVNQIGTILSETLKAVDLAKRNRYASVM SHRSGETEDSTIADLAVATN CMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX					
g652	RSDRMAYNQ LLRIEELAE AAYPGKAAF YQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

a652.seq

1	ATGATCGAAT	TGGACGGTAC	TGAAAACAAA	GGCAATTGGG	GTGCGAATGC
51	GACTTTGGCG	GTTTCTATGG	CGGTTGCACG	CGCCGCTGCC	GAAGACTCAG
101	GCCTGCCCGT	TTACCGCTAC	TGGGCGGGCG	CAGGCCCGAT	GTCCCTGCCCC
151	GTACCGATGA	TGAACGTCAT	CAACGGCGGC	GAACACGCCA	ACAACAGCCT
201	GAACATCCAA	GAGTTTATGA	TTATGCCCGT	CGGCGCAAAA	TCTTTCCGCG
251	AAGCGTTGCG	CTGCGGTGCG	GAAATTTTCC	ACGCCTTGAA	AAACTGTGTC
301	GACAGCAAAG	GCTTCCCGAC	CACAGTCGGC	GACGAAGGCG	GTTTCGCCCC
351	CAACCTGAAC	AGCCACAAAG	AAGCCCTGCA	ACTGATGGTC	GAGGCGACCG
401	AAGCCGCGCG	CTACAAAGCG	GGCGAAGACG	TATTATTCGC	ATTGGACTGC
451	CGCTCCAGCG	AGTTCTACAA	AGACGGCAAA	TACCACTTGG	AAGCCGAAGG
501	CCGCTCCTAC	ACCAACGCGG	AATTGCGCGA	ATATCTGGAA	GGCCTGGTCA
551	ACGAGTTCCC	CATCATCTCC	ATCGAAGACG	GGATGGATGA	AAACGACTGG
601	GAAGGCTGGA	AACTGCTGAC	CGAAAAACTG	GGCGGCAAG	TCCAACCTCGT
651	TGGCGACGAC	CTCTTCGTGA	CCAACCCGAA	AATCCTTGCC	GAAGGCATTG
701	AAAAAGGCGT	GGCAAACGCA	CTATTGGTCA	AAGTCAACCA	AATCGGTACT
751	TTGAGTGAAA	CCCTGAAAGC	CGTCGACTTA	GCCAAACGCA	ACCGCTACGC
801	CAGCGTAATG	AGCCACCGCT	CCGGCGAAAC	CGAAGACAGC	ACCATTGCCG
851	ACTTGGCAGT	CGCCACCAAC	TGTATGCAGA	TCAAACCCGG	TTCTTTGAGC
901	CGTTCCGACC	GCATGGCGAA	ATACAACCAA	CTGCTGCGTA	TCGAGGAAGA
951	ATTGGCGGAA	GCCGCGGACT	ACCCAGCAAA	AGCCGCATTG	TACCAACTGG
1001	GCAATAAA				

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

a652.pep

1	MIELDGTENK	GNLGNATLA	VSMVARAAA	EDSGLPLYRY	LGGAGPMSLP
51	VPMNVINGG	EHANNSLNIQ	EFMIMPVGAK	SFREALRCGA	EIFHALKKLC
101	DSKGFPTTVG	DEGGFAPNLN	SHKEALQLMV	EATEAAGYKA	GEDVLFALDC

1038

151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
 201 EGWKLLETKL GKVQLVGDD LFTVNPKILA EGIKGVANA LLVKVNIQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
a652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
a652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNIQIGTSETLKAVDLAKRNRYASVMHRSGETEDSTIADLAVATNCMQIKTGSLS					
a652	LLVKVNIQIGTSETLKAVDLAKRNRYASVMHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEELAEAADYPSKAAFYQLGKX					
a652	RSDRMAKYNQLLRIEELAEAADYPSKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCCGCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTCGGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTCCGACG GCGACAAATC CCGCTATTCC GGCAAAGCGG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTCCGCGA AGCGTTGCGC TCGCGTGC GG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGTAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCCGCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTGC AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGAAG GCTTGGTTAA CGAATTCCTG ATTATTTCCA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAAATTGG GCAAAAAAGT TCAATTGGTC GCGCAGACT TGTTCGTAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGATCTGG CAAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGCGGAARCC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAACCCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1251 CCGCGCAAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES GVMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSRGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCCA CA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGACGGCG GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGAGC GCGACAAATC CCGTTATTCC GGCAAGGGCG TATTGAAGGC
201 GGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGCGCGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACCGCGCGC AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TCGCGTGGCG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCGCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGCGGACCGA AGCCGCGCGC TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTGGA AGCCGAAGGC CGCTCTTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGCAGCACT TGTTCTGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGCGGAAACC GAAGACAGCA CCATTGCCGA CTGGGAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCAGCAAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES GVMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSRGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLES GVMGRAAVPSGASTGQKEALELRDGDKSRY S					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLES GVMGRAAVPSGASTGQKEALELRDGDKSRY S					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANNSLNIQEFMIMPV GAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANNSLNIQEFMIMPV GAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKLDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA					
g652-1	CGAEIFHALKKLDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEAAEAGYKAGEDVLFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLLT					
g652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLLT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA					
g652-1	EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKCNRYA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEADYPSK					
g652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEAAAYPGK					
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCATTGATAT TTTGCCCCGC GAAATTTTGG ACTCAGCGCG
51  CAACCCACACA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAGA GGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGTTATTCT GGCAAGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCCG TCGGCTGCCG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGCGC ACGAAGCGCG TTTGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGCGCAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAACCTGG GCGGCAAAGT CCAACTCGTT GGCGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGCCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCATAG CAAACCCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECVLLSEGV-VMGRAAVPSG-ASTGQKEALE
51  LRDGDKSRYS KGVVKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGAHA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDN DWEGWKLLT
301 EKLGGKRVQLV GDDLFVTNPK ILAEGIEKGV ANALLVKVNQ IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      70      80      90      100     110     120
            GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      70      80      90      100     110     120
            GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR

m652-1      130     140     150     160     170     180
            AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREARL
a652-1      130     140     150     160     170     180
            AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREARL

m652-1      190     200     210     220     230     240
            CGAEIFHALKFLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      190     200     210     220     230     240
            CGAEIFHALKFLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA

m652-1      250     260     270     280     290     300
            LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLLT
a652-1      250     260     270     280     290     300
            LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLLT

m652-1      310     320     330     340     350     360
            EKLGGVRVQLVGDDLFTVNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      310     320     330     340     350     360
            EKLGGVRVQLVGDDLFTVNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA

m652-1      370     380     390     400     410     420
            SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEEELAEADYPSK
a652-1      370     380     390     400     410     420
            SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEEELAEADYPSK

m652-1      429
            AAFYQLGKX
a652-1      AAFYQLGKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggt GATGTGCGCt ttgccccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTCA TCGGTTCAG GtcgacgaGG
151 AAaacyTGGC TTTCGGTCCG GCCGAAacy atgcgCaaac cgCGTttaac
201 caactcttcc gccATGACGG CAGCATTGAT TTTCATTGT TTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgCGGGCG
301 ATAACGTgca tcaACGGAcc gcCTTGcAGG CTGGGAAGA TGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTGTGG GTGGTAGTg ttACgaaGtc GCAGaatggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAPPMRME VTYGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  RTWLSVRPET MRKPRLTNSS AMTAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLV VVVVTRSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTGACGGT GATGTGCGCT TTGCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTCAG GTCAACGAGG

```


1042

```

151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACCT GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTGGCGGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

```

          10      20      30      40      50      60
m653.pep  MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKRWLSVRPET
          |||||
g653       MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKRWLSVRPET
          10      20      30      40      50      60

          70      80      90      100     110     120
m653.pep  MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
          |||||:|||||
g653       MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
          70      80      90      100     110     120

          130     140     150     160
m653.pep  SWVLSRHKITPPRGPRRLWVVVVVTKSQNGTGLGYSPPATRPAX
          |||||
g653       SWVLSRHKITPPRGPRRLWVVVVVTKSQNGTGLGYSPPATSPAX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGGCGGGCGG AACCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCATTCGGG ATGGCGTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACCT GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTGGCGGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGATTGGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

```

          10      20      30      40      50      60
m653.pep  MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKRWLSVRPET
          |||||
a653       MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKRWLSVRPET
          10      20      30      40      50      60

          70      80      90      100     110     120
m653.pep  MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
          |||||
a653       MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
          70      80      90      100     110     120

          130     140     150     160
m653.pep  SWVLSRHKITPPRGPRRLWVVVVVTKSQNGTGLGYSPPATRPAX
          |||||
a653       SWVLSRHKITPPRGPRRLWVVVVVTKSQNGTGLGYSPPATRPAX

```


1043

130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```
g656.seq
1  ATGCCGCGTT TCTCCGGTTC GATTTCTTCG ATGATTTCCTA TCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCTGG TGAATTTGAC
201 TTCGCTGTT TTGCTGATGC GTCCGACATC GTTGGCCCCC AAATCGATAA
251 GCATAACGTG TTCGGCGgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTCCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTTCCGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```
g656.pep
1  MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIISITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```
m656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCTGG TAACTTTGAC
201 TTCGCCGTT TTAATGATGC GGCCGACGTC GTTGGCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTCCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TCGGTCGCG TCGGACGAGG ATTTCCGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```
m656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLSRTRTR ISGEEPTMWK SPKS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
	: : : : : : : : : : :					
g656	MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPSFKQPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSIINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	: : : : : : : : : : : :					
g656	ILSVTLTSPVLLMRPTSLRPKSIISITCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLSRTRTRISGEEPTMWKSPKSX					
	: : : : : : : : : :					
g656	MTSSRSRTRISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTG GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTGTGTCG TAACTTTGAC
201 TTCGCCGTT TTAATGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTG
301 TTGGCAAGGT CTTCCGCGGG GGTTTGCGG CGCAGGCGCG TGCCGGCGAT
351 GGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTCGGGCG
401 AGGAGCCGAC GATGTGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP K SINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRT R ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM CITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM CITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRP K SINMTCSAI SLASLNKSCS LARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRP K SINMTCSAI SLASLNKSCS LARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRP K SINMTCSAI SLASLNKSCS LARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRP K SINMTCSAI SLASLNKSCS LARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ITSLRSRRT R ISGEEPTMWK SPKSX					
a656	MTSSRSRRT R ISGEEPTMWK SPKSX					
	130	140				
m656.pep	ITSLRSRRT R ISGEEPTMWK SPKSX					
a656	MTSSRSRRT R ISGEEPTMWK SPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGCGCGG GGAATTGACC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGGCGGTta cgACCGAATT TGAAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTCAAGAA AAAGCGTGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGCGCGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattcC ATCGTCcccq CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGACGAC GCGGCAACgc tTGGCGGACG AATTGGATTA TGTCGGCgta
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGCAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAAcctGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTTGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGCGCGAA TGCACACCTG CACCTATACG GAAAAAAAC CGCACAGAAA
1051 GGTCCGAAAA TGGGACACTT TaccgTTTGG ACCACCGATT CGGACaccgc
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pep

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDLKAFF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADELDYVGV

1046

251 LAVEMFVVDG THELLVNETA PRTHNSGHHT IDACAAADQFQ QQVRIMCNLP
 301 PADTKLLSPC CMANILGDVW QEDGGEPDWL PLQSRPNAHL HLYGKKTAKQ
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGGCA TCCTCGGCGG
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTGCCC
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
 201 GGCAAAATGC GCGCGGTGA CCACTGAATT TGAACACGTC AATGCCGATG
 251 CGATGCGCTT TTTGGCAAAA CATAACCAATG TTTCCCTAG CGGCGATTGT
 301 GTGGCGATTG CACAAAACCG CATTCAAGGAA AAGGCATGGA TACGCAAAGC
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
 401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACTCAA
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGA TTGCGTTTG GAAAAAATGG
 551 TGGATTGCG CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC
 601 AACGTGCAAA CTTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
 651 GCGTTATTCC ATCGTCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG
 701 CGCGGCAGAT GCGCAACGC TTGGCGGACG AATTGGATTA TGTCCGCGTA
 751 TTGGCGGTAG AAATGTTTGT TGTCGGTGAC ACGCATGAAT TGGTCGTCAA
 801 CGAAATCGCC CCGCGCCCGC ACAATTCGCG ACACCATACG ATAGATGCCT
 851 CGCGCAGAGA CCAGTTCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
 901 CCTGCCGATA CCAAATTACT GAGTTCTTGC TGTATGGCAA ATATTTTGGG
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTTA ACCACCGATT CGGACACCGC
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDAPAAEFA
 51 DRHLCAPFND QAALDELAKE AAVTTEFENV NADAMRFLAK HTNVSPSGDC
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVVCKA EDITEASAQF LPGILKTATL
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQQARQMAQR LADELQYVGV
 251 LAVEMFVVDG THELVVNEIA PRPHNSGHHT IDACAAADQFQ QQVRIMCNLP
 301 PADTKLLSSC CMANILGDVW QEDGGEPDWL PLQSHPNAL HLYGKKTAKH
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPDAPAAEFA	DRHLCAPFND
g657	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA	DRHLCAPFDD
	10	20	30	40	50	60
m657.pep	QAALDELAKE	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
g657	RAALDELAKE	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	70	80	90	100	110	120
m657.pep	TAPYQVVCKA	EDITEASAQF	LPGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
g657	TAPYQAVCKA	EDITEASAQF	LPGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNNDENVQTFDPAENIHENGILAYSIVPARLSADVQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADELVDYVGVLAEMFVVGDTHELNVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADELVDYVGVLAEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPQSHRNAHLHLYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSXL					
g657	TTDSDTAFQEAKKLHQSXL					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

a657.seq

1	ATGAAAAACA	TATCTCTTTC	TCCGCCCGCC	ATGCTCGGCA	TTCTTGGCGG
51	CGGACAATTA	GGCAGAATGT	TTACTGTTGC	TGCCAAAACC	ATGGGGCTACA
101	AAGTAACCGT	ACTCGATCCC	AACCCGAATG	CGCCGGCAGC	GGAATTGCGC
151	GACCGCCATT	TGTGTGCGCC	GTTTGACAAC	CAAACCGCTT	TGGAAGAATT
201	GGCAAAATGT	GCGGCTGTTA	CGACCGAGTT	CGAAAACGTC	AATGCCGATG
251	CGATGCGTTT	TCTCGCCAAA	CATACCAATG	TTTCCCCCAG	CGGCGACTGC
301	GTTGCCATCG	CGCAAAACCG	CATTCAAGAA	AAGGCATGGA	TACGCAAAAGC
351	AGGCCTGCAA	ACCGCGCCGT	ATCAAGCAAT	TTGCAAAGCC	GAAGACATCA
401	CTGAAGAAAG	CATACAATTT	CTGCCCGGCA	TCCTGAAAAC	CGCTACATTG
451	GGCTATGACG	GCAAAGGCCA	AATCCGCGTC	AAAACGGTGG	ATGAACTCAA
501	AGCCGCGTTT	GCCGAACACC	GCGGCGTGGA	TTGCGTTTTG	GAAAAAATGG
551	TGGAATTGCG	CGGCGAAATT	TCCGTTATCG	TATGCCGTCT	GAACAATGAC
601	AACGTGCAAA	CTTTCGATCC	TGCCGAAAAC	ATTCACGAAA	ACGGTATCCT
651	CGCCTACTCC	ATCGTCCCAG	CCCGACTGAG	TGCCGACATT	CAGCAACAGG
701	CGCGACAAAT	GGCGCAGCGT	TTGGCCGATG	AATTGAACCTA	CGTCGGCGTA
751	TTGGCGGTAG	AAATGTTTGT	TGTCGGCGAC	ACGCATGAAT	TGGTCGTCAA
801	CGAAATCGCG	CCGCGTCCGC	ACAATTCCGG	CCACCATACC	GTCGACGCGT
851	GCGCGGCAGA	CCAATTCCAG	CAACAGGTCC	GCCTGATGTG	CAACCTGCCA
901	CCTGCTGACA	CCAAATTGCT	GAGTTCTTGC	TGTATGGCGA	ATATTTTGGG
951	CGACGTTTGG	CAGGAAGACG	GCGGCGAACC	GGATTGGTTT	CCCCTGCAAA
1001	GCCGGCCGGA	CGCGCACCTG	CACCTTTACG	GCAAAAAAAC	CGCGCACAAA
1051	GGGCGGAAAA	TGGGACACTT	TACCATTTTA	AGCACCGATT	CGGACACCGC
1101	ATTTCAAGAA	GCAAAAAAAC	TGCATCAGTC	CCTATAA	

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

a657.pep

1	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	NPNAPAAEFA
51	DRHLCAPFDN	QTALEELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC
101	VAIAQNRIQE	KAWIRKAGLQ	TAPYQAICKA	EDITEESIQF	LPGILKTATL
151	GYDGKGQIRV	KTVDELKAAF	AEHRGVDCVL	EKMVDLRGEI	SVIVCRLNND
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADI	QQQARQMAQR	LADELNVYGV
251	LAVEMFVVGDT	THELVVNEIA	PRPHNSGHHT	VDACAADQFQ	QQVRLMCNLP
301	PADTKLLSSC	CMANILGDVW	QEDGGEPDWF	PLQSRPDAHL	HLYGKKTAKH
351	GRKMGHFTIL	STDSDTAFQE	AKKLHQSLS*		

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDA PAAEFADRHL CAPFND					

1048

```

|||||
a657 MKNISLSPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDN
      10      20      30      40      50      60

      70      80      90      100     110     120
m657.pep QAALDELAkCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
      |||:|||||
a657 QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
      70      80      90      100     110     120

      130     140     150     160     170     180
m657.pep TAPYQVVCkAEDITEASQFLPGILKTATLGyDGKGQIRVKTLDLKAFAEHGGVDCVL
      |||||:|||||
a657 TAPYQAICKAEDITEESIQFLPGILKTATLGyDGKGQIRVKTVDLKAFAEHRGVDCVL
      130     140     150     160     170     180

      190     200     210     220     230     240
m657.pep EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR
      |||||:|||||
a657 EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQARQMAQR
      190     200     210     220     230     240

      250     260     270     280     290     300
m657.pep LADELdYVGVLAVEMFVVGDTHELvVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP
      |||||:|||||
a657 LADELNYVGVLAVEMFVVGDTHELvVNEIAPRPHNSGHHTVDACAADQFQQQVRIMCNLP
      250     260     270     280     290     300

      310     320     330     340     350     360
m657.pep PADTKLLSSCCMANILGDVWQEDGGEpdWLPLOSHpNAHLHLYGKKTAKHGRKMGHFTVL
      |||||:|||||
a657 PADTKLLSSCCMANILGDVWQEDGGEpdWFPLQSRPDahlHLYGKKTAKHGRKMGHFTIL
      310     320     330     340     350     360

      370     379
m657.pep TTDSDTAFQEAKKLHQSIX
      :|||||
a657 STDSDTAFQEAKKLHQSIX
      370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2135>:

```

g658.seq
1  ATGGTGGCCG GAATTGTGCG TGCGCGGGGC GGTTCATTG ACGAGCAATT
51  CATGTGTGTC GCCGACAACA AACATTCTA CCGCCAAtac GCCGACATAA
101 TCCAATTTCGT CCGCCAagcG TTGCGCGGTC TGCCGCGCCT GTTGCTGCAC
151 GTCGCGCACTC AGCCGCGcgG gGACGATGga atAAGCCAAG ATGCCGTTT
201 CGTGGATGTT TTCGCGGGG TCGAAGGTTT GCACGTTTTC ATCGTTCAGA
251 CGGCATACGA TCACGGAAT CTCGCGCGC AAGTCCACCA TTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGCAAA CGCGGCTTTG AGTTCGTCCA
351 ACGTTTGTAC GCGATTGA CCTTGCCGT CGTAGCCAA CGTAGCCGT
401 TTCAGGATGC CGGGCAAAA TTGCGCGCTT GCTTCAGTAA TGTCTTCGGC
451 CTTGCAAACC GCCTGATACG GCGCGGTTG CAAGCCTGCT TTGCGTATCC
501 ACGCTTTTTC CTGAATGCGG TTTTGTGCAA TGGACACGCA GTCGCCGCTG
551 GGGGAAACGT TGGTATGCTT TGCCAGAGAG CGCATCGCGT CGGCAttgac
601 gTTTTCAAAT TCGGTcgtaA CCGCCGCGCA TTTTGCCAAT TCGTCCAACG
651 CGGCCCGGTC GTCAAACGGC GCGCACAAAT GGCGGTGGC AAATTCGCC
701 GCCGCGCAT TCGGTGCGG ATCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTAGCGGCA ACGGCAACA TTctgcctAA

```

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

```

g658.pep
1  MVAGIVRARG GFIDEQFMCV ADNKHfYRQY ADIIQfVRQA LRRLPRLLLH
51  VGTQPRGDDG ISQDAVfVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

```


1049

```

101 NAIHAAVFGK RGFEFVQRF ADLTFVAVQ RSRFQDAGQK LRACFSNVFG
151 LANRLIRRLG QACFAYPRFF LNAVLCNGHA VAAGGNVGM L CQRAHRVGID
201 VFKEFGRNRR FCQFVQRPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
1  ATGGTGTCCG GAATTGTGCG GCGCGGGGCG GATTTCGTTG ACGACCAATT
51  CATGCGTGTC ACCGACAACA AACATTCTTA CCGCCAATAC GCCGACATAA
101 TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CGGCATACGA TTACGGAAAT TTCACTGCGC AAATCCACCA TTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTGT AGTTCATCCA
351 ATGTTTTTAC GCGGATTGTA CCTTTCGCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTTG CAATCCCGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGGC GCGCACAAAT GCGCGTCGGC AAATTCTGCT
701 GCGGCGCGCT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTTGGCGGCA ACGGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
1  MVSGIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LRHLPRLLH
51  VGTQSRGDDG ISQDAVEFVDV FGRVESLHV IVQAYDYGN FTAQIHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVAVQ RSRFQDAGQK LRACFSNVFS
151 LTNHLIRRLG QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKEFSGHRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENGYFVAHG
251 FGGNGKHSAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

```

m658.pep      10      20      30      40      50      60
MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLHLVGTQSRGDDG
||:||||| ||:| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|
g658          10      20      30      40      50      60
MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLHLVGTQPRGDDG

m658.pep      70      80      90     100     110     120
ISQDAVFVDVFGFVESLHVIVQAYDYGNFTAQIHFFQNAIHAAVFGKRGFEFIQCFY
||||| ||:| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|
g658          70      80      90     100     110     120
ISQDAVFVDVFGGVEGLHVIVQAYDHNLAQVHFFQNAIHAAVFGKRGFEFVQRF

m658.pep     130     140     150     160     170     180
ADLTFVAVQSRFQDAGQKLRACFSNVFSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT
||||| ||:| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|
g658          130     140     150     160     170     180
ADLTFVAVQSRFQDAGQKLRACFSNVFGLANRLIRRLGQACFAYPRFFLNAVLCNGHA

m658.pep     190     200     210     220     230     240
IAARGNIGMFCQKAHRIGIDVFKEFSGHRRFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG
:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
g658          190     200     210     220     230     240
VAAGGNVGM LQRAHRVGIDVFKEFGRNRRFCQFVQRPVVKRRAQMAVGKFRRRRIRVG

m658.pep     250     260
VENGYFVAHGFGGNGKHSAX

```


1050

g658 :|||||:|||||
 IENGYFVAHGFGNGKHSAX
 250 260

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

a658.seq
 1 ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
 51 CATGCGTGTC GCCGACAACA AACATTCTTA CCGCCAATAC GCCGACGTAG
 101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
 151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
 201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTTCAGA
 251 CGGCATACGA TAACGGAAAT TTCGCCGCGC AAGTCCACCA TTTTTCCTAA
 301 AACGCAATCC ACGCGCGCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
 351 CCGTTTTGAC GCGGATTTGG CCTTGCCGT CATAGCCCAA TGTAGCGGTT
 401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
 451 TTTGCAAAAT GCTTGATACG GCGCGGTTTG CAGGCTGCT TTGCGTATCC
 501 ATGCCTTTTC CTGAATGCGG TTTTGCAGCA TGGCAACGCA GTCGCGCGTG
 551 GGGGAAACAT TGTATGTTT GGCAGAAAA CGCATCGCAT CGGCATTGAC
 601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG
 651 CGGTTTGGTT GTCAAACGGC GCACACAAAT GGCGGTCGGC AAATTCCGCT
 701 GCCGGCGCAT TCGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
 751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

a658.pep
 1 MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN
 51 VGTQSGWDDG VGEDTVFVNV FGRIESLHV IVQTAYDNGN FAAQVHHFFQ
 101 NAIHAAVFGK RGFEFIHREF ADLAFVIAQ CSGFQDAGQK LYAFFSDVFG
 151 FANCLIRRLG QACFAYPCLF LNAVL RDGNA VAAGGNIGMF GEKTHRIGID
 201 VFELGRNSRT FCQFFQSLV VKRRTQMAVG KFCRRIRVG IEYGYFVAHG
 251 FGSNSKHS*

m658/a658 75.3% identity in 259 aa overlap

m658.pep	10	20	30	40	50	60
	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLHVGTSQSRGDDG					
a658	10	20	30	40	50	60
	MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGQTLRHLSRLLNVGTSQSGWDDG					
m658.pep	70	80	90	100	110	120
	ISQDAVFVDVFGRVESLHVIVQTAYDYGNTAQIHHFFQNAIHA AVFGKRGFEFIQCFY					
a658	70	80	90	100	110	120
	VGEDTVFVNVFGRIESLHVIVQTAYDNGNFAAQVHHFFQNAIHA AVFGKRGFEFIHREF					
m658.pep	130	140	150	160	170	180
	ADLTFAVVAQRSRFQDAGQKLRFSDVFSLTNHLIRRLGQSRFAYPCLFLNAVLNCRHT					
a658	130	140	150	160	170	180
	ADLAFVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLGQACFAYPCLFLNAVL RDGNA					
m658.pep	190	200	210	220	230	240
	IAARGNIGMFQCAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRAQMAVGKFCRRVRIG					
a658	190	200	210	220	230	240
	VAAGGNIGMFGEKTHRIGIDVFELGRNSRTFCQFFQSLVVKRRTQMAVGKFCRRIRVG					
m658.pep	250	260				
	VENGYFVAHGFGNGKHSAX					
a658	250	260				
	IEYGYFVAHGFGSNGKHSAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

g661.seq

```

1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51 GCGGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151 ACCGGAAAAA CCtgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
201 TGCCGTGCAG ATTGCCGGCA GCGACCCcga acaGATGGCG Gatgcggcgc
251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGTGTC
301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351 CGAGccgctg gttgcCgcca tTTtggaggc ggtggtcAAG GCGGCGGgcg
401 TACCCGTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
451 ctgcCcgccg tcgccaaaat cgcggaagat tgcggcattg ccgccCttgc
501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GCGgcGTTAC
551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601 CGCGGACATC actTCgcccgc AAAAAGCCGC CGccgTCCTC AAACAAACCG
651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
701 TTCCGCGATT TGAAGCATTG TGCCGAACAC GGCCTTTTAC CGCTGCCTT
751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGCGAAAT GCCCGACGGC GAACAGGCGC GCGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

g661.pep

```

1 MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
51 TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDON
151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
251 EFGRMQSRHF EPHPRHARVL WXDRCARHT QTHRLVHRRN ARRTGAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

m661.seq

```

1 ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51 GCGGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCGGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCCGCG TGATGCAGAA
351 CGAGCCGCTG GTTGCGCCCA TTTTGAAGC CGTCGTCCGT GCGGCAGGCG
401 TACCCGTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
501 CGTCC.ACAG ACGCAGCGGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
551 GAATCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACTTCGCCCG AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
701 TTCCGCGATT TGAAACATTA TGCCGAACAC GGTGTTTTC GCCTGCCTT
751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCACATC CGCGCCATAC
801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

m661.pep

```

1 MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51 TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPREFETL CRTCFACAL
251 EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
	: : : : :					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQOMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
	: : : : :					
g661	ADEGGIVAVQIAGSDPEQOMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
	: : : : :					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDDQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPREFTL					
	: : : : : :					
g661	GALRTHRRDQKPSHPGLGQRRHFAAKSRRRPQTNRRRRHHRARRARQAVVFPREFAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
	: : : : :					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCAHRTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGCGGCATT ACCGACAAAC CGTTCCGCGG ACTTTGCCGA GATTTTGCGC
101 CAGGTGCGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCGCTG GTTGGCGCCA TTTTGGAGGC GGTGGTCAA GCGGCGGGCG
401 TACCGGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TCGGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCAGCGCG ACGCAAATGT ACAAAGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGCTCT AACATCCGG TCTGGGTCAA
601 CCGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAACATTA CGCCGAACAC GGTGTTTAC CGCCTGCCTT
751 GAGTTTGCCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTTA CCGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWDDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPREFTL RRTRCFACL
251 EFGRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
	: : : : :					

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60

           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120

           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||:|||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180

           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPREFTL
           |:| |||||:|||||
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPREFTL
           190     200     210     220     230     240

           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           |||||:||||| |:||||| :|||||
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTT GTACTGTATG TTTGTCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGCGGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAACCG TGTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGTctGC CAAATGCCTG AAATCGCTGG TGCGCTACCG CAATAAGCAT
301 TATTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCCGAC GCAACAATTG GGTTTTGTG
601 GATTTTTTCG GCATtcagac GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCCTTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLQFLPF ALLHKKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHEK HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALARGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNNSVFE
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTLO FYPAWSFPS
251 EDQAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DEFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTT GTACTGTATG TTTGTCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGCGGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAACCG TGTGAAACA

```


1054

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCTGCG CGGACGTTTG AAATCGCTGG TGGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTTCGAC GCAACGATTC GGTTTTTGTG
601 GATTTTTCG GTATTCAGAC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CCGCCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAATC CTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTTC TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTTC GCTGCACAAG CGTTTTAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

m663.pep

```

1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51  KCFSEWSEEK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNDSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PVREADNTVTLH FYPAWSFPFG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK					
g663	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKPRRRIGEINLAKCFPEWDEEK					
	10	20	30	40	50	60
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHLYLDDALAAGEKVILYPHFT					
g663	RKTVLKQHFHMAKLMLEYGLYWYASAKCLKSLVRYRNKHLYLDDALAAGEKVILYPHFT					
	70	80	90	100	110	120
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS					
g663	AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS					
	130	140	150	160	170	180
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVTLH					
g663	SAPFLYLPDQDFGRNNSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVTLQ					
	190	200	210	220	230	240
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
g663	FYPAWSFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

a663.seq

```

1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAATT
51  TCTGCCGTTT CCGCTGCTGC ACAAACTGCG TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAAACC CGCCGCCGTA TCGGCGAAAT CAATTTGGCA

```


1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TGGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTT
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTG GGTTTTGTGTC
601 GATTTCTTCG GTATTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCGT CTTGGGAATC CTTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCCTTTTA TCGAGGAACG
801 CGTGCGCGAA CATCCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNRDSVFV
201 DFFGIRTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWESFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

```

          10      20      30      40      50      60
m663.pep MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP RRRIGEINLAKCFSEWSEEK
          |||:|
a663      MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP RRRIGEINLAKCFEWDGKK
          10      20      30      40      50      60

          70      80      90     100     110     120
m663.pep RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIILYPHFT
          |||:|
a663      RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIILYPHFT
          70      80      90     100     110     120

          130     140     150     160     170     180
m663.pep AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS
          |||:|
a663      AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS
          130     140     150     160     170     180

          190     200     210     220     230     240
m663.pep SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVTLH
          |||:|
a663      SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAALANAKVIPAIPVREADNTVTLH
          190     200     210     220     230     240

          250     260     270     280     290
m663.pep FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX
          |||:|
a663      FYPAWESFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
          250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1 ATGATACATC CGCACCATT CCGCGCCTTT TTCATAAAGC GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGCTGAcgg gCGGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTCGGGGAA CTGGTCTTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGGAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGAAA TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCCT TGTTTTCCAT CGCGCCCAT
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCCaa
451 cCggaagcgc gtttcgtcCc acttcatcgC gtTTTTTCAA cgaTTCCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAA ACTCGATTTT

```


551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

g664.pep

```

1  MIHPHHFRAF FINGHGVEIV HLLIADGAHR MGGRACVFGE LVLAQQADV
51  DAAHGAAGAV AGKLLVAEHG QPFLQRKLEP VAAGYAVARP VVEIFVSDHG
101 FNAFEIGIGG GAAVGEDELG VKNVQTLVFH RAHIEIAYGD DHENIQVIFQ
151 PEARFVPLHR VFSTIPRQSR PWVCPLRWCK TRF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

m664.seq

```

1  GTGATACATC CGCACTACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGGCGG GCGCACCGG ATGGGCGGTC
101 GGGCTGCGT CTTGGGGGAA CTGGTGCTGG CGCAGCAGG GGATGTTTTC
151 GATGCGGCGC ACGGCGCGGC TGGCGCGGTC GCCGGAAAAT TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAT TACTCGTGTG CGACCACGGA
301 TTCGATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTCCAT CGCGCCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ATTTTCATCG GTTTT.CAA CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAT ACTCGATTTT
551 GA
```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

m664.pep

```

1  VIHPHYFRAF FINGHGVEIV HLLIAGGAHR MGGRACVFGE LVLAQQADV
51  DAAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGYAVARP VVEILVSDHG
101 FDAFEIGIGG GAAVGKDELG VKDVQTLVFH RAHIEIAHGD DHENIQVVFQ
151 TEARFVPFHR VFXTIPRQSR PWACPLRWCK TRF*
```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRACVFGEVLVAQQADVFDAAHGAAGAV					
	: :					
g664	MIHPHHFRAFFINGHGVEIVHLLIADGAHRMGGRACVFGEVLVAQQADVLDAAHGAAGAV					
	10	20	30	40	50	60
m664.pep	AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAGVKGDELG					
	:					
g664	AGKLLVAEHGQPFLQRKLEPVAAGYAVARPVVEIFVSDHGFNAFEIGIGGGAAGVEDELG					
	70	80	90	100	110	120
m664.pep	VKDVQTLVFHRAHIEIAHGDHENIQVVFQTEARFVPFHRVFXTIPRQSRPWACPLRWCK					
	:					
g664	VKNVQTLVFHRAHIEIAYGDDHENIQVIFQPEARFVPLHRVFSTIPRQSRPWVCPLRWCK					
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

```

1  GTGATACATC CGCACCACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TATCGGCGG GCGCACCGG ATGTGCGGTC
101 GGACCTGCGT CTTGGGGGAA CTGGTGCTGG CGCAGCAGG GGATGTTTTC
151 GATACGGCGC ACGGCGCGGC TGGCGCGGTC GCCGGAAAAT TCTTGGTCGC
```


1057

```

201 GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCTT TGTTTTCCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHFRAF FINGHGVEIV HLLISGGAHR MGRTCVFGE LVLAQQADV
51  DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGRACVFGEVLVAQQADVDAHGAAGAV					
a664	VIHPHHFRAFFINGHGVEIVHLLISGGAHRMGRTCVFGEVLVAQQADVDTAHGAAGAV					
	10	20	30	40	50	60
m664.pep	AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVGKDELG					
a664	AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG					
	70	80	90	100	110	120
m664.pep	AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVGKDELG					
a664	AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG					
	70	80	90	100	110	120
m664.pep	VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVEXTIPRQSRPWACPLRWCK					
a664	VKDVQTLVFHRTHIEIAHGDDHENIQVVFQTEARFVPLHCVFAXAIPRQSRPWACPLRWCK					
	130	140	150	160	170	180
m664.pep	VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVEXTIPRQSRPWACPLRWCK					
a664	VKDVQTLVFHRTHIEIAHGDDHENIQVVFQTEARFVPLHCVFAXAIPRQSRPWACPLRWCK					
	130	140	150	160	170	180
m664.pep	TRFX					
a664	TRFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGg acgaaacgcg cttcgGgttg GAAtatgact tggatatttt
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTCAAGAG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGCGAAG TGGTCCGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTcCaacg CCACGACGGA CAGGCAGTGA
551 CTGCGCAGCA TTTCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCAGTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCAT AAACAAACCG
701 TGCCGCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAACGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CTTTCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

```



```

1001 CCCAACGCT CTACCGTCGC GCCGTGCCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTGCGCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTC GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAA ctGTGGGACG GCACGGAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCAGC AATTGGaccg tcaggcggcg aagCAggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTtcgt cctGCGCGCC GACCCCGCGC acatcgAAAC
1401 TGTGCGCGAA Aaatacggcg AAATGGCGCA AACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGacaa gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCGCC CTTATCGGCT CAAGccgccc cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTC GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTGCG TCATCGGCAG CTCAGCCGC AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCGCAGgtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTGCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NPYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPPPTDM ADKQPMMPV
251 KVGLLNRRNGE AVAFDYQGRK ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLYN PYSDDDLLLL LAHDSDAFTC WEAQAOTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLDNAFKA LLLGVPSAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDROAA KQENQSYEYS PETADWRTL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTTCGGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACCTG ACGGCAACCG GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCGGCGGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCG
401 CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGGCGGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAGTTCG CTTGTGGTA CAGCCAGCGG GGCACGCCCC TTTTGGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCCCAC GCCCGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTGCGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CCTTCCTGCT CGAAGGCGTA ACCGAAGCCG TCGTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCCG GCCGTCGCC CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTC GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGC AAATGGCAGC AATTGAACG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

```



```

1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCGCGCG ACATCGAAAC
1401 CGTTGCCGAA AAATACGCGG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCGG CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCG GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTCCG TCATCGGCAG CTTACGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGGTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1  MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
 51  TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101  RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151  GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201  DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTVPPPTDM TDKQPMMPV
251  KVGLLNRNGE AVAFDYQGRK ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301  GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLATLS
351  DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401  LRYHQAREAL LDTLAVHFLP KWHELNROAA KOENQSYEYS PEAAGWRTL
451  NVCRAFLVLA DPAHIETVAE KYGEMAQNMN HEWGILSAVN GNESDTRNRL
501  LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551  ARSLIGSFSS NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601  CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES					
g665	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES					
	10	20	30	40	50	60
	70	80	90	100	110	120
m665.pep	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGDRAGRAVRRIENIRLLRQNF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
g665	PEDAGPTAHPVRPVSYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQKG MKLYFQRHDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPPTDM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m665.pep	TDKQPMMPV KVGLLNRNGE AVAFDYQGRK RATEAVLLLTAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMMPV KVGLLNRNGE AVAFDYQGRK RATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEEAQTLYRRAVAANLATLSDGVELPKHEK					
g665	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEAAQTLYRRAVAANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
g665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAAKQENQSYEYSPEAAGWRTLNRVCRAFLRADPAHIETVAEKYGEMAQNMT					
g665	KWHELDROAAKQENQSYEYSPETADWRTLNRVCRAFLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVVRTALQH					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
g665	PKFSLENPNKARSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQRIQAEGLSKDVGEIVGKILD					
g665	CNKLEPHRKNLVKQELQCIQAEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG ACGAAACGCG CTTCGGTTTG GAATACGACT TGGATATTTT
51  CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGTGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGTACCGCC
151 ACCGATACCG ATTTTGAAGG CATCGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTG ACGGGCAACC GCGTGACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGTTGACC GTGTTCCGCG ACCAAGAATT TTCCGCGGAC
301 CGCGCCAGCC GCGCCGTGCG CCGTATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGTCCGAC CGCACATCCG GTGCGCCCCG
401 CCGGATATGA GGAGATGAAC AATTCTTACA CCATGACCGT TTATGAAAAA
451 GCGCGGGAAG TGGTGCGGAT GTATCACACC TTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGT ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCTGTTA
551 CCTGCGACGA TTTCGCGCGG GCGATGGTGG ACGCGAACGG CATCAACCTC
601 GACCAATTCT CCTTGTGGTA CAGCCAAGCA GGTACGCCGG TTTTAGATGC
651 TCAAGGGCGT CTGAAAAACA ATGTGTTCTG GTTAACCATC AAACAAACCG
701 TGCCGCCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAATCGGGC TGCTGAACTG CAACGGCGAA GCGGTGGCAT TTGATTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCTG GCTGACCGAA GCCGAACAGA
851 CCTTCCAGTT CGAAAGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACTAT CCGTACAGCG ACGACGACCT
951 GCTGCTTCTG CTCGCCATG ACAGCGACGC CTTACGCGCG TGGGAAGCCG
1001 CACAAACGCT CTACCGCCGT GCCGTCGCGC CCAACCTTGC CGCGCTTTCA
1051 GACGGCGTCG AGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC TTTCAAAGCC CTGCTTTTGG
1151 GTGTGCCGTC TGAAGCCGAG CTGTGGGACG GCGCGGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATATAC TTGCCGTCGG
1251 CTTTCTGCCG AATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAGTACAGC CCGAAGCCG CCGGTTGGCG CACGCTGCGC
1351 AATGTCTGCC GCGCCTTCGT CTGCGCGGCC GATCCGCGCG ACATCGAAAC

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTACGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCCG GCGCAGGAAG GATTGTGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```
a665.pep
1 MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA
51 TDDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM ADKQPMIPV
251 KIGLLNCNGE AVAFDYQGR ATEAVLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLL LAHSDAFTW WEAQAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNROAA KQENQSYEYS PEAAGWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHAEDEG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*
```

m665/a665 97.3% identity in 638 aa overlap

```
10 20 30 40 50 60
m665.pep MKWDETRFGLEYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATDTDFEGIES
a665 MKWDETRFGLEYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATDTDFEGIES
10 20 30 40 50 60

70 80 90 100 110 120
m665.pep VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
a665 VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
70 80 90 100 110 120

130 140 150 160 170 180
m665.pep PEDAGPTAHPVRPARYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG
a665 PEDAGPTAHPVRPARYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG
130 140 150 160 170 180

190 200 210 220 230 240
m665.pep QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM
a665 QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPTPDM
190 200 210 220 230 240

250 260 270 280 290 300
m665.pep TDKQPMIPVKVGLNLRNGEAVAFDYQGRATEAVLLTEAEQTFLEGVTEAVVPSLLR
a665 ADKQPMIPVKIGLLNCNGEAVAFDYQGRATEAVLLTEAEQTFQFESVTEAVVPSLLR
250 260 270 280 290 300

310 320 330 340 350 360
m665.pep GFSAPVHLNYPYSDDDLLL LAHSDAFTW WEAQAQTLYRR AAVANLATLSDGVELPKHEK
a665 GFSAPVHLNYPYSDDDLLL LAHSDAFTW WEAQAQTLYRR AAVANLAALS DGVELPKHEK
310 320 330 340 350 360
```


1062

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
a665	KWHELNRQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRIQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQIRIQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCTTGAA ACCGAACCTGC ATTTCGACAT TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAAACT CTGTGCTGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACAACAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTCCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACCG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCGC GGGCGATTTG GCGGTAACGG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CCGACAAACC
651 CAAGGTCGGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTTGGAA TATGACTTGG ATATTTTCAT GGTGCTCGCC
751 GTAGGCGATT TCAATATGGG CCGGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCCTCG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCGCG
1001 CCGTGCGCCG CATCGAGAAC ATCCGCCTGC TGCGCCAGAA CCAGTTCCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCATACCCCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATT
1251 CCGCGCGGCG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCCGCT
1301 TGTGTGTACG CCAGGCGGGC ACGCCCGTTT TGGAAGCCGA AGGCCGCTCTG
1351 AAAACAATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCCGGCTTC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCT ATTATCAGG CAAACCGCA
1501 ACCGAAGCGG TGTGCTGAT GACCGAAGCC GAACAGCCCT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGATCTT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCACAGACA GCGACGCTTT CACGTGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGTCCGCGC GTCGCCGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTGGGCGG TGCCGTCCGA
1851 AGCCGAAGTG TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTT CCGTCCGCTT CCTGCCGAAA
1951 TGGCACGAAT TGGACCGTCA GCGCGCGAAG CAGGAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCCGG
2051 CCTTCGTCCT GCGCGCGGAC CCCGCGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGTGT GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTT
2251 ATCGGCTCAA GCCGCCGCG CAGACCCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCACTC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG AATTGCAGTG CATTGGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQORAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFRTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDFIMVVA
251 VGDFNMGAME NKGLNIFNTR FVLADSRAT DTDPEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRAVRRIEN IRLLRQNFPP
351 EDAGPTAHPV RPSVYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPPTPDMA DKQPMMPVK VGLLNRRGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNFAFKAL LLGVPSEAEI WDGTEINIDPL RYHQAREALL DTIAVRFLPK
651 WHELDROAK QENQSYEYSP ETADWRTRLN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTM EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QVQVTAHQHP KFSLENPNKA RSLIGSFSRN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAENLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

n665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTTC ATTTTGATAT TAATGAACCG CAACCGTCCG
101 TGAAGTCGCG TTTGACGGTT GAGCCGCAGA GGGTAGGGGA GCCGCTGGTG
151 TTGACCGGTT CGGCGAAACT CTGTCCGCTC AAAATCAACG GGGCGCGCGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCGCGC GGAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGCGCGC AATTGTTTTA CCCAGTGCAG
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCTCAAGT CACCACCACC ATCGTCGCGC ACAAACGAGC CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGCG GCGGAGTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTTCG GGGCGATTG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACCTCAAAAT CGAGTTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGGTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCCTTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAAATTTT CCGCGACCGC GCCAGCCGCG
1001 CCGTGGCGCG CATCGAAAAC ATCCGCGCTG TCGGCCAGCA CCAGTTCCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCCGCA GCTATGAGGA
1101 GATGAACAAAT TTCTACACCA TGACCGTTTA TGAACAAAGC GCGGAAGTAG
1151 TGCGGATGTA TCACACCCCTG CTCGCGCAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTACCT CCGACGATTT
1251 CCGCGCGCGC ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGCGGGCG ACGCCCGTTT TGAAGCGGA AGGTCGCTCTG
1351 AAAACAATA TTTTCAGATT GACCGTCAA CAAACCGTGC CGCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCGTCAGG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCT ACTATCAGGG CAAACGCGCG

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1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCCGCGCCA ACCTTGCCAC GCTTTCAGAC GCGGTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTT CAAAGCCCTG CTTTGGGCGG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTT CCGTCCACTT CCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 ATACAGCCCC GAAGCCGCGG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGTCTT GCGCGCGGAC CCGCGGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCTC
2251 GTCGGCTCAA GCCCGCGCAG CGACACCTG CAACAGGTTG GAACCGCTT
2301 GCAGCATCCG AAATTCAGCC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTCAACCC
2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAAGCTG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGGAT TGTGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YLDLIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTDPEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRHQHFP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYERG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPPTPDMT DKQPMMPVK VGLLNRRGEA VAFDYQCKRA
501 TEAVLLLTEA EQTFLLLEGVT EAVVPSLLRG FSAPVHLNYP YSDDDLLELL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVLPKHEKL LAAVEKVIDS
601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNQRAAK QENQSYEYSP EAAGWRTLRN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AQAADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
851 QEGLSKDVGE IVGKILD*

```

m665-1/g665-1 96.1% identity in 866 aa overlap

	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
g665-1	MSKTVRYLKD	YQTPAYRILE	TELHFDIAEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
	70	80	90	100	110	120
m665-1.pep	KINGAAADYV	LEGETLTIAG	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
g665-1	KINGAAADYV	LEGETLTIAD	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
	130	140	150	160	170	180
m665-1.pep	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS
g665-1	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS
	190	200	210	220	230	240
m665-1.pep	YLFALVAGDL	AVTEDYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGLE
g665-1	YLFALVAGDL	AVTEDRFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGLE
	250	260	270	280	290	300
m665-1.pep	YLDLIFMVVA	VGDFNMGAME	NKGLNIFNTK	FVLADSRAT	DTDPEGIESV	VGHEYFHNWT
g665-1	YLDLIFMVVA	VGDFNMGAME	NKGLNIFNTK	FVLADSRAT	DTDPEGIESV	VGHEYFHNWT

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRRIENIRLLRQHQPFPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRRIENIRLLRQHQFPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHMQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHMQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTFVLEAEGRLKNNIFELTVKQTVPPPTDMDKQPMIIPVK					
g665-1	MADANGINLDQFALWYSQAGTFVLEAEGRLKNNVFELTIKQTVPPPTDMADKQPMIIPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRRNGEAVAFDYQKGRATEAVLLMTEAEQAFPLEGVTEAVVPSLLRGFSAPVYLNYP					
g665-1	VGLLNRRNGEAVAFDYQKGRATEAVLLMTEAEQAFPLEGVTEAVVPSLLRGFSAPVYLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDLLLLLAHDSDAFTRWEEAQTLYRRVAANLATLSDGVLPKHEKLLAAVEKVISD					
g665-1	YSDDDLLLLLAHDSDAFTCWEAQTLYRRVAANLAALSDDIGLPKHEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFKALLLGVPSEAEALWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNQRAAK					
g665-1	DLLDNAFKALLLGVPSEAEALWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDROAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPAEAGWRTLRNVCFVLRADPAHIETVAEKYGEMAQNMTHWEGILSAVNG					
g665-1	QENQSYEYSPETADWRTLRNVCFVLRADPAHIETVAEKYGEMAQNMTHWEGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQRTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQRTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSRNVPFHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSRNVPFHFAQDGGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRIAQEGLSKDVGEIVGKILDX					
g665-1	VKQELQCIRIAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC ATTTTGATAT TAACGAACCG CAAACCATTG
101 TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGACCGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251 AACGCTTCAC CGTCAAGTG GAAACCGAAA TCCTGCCGCG GGAACACAAA
301 TCCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTA CCCAGTGGCA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAACACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GGCGAGTATT CAGACGGCCG

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501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTC GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTTCAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCEGG TTTGCCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCGTGCGC
751 GTGGCGGATT TCAATATGGG TCGGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTTC CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCACCCGCG TGACCTGCCG CGACTGGTTC CAGCTTTCCG TGAAGGAAGG
951 GTTGACCGTG TTCGCGGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCCGCG TATCGAAAAC ATCCGCCTGC TCGCGCCAGCA CCAGTTCCCC
1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCCGCCC GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC CGCGAAGTGG
1151 TCGCGATGTA TCACACCTTG CTCGCGCAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTTACCT GCGACGATT
1251 CCGCGCGCGC ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCT
1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAACAATG TGTTGAGATT AACCATCAAA CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
1451 TGAACGTCAA CGGCGAAGCG GTGGCATTTC ATTATCAGGG CAAACGCGCG
1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCCA
1551 AAGCGTAACC GAAGCCGTCG TTCCTCTGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA GCGACGCCCT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCGGTGCC GTGCGCGCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGCCGAAACA CGAAAACTG CTGCGCGCGC TCGAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCACGAAT TGAACCGTCA GCGGCGAAG CAGGAAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCGG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CTTTCGCTCT GCGCGCGCAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTC
2251 GTCGGCTCAA GCCCGCGCAG CGACACCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAAGCC CGCTCGCTCA
2351 TCGGCGAGCT CAGCCGCAAC GTCCCGCATT TCCACGAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTAAACCC
2451 GCAGGTTCGC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAAGTCG
2501 AGCCGCACCG CAAAACCTTG GTGAAACAAG CATTGCAGCG CATTGGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSERFTVEV ETEILPAENK
101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYS DGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETREGLE YDLDIEMVVA
251 VGDEFNMGAME NKGLNIFNTK FVLADSRTAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRHQHFP
351 EDAGPTAHEV RPARYEEMNN FYTMTVYKRG AEVVRMYHTL LGEEGFQKGM
401 KLYFORHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPPTPDMA DKQPMMPVK IGLLNCNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVLPKHEKL LAVERKVIDS
601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNQAQAK QENQSYEYSP EAAGWRTLRL VCRAPVLRAD PAHIETVAEK
701 YAEMAQNMTH EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QOVQTAHQV KFSLEPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRENQVA ARLVQAFLNC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVGE IVGKILD*

```

a665-1/m665-1 97.2% identity in 867 aa overlap

```

          10      20      30      40      50      60
a665-1.pep MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV
|||||
m665-1     MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV
          10      20      30      40      50      60
          70      80      90     100     110     120

```


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```

          790      800      810      820      830      840
          850      860
a665-1.pep  VKQALQRIRAQEGLSKDVGEIVGKILDX
             |||||
m665-1      VKQALQRIRAQEGLSKDVGEIVGKILDX
             850      860

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1   ATGCTTTGTA TGAATTATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTAGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTT GTATTGGGAC AATACCGCCA
401 AAACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGTCGCT CCGTAGGTAC GCCTGCTATC CCTAAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1   MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTHSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1   ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1   MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

```

          10      20      30      40      50      60
m666.pep  MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE
          |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g666       MLCMNYQSNSGEGVLVAKTYLLTALIMSMVISGCQVIHANQGKVNTHSAVIAGADAHTPE
          10      20      30      40      50      60
          70      80      90     100     110     120
m666.pep  HATGLTEQKQVIASDFIVASANPLATQAGYDILKQGSAADAMVAVQTTL SLVEPQSSGL

```



```
a666.seq
1  ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTGGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGCTAG AGCCACAGTC
351 GTCAGGCTTG GCGGTTGGTG CATTGTGTT GTATTGGGAT AATACGCCCA
401 AAACATTGAC CAGCTTTGAT GGGCGTGAGA CGGCACCGAT CGGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGGAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
```

a666.pep

1	MPCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	ISGCQVIHAN	QGKVNTHSAV
51	ITGADAHTPE	HATGLTEQKQ	VIASDFMVAS	ANPLATQAGY	DILKQGGGSA
101	DAMVAVQTTL	SLVEPQSSGL	GGGAFFVLYD	NTAKTLTTFD	GRETAPMRAT
151	PELFLDKDGQ	PLKEMEAVVV	VARVRRLLSL	N*	

		10	20	30	40	50	60
m666.pep		MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
a666		MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
a666		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGOPLKFMEAVVVVARWVRLLSL					
a666		GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGOPLKFMEAVVVVARWVRLLSL					
		130	140	150	160	170	180
m666.pep	NX						
a666	NX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1  atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  ttcccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aataAttgcg
151 GAtttccttc agcgtgcccg cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTcgcCat atcgtccagC
251 GGCACATTcg ccctcggctG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GGCgTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCGGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATAACG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCCGGA CAGCACCCTG TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCag tACCTTGCAT tcaAAAACAG ACTTGCGCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1  MRFVFLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVAVQAV MQYQVETAA
151 VPADQLRRMF FNQFEKLGNH DFFAIVHLAD GADMNLVLP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHEFVIRQGR RQVIQRTDTL HIGYGFNIES
251 QNRIHGSTLH SKTDLRLLLCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1  ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATTCCGC ATCCGTTTGA
51  TTTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCTTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCGGTCC CCCATATCCC AATAGCGCGC GGCgTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCGGCC
451 GTTCCAACTG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CAGGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCGGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCTG TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1  MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHIPAR GVDVAVQAV MQYQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHNH
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

          10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIAADFLQPARMEC
          ||:  | |::  | ||:||||:| | |||||:| | :  : ||||| | | | | |
```


a667.seq

1	ATGCGGTTTG	TCTTCTGTTT	GGCGGAGAG	ATAGTTTCTG	ATCCGCTTGA
51	TTTCCATTTC	GTATTGCTGT	GCCTGAATC	TGCCGCTGAC	CAGACAGAAA
101	CGCAGATACA	TCAGATAGGT	ATTTACCGCA	TCGGTTTCGC	AATAATTGCG
151	GATTTCCTTC	AGCCTGCCGC	CGTGAACGC	CTCCCACACC	TTGCTGCCGT
201	CATACCCAG	CTTGCCCGGA	AAACCGCACA	GTTTCGCCAT	ATCGTCCAAC
251	GGCACATTCT	CCCTCGGCTG	GTAAGCGCG	AGCAAATCCA	TCAAATTCGA
301	ATGACGTTGG	TGGTGCAGCG	TGATGTAGTT	GTTCCACTTG	AAATCGCGGC
351	TGTCGCCGAA	ATCGCCGTCG	CCCATATCCC	AATAGCGCG	GGCGTTGATG
401	CCGTGTAGCA	GCGAAGCGTA	ATGCAGAACG	GCAGGTCGA	AACCGCCGCG
451	GTTCCAACCT	ACCAGTTGCG	GCGTATGTTT	TTCAATCAAC	TCGAAAAATT
501	TGGCGATAAC	CCTTCTCTCG	CCGTCATACA	TCTCGCGAT	TGTACCGACA
551	TGGACTTTAT	CCTGCCCCCA	ACGCATGCAG	CACGAAATCG	CCACATCTTG
601	ATGAAGATGA	TGCTGCATAA	AATCCCCACC	CGTCTGAGCA	CGGCCATTTT
651	GCTGGGCAAA	CAGCACCAC	TCATCGTCGG	GCACGAGGA	CGGCAAGTCA
701	TACACGCTAG	GCATACACTG	CACATCGGGT	ACGGTTTCAA	TATCGAAAGC
751	CAAAATCGTG	GTCATGACAG	CACCTTGTAT	TTAAAA.CAG	ACTTGCGCCT
801	ATTGTGTCAT	TAA			

a667.pep

1	MRFVFCVLGGE	IVSDPLDFHF	VFVCVESAAD	QTETQIHQIG	IYRIGFAIIA
51	DFLQPVARVER	LPHLAAVHTQ	LARKTAQFRH	IVQRHIRPRL	VKREQIHQIA
101	MTLVVAADPV	VPLEIAAAVAE	IAVAHIPIAR	GVDAV*QRTV	MQNRQVETAA
151	VPTDQLRRMF	<u>FNQLEKFGDN</u>	HFLAVIHLAD	CTDMDFILPP	THAARNRHNL
201	MKMMMLHKIPT	RLSTAFLLKG	QHHFIVGQRG	RQVIQRTDTL	HIGYGFNIES
251	QNRGHDSTLY	LKXDDLRLCH	*		

m667/a667 79.0% identity in 224 aa overlap

	10	20	30	40	50	60
m667.pep	MRLFPGLCGQVIPHFFDFHFVFVRIQPAADQTETQVHQISVCRVGFAIIADFLQPAMEC					
a667	: :: : :: : : :					
	MRFVFCGGEIVSDPLDFHVFVCVESAADQTETQIHQIGIYRIGFAIIADFLQPARVER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m667.pep	LLENLAAVHTQLARKTAQFRHIVQRHVCPRLVKREIQIHQIAVALVITADVVPLEIAAAE					
a667	:					
	LPHLAAVHTQLARKTAQFRHIVQRHIRPRLVKREIQIHQIAMTLVVAADVVPLEIAAAE					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m667.pep	IAVAHIPIARGVDAVYQGAVMGOYQIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD					
a667	IAVAHIPIARGVDAVXQRTVMQNRQVETAAVPTDQLRRMFFNQLEKFGDNHFLAVIHLAD					
	130	140	150	160	170	180
	190	200	210	220		
m667.pep	GADMYFILPPTHAARNRHNLMKMLHKIAARLSTAFVLGNQHHL					
a667	CTDMDFILPPTHAARNRHNLMKMLHKIPTRLSTAFLLGKQHHFIVGQRGRQVIQRTDTL					
	190	200	210	220	230	240
a667	HIGYGFNIESQNRGHDSTLYLKXDLRLCHX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

```

g669.seq
1  ATGCGCCGCA TCGTTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

```

g669.pep
1  MRRIVKKHQP VNAPHIVLEI RIMKLHRAV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```

m669.seq
1  ATGCGCCGCA TCATTAAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```

m669.pep
1  MRRIIKKHQP INAPHIVLEI RIMKLHRAV FLGRKRPHHH DSSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	MRRIIKKHQPINAPHIVLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI					
	EGMGFDFKQI					
g669	MRRIVKKHQPVNAPHIVLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI					
	EGMGFDFKQI					
	10	20	30	40	50	60
	70	80	90	100		

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```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1   ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTG TTCCTTGGGC
101 GGAACGTCC  CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTG TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1   MRRIKKHQP VNAIPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51  EGMGDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRI*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLRQHGIEGMGDFKQI
             |||||:|||||
a669        MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGIEGMGDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1   ATGACTTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGGTGAA
51  AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1   MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51  IIVMPLSAKS FITENTSPTT SGSSAEVGSS NSITRGSIAS PRALATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1   ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGGTAAA
51  AAACGCTTCG GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CCGTTCGTCA AACACATTA

```


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```

251 CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITSATS RANPISWVTHIIVMPLSAKS
               |||||||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITSATS RANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAK PRAIATRCWPPEWEGKASFLCASPTRSK
               |||||||
g670           FITFNTSPTISGSSAEVGSSNSITRGSIAS PRAIATRCWPPEWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARV MFSNTVRCGX
               |||||||
g670           SSIAFFSACS AFCPLTFIGARV MFSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGTTGTA
 51 AAACGCTTCC GGCGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATGGTCA TACCGTTTC CGCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTGTC AACAACATTA
251 CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITSATS RANPISWVTHIIVMPLSAKS
               |||||||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITSATS RANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```


1075

```

              70      80      90      100      110      120
m670.pep    FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              |||||
a670        FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90      100      110      120

              130      140      150
m670.pep    SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
              |||||
a670        SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX
              130      140      150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1   ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAAATG CGGTTGGCAA AGCCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAAcagg cggggTTGGA ACGaggCAAA
201 GGCAGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGaaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTGCTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1   MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAASLAK KKETHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1   ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  ATCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAAcagg CGGGGTTGGA ACGAGGCAAA
201 GGCAGAGGTcG GCGAAGGAGG CGGCaaAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTGCTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1   MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep    MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
              |||||
g671        MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep    RGWNEAKARSAKEAAKSLAKKKETHAAIEPASAITPRIADSTMQAAMTAETRSMGRL

```



```

g671      |||||:|||||:|||||
          RGWNEAKARSAGAAKSLAKKKETTHATIEPASAITPRIVEMTQQAAMTAEARRSAMGRL
          70      80      90      100      110      120

          130      140      149
m671.pep  FIRYLTGDTVYAQFVQIAFGIPC VFIVAX
          |||||:|||||:|||||
g671      FIRYLAGDAVHAQFVQIAFGIPC VFIVAX
          130      140

```

```

a671.seq
1  ATGACCAGCA GGGTAATAAT CAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAATG CGGTGGCAA AGCCCAAACC GACCGCGAA ACTGCCCGG
101 TCAGCAGCA CGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTGGA ACAGTACGAA
201 GCGATGTCG GCGAAGGGTG CCGCAAAGAG TTTGGCGAAA AAAAAGCGAA
251 CCACCCATGC CGCATTGAG CCAGCTCCG CAATCAGCC GCGCATCGCG
301 GATAGCACGA TGCAGCGGC GATGATGGCG GAGACAGGGA GGTTCGGCAAC
351 GGGAGGTTA TTCATTCTT ACCTGACCCG CGATACCGTG TACGCGCAAT
401 TTGTTCAAT CGGCTTCGCG ATCCCTTGGC TTTTATAGT TGCTTGA

```

a671.pep

1	MTSRVIKMP	FNAPNTPPKM	RLAKEPKTAE	TAPVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNDAKAMS	AKGAAKSLAK	KKATTHAAIE	PASAITPRIA
101	DSTMQAAMMA	ETRRSATGRL	FIRYLTGDTV	YAQFVOIAFG	IPCVFIVA*

	10	20	30	40	50	60
m671.pep	MTSRVTIKTTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
a671	MTSRVIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
m671.pep	70	80	90	100	110	120
a671	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					
	70	80	90	100	110	120
m671.pep	130	140	149			
a671	FIRYLTGDTVYAQFVQIAFGIPCIVAX					
	130	140				

g672.seq

1	ATGAGGAAAA	TCCGCACCAA	AATCTGCGGC	ATCACCACAC	CGGAAGACGC
51	ACTGTATGCC	GCCACGCGCG	GCGCAGACGC	ATTGGGACTG	GTTTTTTTACC
101	CCCAAGCCCC	CCGCGCTATC	GACATCATTA	AAGCACAATA	AATCGCCGCG
151	GCACTGCGCG	CGTTTGTTCAG	CGTGTGCGCC	CTTTTCGTCA	CGAAAGACGC
201	GCAAAACATC	CGCCGCATCC	TTGCCGAAGT	GCGGATACAC	ATCATCCAAT
251	TCCACGCGCA	CGAAGACGAT	GCATTCTGCC	GGCAGTTGCA	CGCCCCCTAT
301	ATTAAAGCCA	TTCTGTGTTCA	CACGGCATCA	GACATCCGAA	ACGCGCGCAC
351	GCGCTTCCCC	AACGCTCAGG	GACTGCTGTT	CGATGCCTAT	CACCCTTCGG
401	AATACGGCGG	CACCGGACAC	CGCTTCGact	Ggacgctggt	gscggAATAT
451	TCGGGCAAGC	CGTGGGTGCT	TGCCGGCGGG	CTGACCCCTG	AAAACGTCGG
501	CGAAGCGCTC	CGCATCAGCA	GAGCGGAAGC	GGTGCAGGTA	TCCGGCGGCG
551	TGGAAGCGTC	TAAAGCCAAA	AAAGACCCCG	CCAAAGTCGC	CGCCTTTATC
601	GCAACCGCCA	ACCGCTATC	CCGTTAA		

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
g672.pep
  1 MRKIRTKICG ITPEDALYA AHAGADALGL VFYQSPRAI DIKAQKIAA
 51 ALPPFVSVVA LEVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATREF NAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKPAKVAAFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```
m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCCG CGTTTGTGCG CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGCGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTCGATGTA TCCGGCGGTG
551 TGGAAAGCGT TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep
  1 MRKIRTKICG ITPEDAAAA AAAGADAVGL VFFQSSRAV DIARAKKITA
 51 ALPPFVSVVA LEVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATREF DAQALLFDAY HPSEYGGTGN RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDKAAKVAAFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG ITPEDAAAAAAGADAVGLVFFQSSRAVDIARAKKITAALPPFVSVVA					
	: : : : : : : :					
g672	MRKIRTKICG ITPEDALYAAHAGADALGLVFYQSPRAIDIKAQKIAAALPPFVSVVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m672.pep	LFVNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATREF					
	: : : : : : :					
g672	LFVNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFDRPYIKAIRVQTASDIRNAATREF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m672.pep	DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAESVDV					
	: : : : : : : :					
g672	NAQALLFDAYHPSEYGGTGH RFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAESVDV					
	130	140	150	160	170	180
	190	200	209			
m672.pep	SGGVEASKGKKDKAAKVAAFIATANRLSRX					
	: : :					
g672	SGGVEASKGKKDKPAKVAAFIATANRLSRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

1078

```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCACGCCG GCGCAGACGC ATTGGGACTG GTTTTACC
101 CCCAAGCCCC CCGCGCTGTC GACATCATTA AAGCACAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTCCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GCGGGAATAT
451 TCGGGCAAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
501 CGAAGCCATC CGCATACCGG GAGCGGAAGC GGTGATGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

a672.pep

```

1  MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAV DIKAQKITA
51  ALPPFVSVA LFVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKFWVLGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAEFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

```

          10      20      30      40      50      60
m672.pep  MRKIRTKICGITTPEDAAGADAVGLVFFQGSRAVDIARAKKITAALPPFVSVA
          |||||
a672      MRKIRTKICGITTPEDALYAAHAGADALGLVFPQSPRAVDIIKAQKITAALPPFVSVA
          10      20      30      40      50      60

          70      80      90      100     110     120
m672.pep  LFVNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRF
          |||||
a672      LFVNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRFP
          70      80      90      100     110     120

          130     140     150     160     170     180
m672.pep  DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKFWVLGGGLTPENVGEAVRITGAESVDV
          |||||
a672      DAQALLFDAYHPSEYGGTGHFRFDWTLLEAYSGKFWVLGGGLTPENVDEAIRITGAEAVDV
          130     140     150     160     170     180

          190     200     209
m672.pep  SGGVEASKGKKDAKVAEFIATANRLSRX
          |||||
a672      SGGVEASKGKKDPAKVAEFIATANRLSRX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

g673.seq

```

1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGTAAC CAATGCCCA AGCACACGCC GGTCAATTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGCTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGCGGAGG CGGTCAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAG CGTACCGATG TATCCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAACTCT TCCGCTATTT

```


1079

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCATCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GGCATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGTGTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          |||
g673      MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YDDTAQFVFVDTPGFQTDH RNALNDRLNQ NVTEALGGVDVVVFVVEAMRFTDADRVVLK
          |||

```


1080

```

g673      YTDDTAQFVFDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           |||||
g673      KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVLKVWVKVKS GWADDIR
           |||||:|||||
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDNKVLKVWVKVKS GWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTTC AACCAGCCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTGTGTT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAG CGTGCCGATG TATCCGAAG ATATGTTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGCGGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTTRNRVTGI YTDDTAQFVF VDPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPLESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFDT KVLKVWVKV VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10      20      30      40      50      60

```


1081

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673						
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673						
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR					
a673						
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGGGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
a673						
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673						
	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCCGCCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETYPY
101 VIINEAIEVT KTFGGTDGKH FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCCGCCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCGGAC TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```


51 FFGTQTNAEE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAEE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	::					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAACAG	CCGCCGCGC	TTCCCGCGAG	CTGCGCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAACTT
151	TTCTTCGGCA	CGCAAACCA	TGCGGCAGAG	TACATCCGAC	AAATCCGCCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCCGAAAC	GCCCTACCCC
301	GTCATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTGCC	GCCCAAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAEE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAEE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAEE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcaccgtc
151 gCCACCGTAC CCGGCGCGCT TGAATCCCC ATCGCGCTGA TGAACTTTGC
201 CTCTTCCGAA AAATTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCGGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVC CRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVS NESGAGI
101 GRVALDYNIP IANAVLT TEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAAC TTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACGAAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGCTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVC CRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVS NESGAGV
101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVC CRTLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVC CRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFE LVS NESGAGVSRVALDYNIPIANAVLT TEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFE LVS NESGAGIGRVALDYNIPIANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGE KASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAAC TTGC
201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACGAAAAAC GACGACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGCTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVC CRTLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVS NESGAGV

```


1085

101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg
51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCCGGCGT
151 GTTCAAAACC ACTTCGTGCG CTTGCGCGCG TTTAATCAGG CAACGCGCCA
201 ACGGCGAAAT CCAAGAAATT TTGTTTTCGCG CGGTATCGAT TTCATCGACG
251 CCGACGATT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTGCGCGCG AAAAATACTT GGTGCGTTCG TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTGCTGCG
451 GTCGCCGTTG CTTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GGCCTAATGT AGTTTGTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
1 MPQILVRIFL IRYSEFIWETV RLCRFRHR SRVDFDVDRK DFNFLTAFR
51 VQNHVAFAR FNQATRRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
101 GRAEKYLVR FAQFGIDDDG SLQTFGOETD AAVDFAHAF AVKIVAVFAA
151 VAVACRPVDD LDDEGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCCGGCGT
151 GTTCAAAACC ACTTCGTGCG CTTGCGCGCG TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTTCGCG CGGTATCGAT TTCATCGATG
251 CCGACGATT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC
301 CGTCGCGCGG AAAAATACTT GGTGCGTTCG TTCGCGCAAT TCGGGATCGA
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTGCTGCG
451 GTCGCCGTTG CTTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GGCCTAATGT AGTTTGTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
1 MPQILVRIFL IRYSEFIWETA RLCRFRHR SRVDFDVDRK DFNFLTPFR

1086

51 VQNHFVAFAR FNQTTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLTFFRRVQNHFVAFAR					
g677	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLTFFRRVQNHFVAFAR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m677.pep	FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG					
	:					
g677	FNQATRRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDGRAEKYLVGRFAQFGIDDDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVDFAHTAFVAVFAAFAVACRPVDDLDLDDFGAFFVDQLIKLVFQCL					
g677	SLQTFGQETDAAVDFAHTAFVAVFAAFAVACRPVDDLDLDDFGAFFIDQLIKLVFQCL					
	130	140	150	160	170	180
	190	199				
m677.pep	PSGGRNVVFGFGTHIVCGX					
	-					
g677	PSGGRNVVFGFGTHIVCGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTTG
51	GGAAACGGCG	CGTTTGTGCC	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCATT	TCCTCAGGCC	CTTCGGCGT
151	GTTTAAAC	ACTTCGTCGC	CTTCACGCGC	TTTAATCAGA	CAACGAGCCA
201	GCGCGGAAT	CCAAGAAAT	TTGTTTGCG	CGGTATCGAT	TTCATCGATG
251	CCGACGATT	TGACGGTTG	CTCGCGCCG	TCGCGCGCA	ACAGACCGAC
301	GGTCGCGCG	AAAACACTT	GGTCGGTCG	TTCGCGCAAT	TCGGGATCAA
351	CGACGACGC	GGCTTCCAAA	CGCTTGGTCA	GGAACGGAT	GCGGCGGTCG
401	ATTTCGCGCA	TACGCGTTT	CCCGTAAAG	TAGTCGCGT	TTTCGCTGCG
451	GTCGCGGTT	CCTGCCGCC	AGTTGACGAT	TTGGACGATT	TCGGGCGGTT
501	CTTTATTAAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GGCGTAATGT	AGTTTGTGGT	TTCGGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep

1	MPQILVRIFL	IRYSFIWETA	RLCRFRHRS	SVDFDVFDRK	DFNFLTFFRR
51	V*NFHFAFTR	FNQTTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVVAQQTD
101	GRAEKHLVGR	FAQFGINDDG	GFQTLGQETD	AAVDFAHTAF	AVKVVAVFAA
151	VAVACRPVDD	LDDFGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*

m677/a677 93.4% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLTFFRRVQNHVAFAR					
a677	MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDRKDFNFLTFFRRVXNHVAFAR					
	10	20	30	40	50	60
	70	80	90	100	110	120

1087

```

m677.pep  FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQSDRRAEKHLVGRFAQFGIDDDG
          |||||||||||||||||||||||||||||||||||||||:||||| ||||||||||||||
a677      FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGDAEKHLVGRFAQFGINDDG
          70      80      90      100     110     120

          130     140     150     160     170     180
m677.pep  SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
          ::||:|||||||||||||||||:|||||||||||||||||::|:|||||
a677      GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
          130     140     150     160     170     180

          190     199
m677.pep  PSGGRNVVFGFGTHIVCGX
          |||||||||||||||
a677      PSGGRNVVFGFGTHIVCGX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
51  CTGCATCGTC ATTTCCACGA TCGCGGCGT GATTGCGGAA GCAGgttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTtg ccAAACTCTt tGCCGCACcc
151 ttgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCAATC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATT TGGGCGGTGT ATTCGGTGCA TTGAAAGGCG TTTGATTGT
351 TACCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCCTcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51  FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCGG TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TCGCGGCGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTTT TGCCGCCTCC
151 TTCGCGGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTGCTTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCG TTTGATTGT
351 TACCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51  FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
101 NRILGGVFGA LKGVLIIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

```

      10      20      30      40      50      60
m678.pep  MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ
          |||||:|||||:|||||:|||||:|||||:|||||
g678      MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m678.pep  PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL
          |||||:|||||:|||||:|||||:|||||:|||||
g678      PRLFALALSFISLFVIACLIQKMLRSLTGAWSAVGLGFANRILGGVFGALKGVLIIVTLL
          70      80      90      100     110     120

      130     140     150     160
m678.pep  VMLASKTDLDPTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX
          :|||||:|||||:|||||:|||||: || : ||
g678      IMLASKTDLDPTEEWQSYTVPFFVSLSEAVLNHTDNAPESLDDDX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCGTTGCG ACACCTCCTC GTCTCCGCCA TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGC CGCGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCG CCAAACCTT TGCCGCACCC
151 TTCGCCGACA TCGCCTTTCG ATCGTTCCAA CCGCGCTGT TTGCATTGGC
201 TCTGTCGTTT ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATT TGGCGCGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTTCAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51 FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGILIITLL VMLASKTDL PTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

```

      10      20      30      40      50      60
m678.pep  MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ
          |||||:|||||:|||||:|||||:|||||:|||||
a678      MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m678.pep  PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL
          |||||:|||||:|||||:|||||:|||||:|||||
a678      PRLFALALSFISLFVIACLIQKILRSLTGAWSAVGLGFANRILGGVFGALKGILIITLL
          70      80      90      100     110     120

      130     140     150     160
m678.pep  VMLASKTDLDPTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX
          |||||:|||||:|||||:|||||:|||||:|||||
a678      VMLASKTDLDPTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51 GGCGACGAGG ACGCGCAGGC TGCCGTCTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGTTG

```



```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTAAACTGA TGTTTTCTG TTTCACATGG TCGAGCAGCC
551 GTCCGACGGT GCGCAGCACT ATTTCCGAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTCCA GTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
  1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
  1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
 51 GCGCAGCAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CCGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCGCTT CTGAATGATA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGGCG GCGCACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GCGCAGCAGC ATTTCCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
  1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680      MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFIKSTISRSSRLRFKXVMSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680      TLCLVLQKTIWFIKSTISRSSRLRFKVKSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAELVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

```


1090

```

g680      |||||
          ASLRIGA EKVAEKSRVWRWRG SICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW
          130      140      150      160      170      180

          190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPNKTVWRSGRFLMX
          |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRTVCRSGRFLMX
          190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```

a680.seq
1  ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCCGCGCGG CGATATCGGT
51  GCGCAGCAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCTG ACGCTTTGTT TGGTTTGTGA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTCTTGGCG GCGCACTTCG ACGGTTTCGG GCGCGTTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTGC
451 TCGATAAAAC CCATATCCAG CATA CGGTCTG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GCGCAGCAGC ATTTCCGAGC CGGCACGAGC GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```

a680.pep
1  MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGA EKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

m680/a680 98.6% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||||
a680      MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRFKX MVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||||
a680      TLCLVLQNTMTWFICKSTISRSSRLRFKX MVSTAMMCCSTLALVVS CAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGA EKVAEKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTL FKWMFFCFTW
          |||||
a680      ASLRIGA EKVAEKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTL FKWMFFCFTW
          130     140     150     160     170     180

          190     200     210     220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
          |||||
a680      SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
          190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

```

g681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGgcgacgg

```


1091

```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCcgt cgaggttgGG GCGATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CCGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CCGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CCGCGAGGCT GACGATGCTG AAGTTGTCGG GGTCTCGGT
451  GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTGTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTCGCCGCT TGTCCGCAGA CGGCGCGCGT TTGGTGGTAC
701  AATGTGCCCC GTTTCGAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

g681.pep
  1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
 51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101  RLPVNGLECA AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVGVVG
151  VFVGFVAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
201  CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251  KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
  1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AACTTTTCGG AAGAGGCAAA
 51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101  TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTCGCCGT CGAGGTTGGG GCGATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CCGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CCGCGGTTTC AGGGTTGGTT
401  TTGGCGATGT CCGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCGGT
451  GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTGTTG
551  GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATT
651  TACCACGATT CGTGCCTTGT CCGCAGACGG CCGCGGTTTG GTGGTACAAT
701  GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751  CGCATTCCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
  1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
 51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101  RLPVGDGLECA AVFGKLPCAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIVG
151  VFVGLVAEE TPAAVVFKNG GFAVEEADGP VLFGDGVGGD TAVECRGKCL
201  CKCVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251  RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPLISLV
          |||||
g681       MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
          10      20      30      40      50      60

```


1092

	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSRLPVGDLGECVFGKLPCAA					
	:					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSRLPVGDLGECVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDGVEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
	:					
g681	FGLGKQCGGFRVGFVDGVEADDAEVVGVGVFVGLVAAEETPAAVVFKNGGFAVKEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
	:					
g681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKRIRAVFCGRRX					
g681	LRCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1   ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTC GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTG CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGATGGTG TTCATTGACT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTT AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTGCTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAAATCGG TTCATTGCGG GAATACGTT. GGGGAAAAAC TTGCGGATT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1   IITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGKLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	:					
a681	IITPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSRLPVGDLGECVFGKLPCAA					
	:					
a681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGGFGMPSEGSVLRLPVGDLGECVFCQFPRAA					
	70	80	90	100	110	120

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDGEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
a681	FRLGEQCGGFRVGFVDIGEADDAEVVRVVGVFVGLVAAEETPAAVVFKNGGFAVEEADGL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGXKLTDFTTIRALSADGGGLVVCAPFAAL					
a681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTXGKKLADFTTILALSADGGGLVVCAPFAAL					
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIRAVFCGRRX					
a681	RCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTGTG GTGAATGATG AAATAAAAAT GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTCCGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVSF GKWRKNWDIR YCLLHLIHLF STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. ..EMAMPSEP DWIQTAFDMA YGFIRFPTDR
101 PIRTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

1094

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||: ||| ||: ||||| |||: || ||||| ||||| ||||| ||||| |||||
g682      MRDFAVWVPYGERRKNWDIRYCLPHLIRLSPTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY-----EMAMPSEPDIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR
          ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      PILILIDYICVNDEIKMPSEPDIQTAFCMAGFIRFPTDRPILTRQSGVVRISPRTGFR
          70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
          ||||| |||||
g682      YPTRSLPKSKKAYGX
          120     130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2253>:

```

a682.seq
1   ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:

```

a682.pep
1   MRDFTVWVSY GKWRKNWDIR YCLLHLIHL SSTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIEY.. ..YIRFPTDR
101 PILTRPTGVV RISPTGFRY PTRSLPKSKK AYG*

```

m682/a682 80.6% identity in 129 aa overlap

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a682      MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110     120
m682.pep  PILILIDYEMAMPSEPDIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS
          ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| |||||
a682      PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS
          70      80      90      100

      130
m682.pep  LPKSKKAYGX
          ||||| |||||
a682      LPKSKKAYGX
          110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2255>

```

g683.seq
1   ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTACT
51  CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
151 GACAGTGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTGAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAC ATACCGCTTA
301 AGTTTCGTAC AGTTATTGTA TACAAAAAC ACGGAAATT CCACACAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA

```


401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683 >:

g683.pep

1 MIKETLMRPIL FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTACCAAT CTAAAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..

1 MIKETLMRPIL FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPILFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPILFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
m683.pep	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
m683.pep	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
g683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTACCAAT CTAAAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

1 MIKETLMRPIL FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
a683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
m683.pep	IFQDKKVVVTLNKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTONYTA					
a683	IFXDKKVVVTLNKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
m683.pep	IFQDKKVVVTLNKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTONYTA					
a683	IFXDKKVVVTLNKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
a683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
a683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

```

1  ATGCGCCTTT TCCCATCGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGCGGCGGAA ACCGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCATCAACAC
201 CGCACAAAAC CATGTTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAC CTTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGACAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

```

1  MRLFPIAAL TLAACGTVQS TQYFVLPDSR YIRPATQGGG TAVEVRLAEP
51  LKRGLVYQT DPYRLNTAQN HWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTDKW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD
151 GYAAMTALE QGLKQAAQOM VE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

```

1  ATGCGCCTTT TCCGATTGC CGCCGCCCTG TCGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGCGGCGGAA ACTGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CACGCTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGAAAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CGATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

```

1  MRLFPIAAL SLAACGTVQS TQYFVLPDSR YIRPATQGGG TAVEVRLAEP
51  LKRGLVYQT DPYRLNTAQN HWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTEKW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD

```


Homology with a predicted ORF from *N. gonorrhoeae*

m684/g684 97.7% identity in 172 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

Homology with a predicted ORF from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFP	IAAALS	LAACGTVQSTQYFVLPDSRYIRPATQGG	ETAVEVRLAEPLKRGGLVYQT		
a684	MRLFP	IAAALT	LAACGTVQSTQYFVLPDSRYIRPATQGG	ETAVEVRLAEPLKRGGLVYQT		
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTA	NHVVADTLD	DMLEAALSNAFNRLDSTRIFV	PASRSGSTEKWT	VYIDAFQGS	
a684	DPYRLNTA	NHVVADTLD	DMLEAALSNAFNRLDSTRIFV	PASRSGSTEKWT	VYIDAFQGS	
	70	80	90	100	110	120
	130	140	150	160	170	

g685.seq

1	TTGTTTTGCC	GTATCGGGAA	TTTTGCGTTT	TGCGGCGTGG	TTTCTGCAGG
51	TTGTTTGCTT	AATAATAAAC	ATTCTTATTC	GTATGCAAG	GAACCGCACA
101	CCGTGA AAC	CGCTTTTAT	TGGCGACcct	CGCGCTTCTT	CGCCGCCGCC
151	TGTTTCGCCG	AACCTTGGCG	CGAAAAAACT	GTATcgcCGG	CATCCCAAG
201	CGCATCCACA	CCTGTCGCCA	CGCTGACCGT	CGCGACCGCG	CGGGGCGATG
251	CCGTTGTGCC	GAAGAAATCC	GAACgcgtcg	cgctgtAcga	CtggcCGCGG
301	TtgytACGCG	TGACCGAGCC	GGCGCTGAAT	TGGCGCGCAA	CCACCGCGCC
351	GGTGCCTGTG	GACTATTTCG	AGCCTGCAIT	TGACAAGCGG	GCAACGGTGG
401	GGACGCGTGT	TGAGCCCGAT	TGCGAATCCC	TGCACCGCCA	CAATCCCGAG
451	TTTGTCAAT	CCGGCGGGCG	GGCTGCGGAA	CGGTATGAAC	AGTTTGGCGAA
501	AAACGCGACAG	ACCATAGATT	TGACGGTGGG	CAACGGCAAT	ATCCGCGACCA
551	CGCGCGAGAA	CGAGATGGAG	ACCGTGTCCG	GGATTTTCGG	TAGGAAGCG
601	CGCGTGGCGG	AATTGAATGC	CGCATTTGAC	GGCGTGTTCG	CCCAAGAACCG
651	CGAAGCGGCC	AAAGCGAAAG	GACGCGGGCT	GGTGTGTGTCG	GTTACAGGCA
701	ACAAGGTGTC	CGCCTTCCGC	ACGCAATCCG	GCTTGGCAAG	TTGGATACAC
751	CGCGACATCG	CGCTGCCCGC	CGGTGACGAA	TCTTTACGCA	ACGAAGGGCA
801	CGGCGAGCCC	GTTTCTTTCG	AATACATCAA	AGAGAAAAAC	CCCGGCTTGA
851	TTTTCATCAT	CGACCGCAC	GCCCGCATCG	GGCAGGAAG	CGCGGCTGCC
901	GTGGAAGTGT	TGGATAACGC	CTGTGTATCG	GGCAGCAACG	CTTGGAAAGC
951	CAAGCAAATC	ATCGTCATGC	CTGCCCGGAA	CTACATTGTC	CGCGGCGGGG
1001	CGCGGCAAGT	GATACACGCG	CGGGAACAGT	TGAAGCGCGC	GTTTGAAGAG
1051	CGAAGAACCCG	TTTCCGGCGCA	GTAG		

g685.pap

1	LFCRIGNFAF	CGVVSAGCIL	NNKHSYSYAK	EPHTVKPRFY	WAACAVLPAA
51	LSPEPAEAKT	VSAASQAAST	PVATLTVPFA	RGDAVVPKNP	ERVAVYDWAQ
101	LDLTTEPEGVN	VGATTAIPVRV	DYLPQAFDKA	ATGTGLEPND	CESLHRHNPQ
151	FVITGGPGGAE	AYEQIAKNAT	TIDLTVDNGN	IRTSGEKQME	TLSRIFGKEA
201	RVAELNAQID	ALFQAQKREA	KGKGRGLVLS	VTGNKVSAGF	TQSRLASWII
251	GDIGLPPVDE	SLRNEGHQSP	VSEFYIEKKN	PWGIFITDRT	AAQGLGEPAA
301	VEVLDNALVC	GTNAWKRKQI	IVMFAANYIV	AGGARQLIQ	AEQLKAAFEK
351	AEVPAWA*				

u685.seq

1	TTGTTTTGCC	GTATCGGGAA	TTTTGCGTTT	TGCGGCGTGG	TTTCTGCAGG
51	TTGTTTTGCTT	AATAATAAAC	ATTCCTATTCC	GTATGCAAG	GAACCCGACA
101	CCGTGAACAC	CGCTTTTAT	TGGCGACCT	CGCGCTTCT	GCTGACCCCC
151	TGTTGCGCCG	AACCTGCCGC	CGAAAAAACT	GTATCCGCCG	CATCCGCAAT
201	TGCCCGCCAG	CTGACCGTGC	CGACCGCGCG	GGGCGATGCC	GTTGTGCCGA
251	AGAAATCCGA	ACGCGTCGCC	GTGTACGACT	GGGCGGCGTT	GGATACGCTG
301	ACCGAATTGG	CGGTGAATTG	GGGCGCAACC	ACCGCGCCGG	TGCGCGTGA
351	TTATTTTCAG	CCTGCATTTG	ACAAGCGCGC	AACGGTGGGG	ACGCTGTTCG
401	AGCCCGATTA	CGAAGCCCTG	CACCGCTACA	ATCCTCAGCT	TGTCATTACC
451	GGCGGGCCGG	GCGCCGAAG	GTATGAACAG	TTAGCGAAAA	ACGGCACCAC
501	CATAGATTCT	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC	GGCGAAAAAGC
551	AGATGGAGAC	CTTGGCGCGG	ATTTTCGGCA	AGGAAGCGCG	CGCGCGCGAA
601	TTGAAGGCGC	AGATTACGCT	GCTGTTTCGC	CAAACGCGCG	AAGCCCGCAA
651	AGGCAAAAGGA	CGCGGGCTGG	TGCTGTCCGT	TACGGGCAAC	AAGGTGTCCG
701	CTTCCGGCAC	GCASTCCGGT	TGTGCAAGTT	GGATACACGG	CGCATCTGCT
751	CTACCGCGTG	TAGACGAATC	TTTACGCAAC	GAGGGCGACG	GGCAGCCTGT
801	TTCCTTCCAA	GATCATCAAG	AGAAAAACCC	CGATTGGATT	TTCATCATCG
851	ACCGTACCCG	CGCATCCGGG	CAGGAAGGCG	TGGCGGCTGT	CGAAGTATTG
901	GATAACGCGC	TGGTACGCGG	CACGAACGCT	CGGACGCGCA	AGCAAAATCAT
951	CGTCATGCCCT	GCCGCGAACT	ACATTGTCGC	GGGCGGCGCG	CGCGCAATTGA
1001	TTCAGCGGGG	GGAGCAGTTG	AAGCGGCGGT	TTAAAAAGGC	AGAACCCGTT
1051	GCGGCGGGGA	AAAAGTAG			

п685.рер


```

1  LFCRIGNFAF CGVVSAGCIL NNKHSYSYAK EPHI
51 CSPEPAEKT VSAASASAAT LTVPTARGDA VVPI
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFI
151 GPGGAEAYEQ LAKNATTIDL TVDNGNIRTS GEK
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSJ
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIII
301 DNALVRGTNA WRRKQIIVMP AANYIVAGGA RQLJ
351 AAGKK*

```

Computer analysis of this amino acid sequence
Homology with a predicted ORF from *N. gonc*
 ORF 685 shows 94.4% identity over a 356 aa overlap
N. gonorrhoeae:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30
m685.pep      LFCRIGNFAFCGVVSAGCLLNKHSYSYAKEPHT
g685           |||||
              10      20      30
              70      80      90
m685.pep      VSAASASA----ATLTVPTARGDAVVPKNPERVA
g685           ||||| :| |||||
              70      80      90
              120     130     140     150
m685.pep      DYLPAPFDKAATVGTLEFPDYEALHRYNPQLVIT
g685           ||||| ||||| :|||:|:|:|
              130     140     150
              180     190     200     210
m685.pep      IRTSGEKOMETLARIFGKEARAAELKAQIDALFA
g685           ||||| ||||| :|||:|:|:|
              190     200     210
              240     250     260     270
m685.pep      TQSRLASWIHGDIPLPPVDESLRNEGHPVSFE
g685           ||||| ||||| ||||| |||||
              250     260     270
              300     310     320     330
m685.pep      VEVLDNALVRGTNAWRRKQIIVMPAANYIVAGGA
g685           ||||| ||||| ||||| |||||
              310     320     330

```

The following partial DNA sequence was ident

```

a685.seq
1  TTGTTTGCC GTATCGGGAA TTTGCGTTT TGCG
51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTAT
101 CCGTGAAACC GCGTTTITAT TGGGCAGCCT GCGC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAAT GTAT
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGC
251 AGAATCCCGA ACGGTCGCC GTGTACGACT GGGC
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCG
351 TTATTTCAG CCTGCATTG ACAAGCGGCG AACG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCC
451 GCGGGGCGG GCGCGGAAGC GTATGAACAG TTGG
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGA
601 TTGAAGGCGC AGATTGACGC GCTGTCGCC CAAG
651 AGGCAAGGA CGCGGGCTGG TGCTGTGGT TACG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGAT
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGG
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGAT

```



```

VYDWAALDTLTPEGVNVGATTAPVRV
100      110      120

160      170
GGPGAEAYEQLAKNATTIDLTVDNGN
|||||
GGPGAEAYEQLAKNATTIDLTVDNGN
160      170      180

220      230
QTREAAKGKGRGLVLSVTGNKVSAPG
| |||||
QKREAAKGKGRGLVLSVTGNKVSAPG
220      230      240

280      290
YIKEKNPDWIFIIDRTAAIGQEGPAA
|||||
YIKEKNPDWIFIIDRTAAIGQEGPAA
280      290      300

340      350
RQLIQAAEQLKAAFKKAEPVAAQX
|||||
RQLIQAAEQLKAAFKKAEPVAAQX
340      350

```

ified in *N. meningitidis* <SEQ ID 2271>

```

3CGTGG TTTCTGCAGG
3CAAAG GAACCGCACA
3GTCTT GCTGACCGCC
3CGCCG CATCCGCATC
3ATGCC GTTGTGCCGA
3GCGTT GGATACGCTG
3GCCGG TGCCTGTGGA
3TGGGG ACGCTGTTTG
TCAGCT TGTCATTACC
3GAAA ACACGACCAC
ACACGC GCGGAAAAGC
AGCGCG CGCGCGGAA
3GCGCG AAGCCGCCAA
3GCAAC AAGGTGTCCG
ACACGG CGACATCGGC
3GCACG GGCAGCCTGT
3GGATT TTCATCATCG

```

PCT/US99/09346

999

```

TVKPRFY WAACAVLLTA
QNPVERA VYDWAALDTL
EPDYEAL HRYNPQLVIT
METLAR IFGKEARAAE
IFGTQSR LASWINGDIG
ORTAAIG QEGPAAVEVL
QAAEQL KAAFKKAEPV

```

gave the following results:

rrhoeae

overlap with a predicted ORF (ORF 685) from

```

40      50      60
TVKPRFYWAACAVLLTACSPPEAAEKT
|||||
TVKPRFYWAACAVLPAACTPEAAEKT
40      50      60

```

```

100      110
VYDWAALDTLTGTVNVGATTAPVRV
|||||

```


1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAGCGCA AGCAAATCAT
951 CGTCATGCGT GCCGCGAAGT ACATTGTGCG GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPTYEAL HRYNPQLVIT
151 GGPGEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGGK RGLVLSVTGN KVSAGTQSR LASWINGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

```

m685/a685 98.9% identity in 355 aa overlap

      10      20      30      40      50      60
m685.pep  LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAEKT
          |||
a685      LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAEKT
          |||

      10      20      30      40      50      60
m685.pep  VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
          |||
a685      VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
          |||

      70      80      90     100     110     120
m685.pep  VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
          |||
a685      VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
          |||

      70      80      90     100     110     120
m685.pep  VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
          |||
a685      VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
          |||

      130     140     150     160     170     180
m685.pep  PAFDKAATVGTLFEPTYEALHRYNPQLVITGGPGAAYEQ LAKNATTIDLTVDNGNIRTS
          |||
a685      PAFDKAATVGTLFEPTYEALHRYNPQLVITGGPGAAYEQ LAKNATTIDLTVDNGNIRTS
          |||

      130     140     150     160     170     180
m685.pep  PAFDKAATVGTLFEPTYEALHRYNPQLVITGGPGAAYEQ LAKNATTIDLTVDNGNIRTS
          |||
a685      PAFDKAATVGTLFEPTYEALHRYNPQLVITGGPGAAYEQ LAKNATTIDLTVDNGNIRTS
          |||

      190     200     210     220     230     240
m685.pep  GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGKRLVLSVTGNKVSAGTQSR
          |||
a685      GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGKRLVLSVTGNKVSAGTQSR
          |||

      190     200     210     220     230     240
m685.pep  GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGKRLVLSVTGNKVSAGTQSR
          |||
a685      GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGKRLVLSVTGNKVSAGTQSR
          |||

      250     260     270     280     290     300
m685.pep  LASWINGDIGLPPVDESLRNEGHPVSFEYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
          |||
a685      LASWINGDIGLPPVDESLRNEGHPVSFEYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
          |||

      250     260     270     280     290     300
m685.pep  LASWINGDIGLPPVDESLRNEGHPVSFEYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
          |||
a685      LASWINGDIGLPPVDESLRNEGHPVSFEYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
          |||

      310     320     330     340     350
m685.pep  DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPPVAAGKKX
          |||
a685      DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQLKEAFKAEPVAAGKEX
          |||

      310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

```

g686.seq (partial)
1  ..AATTCTCCTT GCCGCGCGCA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCCGTCAGCA TAGCGCCGGC
151 ATTGTGGAAA CGGTCCGGCA GCCGTTGTCC GGTGCTCGCG TTGTCGGTCA
201 GGTGTAGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```


This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686>:

g686.pep (partial)
 1 ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
 51 IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
 101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..
 1 ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTGGC
 51 GGCCTGCGGC GGTTCGGAAG CCGGCAGCGG AGCGNNNNNN NNNNNNAATT
 101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTGAA
 151 GGCTTCGCGC GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
 201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGCG TCAGCATACT ACCGGCAATTG
 251 TGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
 301 GAGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
 351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
 401 TCGGCGGGAT GGTGTTTCGTA TCCGTCCCAA TGGATCGCGT AAAGGCTAAA
 451 TCCGTCAACG GGACTACCGG CTTATCAGA ATCGGAATGT GA

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep
 1 MMLKKFVLGG IAAVLAAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
 51 GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
 101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
 151 SVNGTTGFIR IGM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACG	GS	EGGSGAXX	XXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG		
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYS	SLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS			
m686		AVSGGAFESVAYS	SLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS			
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPVIAVGGMVFVSV	PMDAVKAESVNGTTGFVRIGMX			
m686		GIAAALWPVIAVGGMVFVSV	PMDAVKAKSVNGTTGFIRIGMX			
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)
 1 ..AATTTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
 51 TGAAGCTTC GCGGCGATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
 101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGGTCAGCA TACTACCGGT
 151 ATTGTGGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
 201 GGTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
 251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
 301 CCGTCGCGG GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC
 351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

```

      10          20          30          40          50          60
m686.pep    LKKFVLGGIAALVLAACGGSEGGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
              |||   ||||:|||||:|||||
a686         NFSCRADDDVEDDICSAVESFGGIARSVQLG
                  10          20          30

      70          80          90          100         110         120
m686.pep    AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGVQEADILGNIFYVVAVYIPRAFGS
              |||   ||||:|||||:|||||
a686         AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGVQEADILGNIFYVVAVYIPRAFGS
                  40          50          60          70          80          90

      130         140         150         160
m686.pep    GIAAALWPFVIAGGMVFVSVPMDAVKAHSVNGTGFIRIGMX
              |||   ||||:|||||:|||||
a686         GIAAALWPFVIAGGMVFVSVPMDAVKAESVNGTGFIRIGMX
                  100        110        120        130

```

q687.req

1	ATGAAATCCA	GACACCTCGC	CCTGCCTCTC	GGCGTTGCCG	CCCTGTTCCG
51	CTCTGGCGCG	TGGCGACAGA	AAGTGCACAA	CAGGCTCCCC	GCCGACAGCG
101	CGCTTGGCGC	TTGGCGAGCC	GCGCCCGCGG	CAGAGTGGCT	CGAAGGGCAG
151	AACTACACCG	TCCTTGCCAA	CCCGATTCCC	CAACAGCAGG	CAGGACAGGT
201	TGAAGTGCTT	GAGTGTTCGC	GCTAATTTTG	TCGCCATGTC	GCCCGCCTcg
251	AACCTGTTT	GACCAAAAC	GCCAAGTCT	TTAAAGACGA	TATGTACCTG
301	CGTACCGAAC	ACGTCGTCGT	GCAGAAAGAA	ATGCTGCCCG	TGGCAGCGct
351	cGCCCGCGCC	CTGCATATGG	CTGCCCGCGA	AAACAAGATG	GTGGCGAACA
401	GCCATATTT	CGATGCGATG	GTCACACCAA	AAGTCAAGCT	GCAAGAGCCG
451	GAAGTCTCTA	AAAAATGGCT	GGGCGAACaa	ACgcctTTTG	ACGGCGAAAA
501	ATGCTCTGCC	GCCTACGAAT	CCCCCGAAG	TCAGGCGCGC	GcgygcAAAA
551	TGCAGGAGCT	GACCGGAAAC	TTCCAAATCG	ACGGTACGCC	CCGGTTATAC
601	GTCGGCGGCA	AATATAAAGT	CGAATTTGCC	GACTGGGAGT	CCGGTATGAA
651	ACCATTCGAC	CTTTTGCGCG	ACAAAGTACG	TGAAGAACAA	AAAGCCGCGC
701	AGTAG				

q687.pep

```

1  M K S R H L A L A L   G V A A L F A L A A   C D S K V Q T S V P   A D S A P A A S A A   A A P A G L V E Q G
51 N Y T V L A N P I P   Q Q O A G K V E V L   E F F G Y F C P H C   A R L E P V L S K H   A K S F K D D M Y L
101 R T E H V V W Q K E   M L P L A R L A A A   V D M A A A E S K R   V A N S H I F D A M   V N Q I K L Q E P
151 E V L K W I L G E Q   T A F D G K V K V L A   A Y E S P E S Q A R   A G K M Q E L T E T   F Q I D G T P T V I
201 V G G K Y K V E F A   D W E S G M N T I D   L L A D K V R E E Q   K A A O *

```

m687.beq

1	ATGAAATCCA	GACACCTTGC	CCTCgGCGTT	GCCGCCCTGT	TCGCCCTTGC
51	CCGCTGGCGAC	AGCAAAGTCC	AAACCCAGGT	CCCCGCCGAC	AGCGCGCCTG
101	CCGCTTCCGC	AGCCGCGCCG	CCGCGACGGC	TGGTCCAAGG	GCAAAACTAT
151	ACCGTCCCTTG	CCAACCGGAT	TCCCCAACAG	CAGCGAGCCA	AAGTCGAAGT
201	CTCTGAAGTTT	TTCGGCTATT	TCTGTCCGCA	CTGCGCCAC	CTCGAACCTG
251	TTTTAAGCAA	ACACGCCAAG	CTTTTAAAG	ACGATATGTA	CCTGCGTACC
301	GAACACGTCG	TCTGGCAGAA	AGAAATGCTG	ACGCTGGCAC	GGCTGCGCGC
351	CGCCGTCGAT	ATGGCTGCCG	CCGACAGCA	AGATGTGGCG	AACGAGCCATA
401	TTTTCGATGC	GATGGTCAAC	CAAAAAATCA	AGCTGCAAAA	TTCGGAAGTC
451	CTCAAAAAAT	GGCTGGGCGA	ACAAACCGCC	TTTGAAGCGCA	AAAAAGTCTC

1103

```

501 TGCCGCTAC GAGTCCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
1  MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGyFCPhCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNEPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687 97.0% identity in 234 aa overlap

      10      20      30      40      50
m687.pep  MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
          10      20      30      40      50      60

      60      70      80      90     100     110
m687.pep  QQQAGKVEVLEFFGYFCPhCAHLEPVLSKHAKSFKDDMYLRTHEHVWVQKEMLTLARLAAA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      QQQAGKVEVLEFFGYFCPhCARLEPVLSKHAKSFKDDMYLRTHEHVWVQKEMLTLARLAAA
          70      80      90     100     110     120

     120     130     140     150     160     170
m687.pep  VDMAAADSKDVANSHIFDAMVNQKIKLQNEPEVLKKWLGEQTAFDGKKVLAAYESPESQAR
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      VDMAAAESKDVANSHIFDAMVNQKIKLQNEPEVLKKWLGEQTAFDGKKVLAAYESPESQAR
          130     140     150     160     170     180

     180     190     200     210     220     230
m687.pep  ADKMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      AGKMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
1  ATGAAATCCA AACACCTCGC CCTCGGCGTT GCGGCCCTGT TCGCACTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCC GCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACTGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CTTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTGACGGCA AAAAAAGTCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGyFCPhCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNEPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N. meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

	10	20	30	40	50	60
m687.pep	MKSRLHAGVAALFALAACDSKVQTSVPADSAPASAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSRLHAGVAALFALAACDSKVQTSVPADSAPASAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
m687.pep	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVWQKEMLTARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVWQKEMLTARLAAAVD					
	70	80	90	100	110	120
m687.pep	MAAADSKDVANSHIFDAMVNQIKLQNEVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKLQNEVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
m687.pep	KMQLTETTFQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX					
a687	KMQLTETTFQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTGACACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAT	CATCCAAGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTCGCCCGCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688>:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERSVLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGLVLRTEG	DALQNAEAL	RAKQNAADKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTGACACAG	AAAGGCATT	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCCTGTTC	CCCTCGTACA	AACTCAAAT	CATACAGGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTCCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCTCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAAACATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERSVLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGLVLRTEG	DVLQNAEAL	KDRQNTDKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

```
m688/g688    90.6% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYPSRFAQKGISVNKTLILALSALLGLAACSAERVSFLFPSYKLKIIQGNELEPRAVAA
              |||  |||||  |||||  |||||  |||||  |||||
g688          VLHXTSRFAQGSPVNKTLILALSALFSLTACSVERVSLFPSYKLKIIQGNELEPRAVAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLTVYFENGVLVRTEG
              |||  |||||  |||||  |||||  |||||  |||||
g688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLTVYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDRPX
              |||  |||||  |||
g688          DALQNAAEALRAKQNAADKQX
              130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```
a688.seq
 1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51  AACCCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCACTGTTC CCCTCGTACA AACTCAAAAT CATAcAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCCGCCCGG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTT GAAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```
a688.pep
 1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSFL PSYKLKIIQG
51  NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLTVYF ENGVLVRTEG NALQNAAEAL RVKQNAADKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

```
m688/a688    93.5% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYPSRFAQKGISVNKTLILALSALLGLAACSAERVSFLFPSYKLKIIQGNELEPRAVAA
              |||  |||||  |||||  |||||  |||||  |||||
a688          VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFPSYKLKIIQGNELEPRAVAS
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLTVYFENGVLVRTEG
              |||  |||||  |||||  |||||  |||||  |||||
a688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLTVYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDRPX
              |||  |||||  |||
a688          NALQNAAEALRVKQNAADKQX
              130     140
```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCTAC CTGCCCCGCA
101 TTCCCGAAAT GCGCGAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTATGT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GCGCGAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGGCGAG GCATGGCTGT
351 AGTCATCGTc ggtgcatggt tgcgcgatTA TTATTCCGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCAITC TGATGGTTGT GCCCGTGGCC
451 GCACCCATGG TCGGCGCATT GTTGCGAGGA TTGGGCGGAT GCGGGGCGAT
501 TTTTCGTTTC ttggcGgcgt ATTCCGCCGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTCTGC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTC
601 GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTCAGG CATTGAGCTT CGGTTCGATG TTCGCCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CGGTACGCAT GGTGTGTTGC ACTCAACATC ATCAGCATGA TGTTTTTCAG
801 CCGCGTTACC GCGTGGCGGC TTAACCCGCG CGGCATCCG CAAAGCATCC
851 TGCTCGGGGG GATTGTGCTC CAATTGCGCG CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTTT TGGCTGCCGG TCGCGTCCGT
951 GATGTTTTCC GTCGGTACGC AGGGCCTGGT CGGTGCCGGC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTG
1051 GGTGTATGCC GGTCTTAAT CGGCGCGGCG GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCCCT TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGAAGGAAA ACGAAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689 >:

g689.pep (partial)

```

1  ..SPPLPPMSGK IMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFGTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLLNLRAVOA FGAGMAVVIV GAMVRDYYSG RKAQMFIALI GIILMVVPLA
151 APMVGGALLQG LGGWRAIFVF LAAYSPVLPQ LVQYFLPNPA VGGKIGRDVF
201 GLVAGREFKRV LKTRAAMGYL FFOAFSFGSM FAFLETSEFV YRQLYHVTPH
251 RYAWVFALNI ITMMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSQLA
301 AVLFFGLPPF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCGG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCCGACG AGAATTTATG
151 CTTCTGTCGG ATTATCCTGA AATGAGCGAA AAACATGATG CGGTTTGTAT
201 GGCATGCTG GTTACGCTGA TCGCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCCG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCTTGCC GTTGCCGCCA TCGTATTGTT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGGT CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGTTAC
701 AGTATTTCTT GCCCTGCTCC GCGTCCGGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTCCGTTCC ATGTTCCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCG TGTACGCCT
901 CATCAATACG CTTGGGCGTT TGCACCTAAC ATCATCAGCA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTC GTCCCAACTC
1051 GCCGCGGTGC TGTTTTTCGG GTTGCCCGCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCCGTA CGCAGGGGCTT GGTCCGTGCA AACACGCGAG
1151 CGTGTTTTAT GTCTTATTC AAAGAAGAGG GCGGCGAGCG AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTTGACG GACGGTTCGG CAACCGTGAT GCGGCGAACG ATGACCGCGT
1301 CCACCTCTTG CCGCATTGCG CTTCTGTGGC TCTGCTCGCA TCGTGGCTGG

```


m689.pwp

m689/a689 88.0% identity in 408 aa overlap

		30	40	50	60	70	80
m689.pep		CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPPEMSEKLMAVLMAMLVLTLMPPSIDAY					
g689				SPPLPPMSGKLMAMVLMAMLVLTLMPPSIDAY			
				10	20	30	
		90	100	110	120	130	140
m689.pep		LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV					
g689		LPAIPEMAQPLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
		40	50	60	70	80	90
		150	160	170	180	190	200
m689.pep		AAIVFVSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYYSGRKAQMFALIGIILMVVFLV					
g689		AAIVFASSTEQLLNLRVAVQAFGAGMAVVIVGAMVRDYYSGRKAQMFALIGIILMVVFLA					
		100	110	120	130	140	150
		210	220	230	240	250	260
m689.pep		APMVGALLQGLGCGWAIFVFLAAYSLVLGLVQYFLPKPAVGGKIGRDVFGLVAGRFRKV					
g689		APMVGALLQGLGCGWRAIFVFLAAYSPVLEGLVQYFLPNPAVGGKIGRDVFGLVAGRFRKV					
		160	170	180	190	200	210
		270	280	290	300	310	320
m689.pep		LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689		LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMMFFSRVT					
		220	230	240	250	260	270
		330	340	350	360	370	380
m689.pep		AWRLKTGVHPQSIILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMFVSGTQGLVGAN					
g689		AWRLKTGAHPQSIILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMFVSGTQGLVGAD					
		280	290	300	310	320	330
		390	400	410	420	430	440
m689.pep		TQACFMSYFKEEGGSANAVLGVSFLQSLGAGVGMATFLLHDGSATVMAATMTASTSCGIAL					
g689		TQACFMSYFKEEGGSANAVSGVFRSLGAGVVMAT-----VMAATMTASASCGIAL					
		340	350	360		370	380
		450	460				
m689.pep		LWLCSHRAWKENGQSEYLYX					
g689		LWLCSHKAWKENCKRIL					
		390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

a689.seq

```

1   TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CGGGGCTTTT
51  GTTGCCGCGT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCGG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTATG
151 CTTTCTGCCC ATTATCCTGA AATGAGCGAA AAACGTATGG CCGTTTGTAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGTCTA CTGCCCTGCC GTTCCGCCCA TCGTATTTCG TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTTCGGT CCGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCCGGA TTATTATTCC GGACGCAAAG
551 CCGCCAGATG GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGCG
651 GATTTTGTGT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCCG
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTTCGGTTC ATGTTTCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCAGTACG CTTGGGCGTT TGCATCAAC ATCATCAGCA TGATGTTTTT
951 CAACCGTATT ACCGCGTGCC GGCTCAAAAC CCGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATGTGC GTCCAGTTTG CCGCAACCTC GTCCCAACTC
1051 GCGCCCGTGC TGTTTTTTCG GTTGCCCGCG TTTTGGCTGC TGGTCGCGTG
1101 CCGTATGTTT TCCGTCGGTA CGCAGGGCTT GGTTCGGTGA AACACGCAGG
1151 CGTGTTTTAT GTCCTATTTC AAAGAAGAGG CCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTTGACG GACGGTTCGG CAACCGTGAT GCGGCAACC ATGACCGCGT
1301 CTACCTCTTG CCGCATTCGC CTTTGTGGC TCTGCTCGCA TCGTCCGTGG
1351 AAAGAAAACG GCAAGCGA ATACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

a689.pep

```

1   LLIHIVPVR PVLPGLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVO AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAI FV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFOAFSFGS MFAFLTESSF VYQQLYHVTP
301 HQYAWAFALN IITMFEFNRI TAWRLKTGVH PQSILLWGI VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTA TSCGIA LLWLCSHRAW
451 KENGQSEYL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

	10	20	30	40	50	60
m689.pep	LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
a689	LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
	10	20	30	40	50	60
m689.pep	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
a689	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
	70	80	90	100	110	120
m689.pep	SDIKGRKPVALTGLIVYCLAVAAIVFVSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYYS					
a689	SDIKGRKPVALTGLIVYCLAVAAIVFVSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYYS					
	130	140	150	160	170	180
m689.pep	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP					
a689	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP					

1109

```

|||||
a689      GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSILVLLGLVQYFLPKP
          190      200      210      220      230      240
          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFRKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSEFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFGVLVAGRFRKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSEFVYQQLYHVTP
          250      260      270      280      290      300
          310      320      330      340      350      360
m689.pep  HQYAWAFALNIIITMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          |||||
a689      HQYAWAFALNIIITMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          310      320      330      340      350      360
          370      380      390      400      410      420
m689.pep  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMMAATFLH
          |||||
a689      FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMMAATFLH
          370      380      390      400      410      420
          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEY LX
          |||||
a689      DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEY LX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

g690.seq (partial)

```

1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTCCGCG TCATCGGCTT CTCCCAAAC CGATTGCAA
151 CCGCCGCGAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCTGC ACCCGCCGC CGGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTGC CCTTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GCGGCGGCT ATGACAACAT
351 ACAGCGGctG CTgtttCCCG ACATCCGCC TGAAGATCCC GACTACCATC
401 AGAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACC CGG GgCaAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCGGCAAC ATCtgCCtAt
601 TTgaaccggC ACAacaacGG ACTTggcgGC AATTTCCAAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTtagAC
751 ATCCATTTG ACGAAAATGG CAAAATCAG CGTATTGTCG TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

g690.pep (partial)

```

1  MNKNTSSLPL WLAAILAAR SPSKEDKTE NGASAASSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQIAEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQSEEPKRAR YFEVSATSAY
201 LNRHNNLGG NFOYIGQLPG YLKMHEMLE NQSLFRLSNR ERNPDKPFLD
251 IHFDENGKIT RIVVYEKNY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

m690.seq..

```

1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
101 CCGTGTCTTC GTCTCCGCG TCATCAGCTC CTCCCAAAC CGATTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTGC CCTTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGCTGCT ATGACAACAT
351 ACAGCGGCTG CTGTTCCCG ACATCCGCC TGAAGATCCC GACTACCATC
401 AGAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCAGCATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACC CGG GgCaAAGGCG

```


1110

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551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTC CAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCTG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
1  MNKNTSSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLO
51  PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQOIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEPEKTRR YFEVSATPAY
201 SSRHNNGLGG NFOYISQLPG YLKHGEMLE NQSLFRLSNR ERNPDKPFLLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690    89.3% identity in 408 aa overlap

      10      20      30      40      50      60
m690.pep    MNKNTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPSQTDLOPTASAPDNVK
g690         MNKNTSSLLPLWLAAILAARSPSKEDKTKEVGASAASSASSASSQTDLOPAASAPDNVK
      10      20      30      40      50      60

      70      80      90     100     110     120
m690.pep    QAESAPPSNCTSLHPATGIDDLMQOIAEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
g690         QAESAPLNKNTGLHPAAGIGDLIQOIAEHIDSDCLFALSHNELETRFGLPGGGYDNIQRL
      70      80      90     100     110     120

      130     140     150     160     170     180
m690.pep    LFPDIRPEDPDYHQKIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
g690         LFPDIRPEDPDYHQKIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSOKTR
      130     140     150     160     170     180

      190     200     210     220     230     240
m690.pep    GQGEPEKTRTRYFEVSATPAYSSRHNNGLGGNFOYISQLPGYLKHGEMLENQSLFRLSNR
g690         GQGEPEKRRARYFEVSATSAYLNRHNNGLGGNFOYIGQLPGYLMHGEMLENQSLFRLSNR
      190     200     210     220     230     240

      250     260     270     279
m690.pep    ERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
g690         ERNPDKPFLLDIHFDENGKITRIVVYEKNIY
      250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51  GACCGCGTGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCGCGCTC GTCCACGGCA TCCGCGGCTT CGTCTTCCGC GCCCAAACC
151 GATTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCGC TCAAAATGCA CCGACCTGCA CCCC GCCACC GGCATTGACG
251 ATCTCATGCA GCAAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTCCTCGA CATCGCCCTT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAAG
451 CGCAGGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGCGCA GGAGCCGAAA CGCAGCGGTT ATTTTGAAGT TTCGCAACC
601 CCGCCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

```


1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTTAGACA TCCATTTTGA CGAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAA AACATCTACT TCAATCCAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep

1 MKNKTSLLLL WLAAMLTAC SPSKEDKTE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFFDIRP EDPDYHQII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT
 201 PAYSSRHNG LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPGLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

	10	20	30	40	50	
m690.pep	MKNKTSLLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPS---	QTDLQPTASAPD				
a690	MKNKTSLLLLWLAAMLTACSPSKDDKTKEVGASAASSASSAPS---	QTDLQPTASAPD				
	10	20	30	40	50	60
	60	70	80	90	100	110
m690.pep	NVKQAESAPPNSCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI					
a690	NVKQAESAPPNSCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI					
	70	80	90	100	110	120
	120	130	140	150	160	170
m690.pep	QRLFFDIRPEDPDYHQIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ					
a690	QRLFFDIRPEDPDYHQIILAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m690.pep	ETRGQGEPEKRTTRYFEVSATPAYSSRHNGLGGNFQYISQLPGYLKIHGEMLNQLFRL					
a690	ETRGQGEPEKRTTRYFEVSATPAYSSRHNGLGGNFQYISQLPGYLKIHGEMLNQLFRL					
	190	200	210	220	230	240
	240	250	260	270	279	
m690.pep	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPGLGR					
a690	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPGLGR					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq

1 GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTTT
 51 AAGTATGGCT TTGCTTTCTT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTTCAA CCGAAGTGGC ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT
 201 GCGCGGCGAC AGGCGCGGTT TGAAGGTTAT GCATTCGGA CACAGCCGCC
 251 GCGGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGGCGGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTGCGGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep

1 VPLEPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGHNELRK IRAAFKMGD RARLKVHSE HSRRSVVEI ISSDVFNENE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GCGGCTCTGT CGTCGAAATC ATTTCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTTC TCCGGTATGG ATTTTGGCGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFRMAGD RARLKMVHSE HSRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691  97.2% identity in 144 aa overlap

      10      20      30      40      50      60
m691.pep  VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
          |||
g691       VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQGOHNELRK
          |||

      70      80      90     100     110     120
m691.pep  IRTAFKMGDRARLKMVHSEHSRRSVVEI ISSDVFNENE ARDYVESRYLSGMDFAVDEL
          |||
g691       IRAAFKMGDRARLKMVHSEHSRRSVVEI ISSDVFNENE ARDYVESRYHSSMDFAVDEL
          |||

      70      80      90     100     110     120
m691.pep  EIQRFFHILTPQQQMWLS SCLKX
          |||
g691       EIQRFFHILTPQQQMWLS SCLKX
          |||

      130     140
m691.pep  EIQRFFHILTPQQQMWLS SCLKX
          |||
g691       EIQRFFHILTPQQQMWLS SCLKX
          |||

      130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCGCCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTTCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTTC TCCGGTATGG ATTTTGGCGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQGOHNELRK IRAAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

m691/a691 97.2% identity in 144 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2309>

g692.seq

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

g692.pap

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2311>:

m692.seq

1	GTGTTGCAC	CGGTTTGTG	CTGTTCCGAA	TCGATACGCC	GGATTCCGGC
51	GAATGCAGC	GAATGCGGGA	TTTAAGGACA	AAAATCGCGT	CTGAAACCGG
101	ATACAGTTC	GACGCCATCA	TTTATACAGA	TCGCCTTATT	TGGCTGCGCC
151	TTGATTCCAT	CGCGCAGGGG	ATTGTGAGCC	CTCGAAGCGT	TGTGTGCGGT
201	ACGGCTTTGA	CGCGTCGGAG	TTTATAGCGT	CGGTTACGTC	TTTAAGCCAT
251	TGCGTGTCT	TGTGCGCGGT	TTTGACGGCA	GACCACTTGA	CATAGCCAAA
301	GCTCGGTTCT	TGGAACAGGG	CTTCGGTTCG	CTTCATCGCG	CTCGTTATGG
351	CGTAGTTGCC	TTTGACGAGC	GCAAAAATCCA	CGTCGGCGCG	GCTACGCGGC

m692.ppt

1	VLHTLCRCSE	SIRRIRRNGR	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA
51	FIPCGRGFVA	LEAFVYVVGFE	RVGIGILGYV	FKPLAVFVGG	FDGRPVDIGK
101	ARFLEQCGFCQ	LHAAAYGVVA	VDDGKIHWGA	ATRQLRGFKL	DDDFVQFVLG
151	DVRFEGCGQRI	DAVEFDPTQ	FVEHHQDAGE	GVRRVGRGGL	AAVEFDFFQLG
201	QLARVQSQRR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV	QLALSQCQIR
251	AYIVVGKLDQF	DGVAFFLQLG	LDLFFDHIAE	VADGRAEDDF	FFRRRAVVGGG
301	RSCGCGGRAVF	LTAAGGEDER	ECGGGKGFEF	GFHTFS*	

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m692.pep	VLHTLCRCSESIRRI	RNRNGREWRIK	GKQCRLNTDT	VQTASFYTTAL	FGCAFI	PCGRGFVA
g692	VSHTRCRCSESIRRI	WRNGREWRIK	GKQCRLNTDA	VQTASFYTTAL	FGCAFI	PCGRGFVA
	10	20	30	40	50	60
m692.pep	70	80	90	100	110	120
	LEAFVVRVGFERV	GVIGLGYVFKPL	AVFVGGFDGR	PRPVDIGARF	LEQGFGQLH	AAAYGVVA
g692	LEAFVVRVGFERV	GVIGLGYVFKPL	AVFVGGFDGR	PRPVDIGARF	LEQGFGQLH	AAAYGVVA
	70	80	90	100	110	120
m692.pep	130	140	150	160	170	180
	VDDGKIHVGAA	TRQLRGFKL	DDFVQV	LGDVRF	CGGQRIDAV	FEFDPTQF
g692	VDDGKIHVGAA	AAARQLCGF	KLDDFVQ	VFVRDVG	FGCGQRIDAV	FEFDPTQF
	130	140	150	160	170	180
m692.pep	190	200	210	220	230	240
	VGRVVRGRGY	GAAVDFDFF	QRFQRLAR	VQSORRG	RHLEDFG	DVQIVFFFE
g692	VGRVVRGRGY	GAAVDFDFF	QRFQFARI	QSORRG	RHLEFG	DVQVVF
	190	200	210	220	230	240
m692.pep	250	260	270	280	290	
	QLALSQCQIR	AYIVGKLD	QDFGVAFF	LQLGLDL	FFDHHIAE	VDAGRAED
g692	QLALRQCQIR	AYIVGKFD	QDFGVAFF	LQLGLDL	FFDHHIAE	VAHGRAED
	250	260	270	280	290	300
m692.pep	300	310	320	330		
	GGRSGCGG	RAVFLTA	AGGEDERE	CGGGKGF	EEGFHI	FSX
g692	GGRSGCGG	RAVFLTA	AGCEDERE	CGGGKGF	EEGFHI	FSX
	310	320	330			

a692.seq

1 GTGTTGCACA CGCTTTGTCG CTGTTCCGAA TCGATACGCC GGATTCGGCG


```

51 GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CCGCTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTGCGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCGGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGTACAGTC CCAAAGGCGG GGTGCGCACT TGAAGACTT
651 CCGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCCG
751 GCGCACATAG TCGGTAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGATTTTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCGGA AGACGATTTC TTTTTCGCC GCGCCGTTGT CCGCGCGCGC
901 AGAAGCGGAT GCGCGGGGCG CGCTATCTTT TTGACCGCCG CAGCGCGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTCATCA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1 VLHTLCRCSE SIRRIIRNGR EWRIGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGFE RVGVIGLGYV FKPLAVEVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151 NVRFQCGQRI DAVFEFDPQT FVEHHQDAGE VGRVVGGRYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVGGG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

```

          10      20      30      40      50      60
m692.pep  VLHTLCRCSESIRRIIRNGREWRIKGQKCR LNTDTVQTASFYTTALFGCAFI PCGRGFVA
          |||||
a692      VLHTLCRCSESIRRIIRNGREWRIKGQKCR LNTDTVQTASFYTTALFGCAFI PCGRGFVA
          10      20      30      40      50      60

          70      80      90     100     110     120
m692.pep  LEAFVRVGFERVGIVGLGYVFKPLAVFVG GDFGRPVDIGKARFLEQGFQ LHAAYGVVA
          |||||
a692      LEAFVRVGFERVGIVGLGYVFKPLAVFVG GDFGRPVDIGKARFLEQGFQ LHAAYGVVA
          70      80      90     100     110     120

          130     140     150     160     170     180
m692.pep  VDDGKIHVGAATRQLRGFKLDDFVQV LGGDVRFGCGQRI DAVFEFDPQTQFVEHHQDAGE
          |||||
a692      VDDGKIHVGAATRQLRGFKLDDFVQV LGGDVRFGCGQRI DAVFEFDPQTQFVEHHQDAGE
          130     140     150     160     170     180

          190     200     210     220     230     240
m692.pep  VGRVVGGRYGAAVDFDFQRFQLARVQSQR GRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
          |||||
a692      VGRVVGGRYGAAVDFDFQRFQLARVQSQR GRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
          190     200     210     220     230     240

          250     260     270     280     290     300
m692.pep  QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDF FFRAVVGGG
          |||||
a692      QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDF FFRAVVGGG
          250     260     270     280     290     300

          310     320     330
m692.pep  RSGCGGRAIFLTAAGGEDERECGGKGFE EGFHIFSX
          |||||
a692      RSGCGGRAIFLTAAGGEDERECGGKGFE EGFHIFSX

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

g694.seq

```

1   TCGGCATTG TGTGCCCCA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGCGCCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCA CAAACACGATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
401 GTTTCGCGGT TGGTCGTCCG ATAGCAGATG TCTTCCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGCG GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTC GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAAGC TGCCCCATCG TGCTTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTCACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
701 TGCACTTTCG TCACCAGCGG GCAAGTCGCA TCAAATACCC GGAAACCGCG
751 CTCGCGCGCT TCCTGCTGCA CCGCCTTCGA TACGCGGTGT GCCGAATAAA
801 CCAGTGTCCG GCCCGCGCGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CTTTTTTCGG GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGGCGCGC CGAATTCCTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCC ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTTC CGTTCATAAG TTTTGCAATC CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTCG TNNATCTTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

g694.pep

(partial)

```

1   SAFVLPKHEM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPPAHG
51  FMPPSAYGCQ YFPHQHFRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHQR ASRIKYPETA
251 LRRFLHLRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQVV HDEFVVDFFV
301 AHINRRAEFF QSTFDNTDCP IHTGAEEAARI GKDDGFSVHK FCIPCSDGII
351 VFLLXLCDDR YQAPPTPHR RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

m694.seq

```

1   TTGGTTTCGG CATCCGGCAC ACGGCAAAAA TGCCCTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCCGAC TTTGTTTTTG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCCTTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGGATGT CGCACTGTTC TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTGCTGCGA TAGCAGATAT CTTCCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTCGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCGAAGCT
651 GCGCCATCGT TCCTTCGACC TCGACGTGCC CCTATGCCC GATCATGATG
701 ATTTACAGT CTGCGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACGAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCGCGCGGCA CTTCGCGCAA GTCTTCAATA AACACCGCAC CTTTTTCAGC
901 CAGGTTGTCC ACGAGCAATF TGTGTTGAAC GACTTCGTGG CGCACATAAA
951 TCGCGCGGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACGAG CGCAGAAAGC GCGCGGATTG GCAAGGATGA TGGTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCACAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

m694.pep

```

1   LVSASGTRQK CRLKPVTQAF VLPRHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV

```


Homology with a predicted ORF from *N. gonorrhoeae*

m694/g694 86.8% identity in 372 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1      TTGGTTTCCG CATCCGGCAC ACGCGAAAAA TGCCGCTCTGA AGCCTGTTCAC
51     GACGGCATTT  GTGTGGCCCA AACATTC AAC GCCTGCGTCA ACCTTTGCAC
101    AAATCGGGTT TGTTTTCGCC CTCGGGGCGC AACTCTTTGG GCAGGACGAA
151    CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTAGCGTT TCGTGCCCCC
201    ATCCGCGTAT GTTGGCCAGT ACCTCCGCGA CCAACACTTC GGGCGGGAC
251    GCGCCTGCCG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301    CAGGTAGCCT GCATTATCCA CATATACGC ATCGATTCCG CGCGATCGCG
351    CCACITTCGGC CAAAGCGGTG CTGTTGAGCA AATGGGCGCA ACCGACCACA
401    ATCACGATGT CGCACTGTTT TGCCAACCTT TTGACGGCGG TTTGCCGGTT
451    GGTCGTCGCA TAGCAGATAT TCTCTTGTGT CGGATTTCGG ATATTGGGGA
501    AACCGCGGTT GACGCGGGG ATGATGTCTT TGGTTTCACT GACGAGAGC
551    GTGGTTTGCG TGACATAGCG GAGTTTGTG GGGTTTCTGA CTTGAGTTTT
601    TGCCACATCT CCGACAGGTT CGACCAAAGC CATTTTGGCC GGCGCAAGCT
651    GCCCATCGT TCTCTCGACC TCAGCGTGCC CTTATGCCC GATCATATG

```


1118

```

701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGCCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACCTCTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTAC GGTGGACGAT GTTGCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

a694.pep

```

1  LVASAGTRQK CRLKPVQTAFLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
151 GRRADIPLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPFR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVFN DFVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

	10	20	30	40	50	60
m694.pep	LVASAGTRQKCRKLPVQTAFLPKHSTPAS TFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
a694	LVASAGTRQKCRKLPVQTAFLPKHSTPAS TFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m694.pep	AYGFVPPSAYGCQYFFPHQHFGRGRACRYAD FVFALKPCALQVACIIHHIRIDSARCRHFA					
a694	AYGFVPPSAYGCQYFFPHQHFGRGRACRYAD FVFALKPCALQVACIIHHIRIDSARCRHFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m694.pep	QAVAVGRIGR TDHNDVALFCQLFDGGLPVGRRADIPLVRIADIGETRVQRGDDVFGFI					
a694	QAVAVGRIGR TDHNDVALFCQLFDGGLPVGRRADIPLVRIADIGETRVQRGDDVFGFI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m694.pep	DRERGLADIGEFVGVSDFEFCHISDRFDQKH FARRKLP HRSFDLDVPLMPDHDDFTVLGI					
a694	DRERGLADIGEFVGVSDFEFCHISDRFDQKH FARRKLP HRSFDLDVPLMPDHDDFTVLGI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m694.pep	QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT					
a694	QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m694.pep	QVVHDEFVFNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD					
a694	QVVHDEFVFNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD					
	310	320	330	340	350	360
	370	380				
m694.pep	GINIFLLGFYGGRCCTPTPHRRRX					
a694	GINIFLLGFYGGRCCTPTPHRRRX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

g695.seq

```

1   TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATT TCAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCTCATC ACCCTGCCCG TCGGCGACGG TTTGACCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG AGGGCAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAAATA
451 CACCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTAATACCG AAGGCGGCAG CGCATCCGCA CATAACGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACTA TCAAAACGGC
601 AGGTTTCTG CCGCAGCCCG CTTGTTGAAG GGGCGGACG GCGGAGACGG
651 CCGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCGCGCGCA
901 GCCGTACGCA AACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

g695.pep

```

1   LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCONSQR QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPEGRSTEM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMING KVKALEHTKI
151 HPSGRYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYQNG
201 RFSAAALLK GADGGDGGSI AQRSMYLLQ SRARMNCES VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQQKDIARA TWRSLIQTYP GSFAAKRAAA
301 AVRKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

m695.seq

```

1   TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATT TCAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACTA TAAAGCGGC
601 AAGTTTCTG CCGTGCCTC CTTGTTGAAA GGCGCGGACG GAGGCGACGG
651 CCGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCCGA AACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

m695.pep

```

1   LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAONLY NQALKHYKSG
201 KFSAAASLLK GADGGDGGSI AQRSMYLLQ SRARMNCES VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQQKDIARA TWRSLIQTYP GSFAAKRAAA
301 AVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHHRHQYFAERKGDARSGFRCAAQRRHPORFQSKPAERPAHRPHHPARRRR					
g695	LPQTRPARRHHRHQYFVERKGDARSGFXCAAQCNQSRFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
m695.pep	70	80	90	100	110	120
	LDPASEKIMKIKLPLFIWLVSASCSVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
g695	FDPASEKIMKIKLPLFIWLVSASCSVLPVPEGSRTemptQENASDGIPYPVPTLQDR					
	70	80	90	100	110	120
m695.pep	130	140	150	160	170	180
	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASA					
g695	LDYLEGKIVRLSNEVEMLNCKVKALEHTKIHPSCRTYVQKLDLDRKLKEHYLNTEGGSASA					
	130	140	150	160	170	180
m695.pep	190	200	210	220	230	240
	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGSIQSRMYLLQLSRARMGNCS					
g695	HTVETAQNLYNQALKHYQNGRFSAAALLKGADGGDGGSIQSRMYLLQLSRARMGNCS					
	190	200	210	220	230	240
m695.pep	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
	250	260	270	280	290	300

m695.pep AVRKRKX
|||||

g695 AVRKRKX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

```

1  TTGCCTCAAG CTTGTCCGGC AAGGCGGCAT CATTGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATT TAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCCGTATCCG
251 CCGCTGTTC TTCCCTGTT TCCCGCAATA TTCAGGATAT CGCGCTCGAA
301 CCGCAGGCAG AGGCAGGTAG TTCGGACGCT ATTCCCTATC CCGTTCCAC
351 TCTGCAAGAC CGTTTGGATT ATCTGGAAGG CACACTCGTC CGCTGTGCGA
401 ACGAAGTGGA AACCTTAAAC GGCAAGTCA AAGCACTGGA GCATGCGAAA
451 ACACACCCCT CCAGCAGGGC ATACGTCCAA AAACTCGACG ACCGCAAGTT
501 GAAAGAGCAT TACCTCAATA CCGAAGGCGG CAGCGCATCC GCACATACCG
551 TCGAAACCGC ACAAACCTC TACAATCAGG CACTCAAACA CTATAAAGC
601 GGCAGGTTT CTGCCGCTGC CTCCCTGTTG AAAGCGCGG ACGGAGGCGA
651 CGGCGGCAGC ATCGCGCAAC GCAGTATGTA CCTGTTGCTG CAAAGCAGGG
701 CGCGTATGGG CAACTGCGAA TCCGTATCG AAATCGGAGG GCGTTACGCC
751 AACCGTTTCA AAGACAGCCC AACCGCGCCT GAAGCCATGT TCAAAATCGG
801 CGAATGCCAA TACAGGCTTC AGCAAAAAGA CATTGCAAGG GCGACTTGCC
851 GCAGCCTGAT ACAGACCTAT CCCGGCAGCC CGGCGGCAAA ACGCGCCGCC
901 GCAGCCGTGC GCAAACGATA G

```

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

```

1  LPOACPARRH HCHRQYFVER KGDARSGFRC AAQRRHPORF *SKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIWL SVSAACSSPV SRNIQDMRLE
101 PQAEAGSSDA IPYPVPTLQD RLDYLEGLTV RLSNEVETLN GKVKALEHAK
151 THPSSRAYVQ KLDDRKLKEH YLNTEGGSAS AHTVETAQNL YNQALKHYKS
201 GRFSAASLL KGADGGDGGG IAQRSMYLLL QSRARMGNCE SVIEIGGRYA
251 NRFKDSPTAP EAMFKIGECQ YRLQKDIAR ATWRSLIQTY PGSPAAKRAA
301 AAVRRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

```

      10      20      30      40      50      60
m695.pep  LPQTRPSRRHHRHQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR
a695      LPQACPARRHCHROFYFVERKGDARSGFRCAAQRRHPQRFQSKPAERYADCPHHPARRRR
      10      20      30      40      50      60

      70      80      90     100     110
m695.pep  LDPASEKIMKIKLPLFIWLSVSASCASVSPVPAGSQT--EMSTRENASDGIPYPVPTL
a695      FDPASEKIMKTKLPLFIWLSVSAACSS--PVSRNIQDMRLEPQAEAGSSDAIPYPVPTL
      70      80      90     100     110

      120     130     140     150     160     170
m695.pep  QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTGGGS
a695      QDRLDYLEGTIVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLDLDRKLKEHYLNTGGGS
      120     130     140     150     160     170

      180     190     200     210     220     230
m695.pep  ASAHTVETAQNLQALQKHYKSGKFSAAASLLKGADGGDGGGSIQQRSMYLLQSRARMGN
a695      ASAHTVETAQNLQALQKHYKSGRFSAAASLLKGADGGDGGGSIQQRSMYLLQSRARMGN
      180     190     200     210     220     230

      240     250     260     270     280     290
m695.pep  CESVIEIGGRYANREFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTPGSPAARR
a695      CESVIEIGGRYANREFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTPGSPAARR
      240     250     260     270     280     290

      300
m695.pep  AAAAVRKRXX
a695      AAAAVRKRXX
      300

```

The following partial DNA sequence was identified in *N. gonorrhoeae*
g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:
g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

```

m696.seq
1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGCTGCGC CTTCCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGCTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGCGCAGAA
251 GCCGCAGTGT CTTTAACATC GGACTCAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTTG GCTTCTTTCG AACAGCTGC CAAGGCAGCC GCCATCATTC
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

```

m696.pep
1  LGCROASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCNGQ *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:
a696.seq

1122

```

1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TGTCGTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTTG GCTTCTTTCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1  LGCRQAASHH FCQGNKLFPG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRVFN IGLNLRFLN
101 LLFGFLRTSC QGSRHHCNGQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696 100.0% identity in 120 aa overlap

      10      20      30      40      50      60
m696.pep LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
a696      LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
      10      20      30      40      50      60

      70      80      90      100     110     120
m696.pep ISRSIFDLVFRFFDGRSGRLGGRSRVFNIGLNLNRLNLLFGFLRTSCQSRHHCNGQ
a696      ISRSIFDLVFRFFDGRSGRLGGRSRVFNIGLNLNRLNLLFGFLRTSCQSRHHCNGQ
      70      80      90      100     110     120

m696.pep  X
          |
a696      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1  ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTT GGTGATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTGC
151 CGCGTGGAGG ATTTGGGTTT CCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGCG AAATTGATGT GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTC CTTAACCGGC GGGGCATCCG
501 GCTGTCCGTT TGTTTATAT TGTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTC GATGCGGCG
751 GTGGGGGTGG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTTTGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1  MSSIMTLEFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLIGVSL
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSFW RIGGKGKGV
101 VGVSGSVRQL GCVLLGEVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLGG LFAASADGV SWTKGLAMAS

```


m700.seq

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLLIGVSLSRVEDLGSRLD					
	: : :					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGLFPWRIGKGKGVSVGVSGSVGQLGCVLLGFAFG					
	:					
g700	DMALTVLWLFVCTVGANLLALAVLGLSPWRIGGKGKGVSVGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSESAGMYCMLLVFLIGVQLKSSGVSLRQVLVNRGRIRLSVWFMLSSLSGG					
	:					
g700	KLMCDIWMPSENAGMYCMLLVFLIGVQLKSSGVSLRQVLVNRGRIRLSVWFILSSLSGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGVMTEAYGAVWGSIMLLNDLARELFALAFIP					
	:					
g700	LLFAASADGVSWTKGLAMASGFGWYSLSGVMTEAYGAVWGSIMLLNDLARELFALAFI					

1124

	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

a700.seq

```

1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTATATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCG
151 CGCGTGGAGG ATTTGGGTTC GCGGTGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AACTGATGC GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTTG GTCAACCGCA GGGGTATTCG
501 GTTGTCCGTC TGGTTATATG TTTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTGGCA CGAGAGCTGT
701 TCGCGCTGCG ATTTATTCCG CTGCTGATGA AGCGTTTTC CGATGCGGCA
751 GTGGGGTTCG GCGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTTC
801 GGTGCGGGC GGCTTGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCGCTCCG TTTCTGATGG TGGTGTTCG CGCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

a700.pep

```

1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSLS
51  RVEDLGSRLD DMALTIVLWLF VCTVGANLLA LAVLGKLFPP RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVOLK
151 SSGVSLRQVL VNRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYLSLGL VMTEAYGAVW GSIALNLNLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF TLPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
m700.pep	DMALTIVLWLFVCTVGANLLALAVLGKLFPPWRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
a700	DMALTIVLWLFVCTVGANLLALAVLGKLFPPWRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

1125

	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASFGWYSLSGGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
a700	LLFAASADGVSWVKGLAMASFGWYSLSGGLVMTEAYGAVWGSIALLLNDLARELFALAFIP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFLTPVIQAGGLEVPVAVSFGVVVNIAAPFLMVVSALG					
a700	LLMKRFPDAAVGVGGATSMDFLTPVIRGAGGLEAVPVAVSFGVVVNIAAPFLMVVSALG					
	250	260	270	280	290	300
m700.pep	X					
a700	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

```

1  ATGTCTTGCC ACATATTCCA AGTTGCAGGG ATACCGACCG CTCGATGGC
51  ACAATCTACG CCGTCTTCGC CGACGATGGC GAAACTTGT TTGGAGACGT
101 CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCACTC TTTCGCCGT
151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA
201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCGA
251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCG GTAAAGCGTC GCTCAACAGC AGGGCGATTT CTTCGTTGAC
351 GTTGTCGTGC GCGGCACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

```

1  MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWAPNSFAG
51  FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISLTLSC GSTRLLSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

```

1  ATGTCTTGCC ACATATTCCA TGTAGCAGGG ATACCGACCG CTCGATGGC
51  GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGATTT CTTCGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

```

1  MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPEAGLM VVWAPNSFAS
51  FKRFSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISLTLSC GSTRLLSA*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with menB

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTC	LDTSPEAGLMVVWAPNSFAS	FKRFSISQT			
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTC	LETSPEAGLMVVWAPNSFAG	FKRFSISHT			

1126

	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	: : : : : :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISLTLSC					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
	:					
g701	GGTRLLSAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
  1  ATGTCTTGGC ACATATCCA AGTTGCAGGG ATACCGACGG CTTCGATCGC
 51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101  CGCCGGAAGC AGGGTTAATG GTATGGGTTG CGCCCAACTC TTTCGCCAGT
151  TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201  CAGTTGGGCG GTCCGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251  TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301  TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351  GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
  1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VVWVAPNSFAS
 51  FKRFSSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101  CAVGKASLNN RATSSLTLSG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSSISQT					
	: : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASFKRFSSISQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	: : : : :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSG					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
a701	SGTRLLSAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
  1  ATGCCGTGt ccaAAGCCAG TTGGACTTCG CCGGAGtgg cAACGCCGGG
 51  AATCAGGGGA ATGCCGTGT TCGGCCGGC TCTGGCGAGG GATTCGTGCA
101  AACC CGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151  TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201  TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251  TTTTCGAGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301  GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAACTG CGCCGGCGGT
351  CAGGATTTTC cggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

1127

1 MPCSKASWTS PGVATPGIRG MPLLRPALAR DSCKPGLMAK TAPASSTALS
 51 CSGLVTVPPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
 101 AVLKSSIAIT GTTAPAVRIS RGVSV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

m702.seq
 1 ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
 51 AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
 101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
 151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
 201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
 251 TTTGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
 301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACCTG CGCCGGCGGT
 351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
 401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

m702.pep
 1 MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
 51 CSGLVTVPPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
 101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP					
g702	MPCSKASWTS PGVATPGIRGMPLLRPALARDSCKPGLMAKTAPASSTALSCSGLVTVPPAP					
	10	20	30	40	50	60
m702.pep	TMALGTSIAIRRMASRPTGVRRVISRVGMPPSTRAWDKSM AVLKSSIAIT GTTAPAVKIS					
g702	MMALGISLAI RRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAIT GTTAPAVRIS					
	70	80	90	100	110	120
m702.pep	RGVSLDISVL RVEWGILLRW DRLX					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

a702.seq
 1 ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
 51 AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
 101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
 151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
 201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
 251 TTTGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
 301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACCTG CGCCGGCGGT
 351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGAAT
 401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

a702.pep
 1 MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
 51 CSGLVTVPPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
 101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

m702/a702 100.0% identity in 143 aa overlap

10 20 30 40 50 60

1128

```

m702.pep      MPCSKASWISPGVATPGIRGMPDLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVVPAP
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702           MPCSKASWISPGVATPGIRGMPDLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVVPAP
                10      20      30      40      50      60

                70      80      90      100     110     120
m702.pep      TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702           TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
                70      80      90      100     110     120

                130     140
m702.pep      RGVSLDISVLRVEWGILLRWDR LX
                ||||||||||||||||||
a702           RGVSLDISVLRVEWGILLRWDR LX
                130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

g703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TCGCGAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAC AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TCGCCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGTT
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGCC GTTTACGACA ATATCAGCGG TTTTATATAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCCT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTctgTgc gcTGTgggt aaggCAAACA
851 TCAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

g703.pep

```

1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKDL E QGVPLYQAI KDLKKGEFTA TPLKNGDFY G VYYVND SREV
251 KVPSFDEMKG QIAGNLQAER IDRVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

m703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TCGCGAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAC AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TCGCCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGTT
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```


п703.рер

1	<u>MKAKILRTSVA</u>	<u>LLACSGSLFA</u>	QTLATVNGQK	IDSSVIDAQV	AAFRAENSRA
51	EDTPQLRSQT	LENEVVNTV	AQEVKRLKLD	RSAEFKNLA	KLRAAEAKSGS
101	DDKKPSFKLV	WQAVYKGLNG	EAYALHIART	QPVEQEYKA	AYDNISEGYK
151	GTQEVQLGEI	LTDKEENAKK	AVADLKAKKG	FDAVLKQYSL	NDRTKQTGAP
201	VGYVPLDKLE	QGVPPLYQAI	KDLKKGGEFA	TPLKNGDFGY	YVVYNDNSREV
251	KVPSFDEMGK	QIAGNLQAOER	IDRAVGALLG	KANIKPAK*	

m703/g703

	10	20	30	40	50	60
m703.pep	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m703.pep	LENEVVNTVVAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVVNTVVAQEVKRLKLDRSAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m703.pep	EAYALHIAKTQPVSEQEVKAAAYDNISGFYKGTQEVQLGEILTDKEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDKEENAKKAVADLKAKKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m703.pep	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
	250	260	270	280	289	
m703.pep	VYYVNSDREVKVPSFDEMKGQIAGNLQAEIRIDRAVCALLGKANIKPAKX					
g703	VYYVNSDREVKVPSFDEMKGQIAGNLQAEIRIDRAVCALLGKANIKPAKX					
	250	260	270	280		

a703.seq

1	ATGAAAGCAA	AAATCCTGAC	TTCGGTTGCA	CTGCTTGCC	GTTCCGGCAG
51	CCTGTTTGCC	CAAACGCTGG	CAACCGTCAA	CGGTGAGAAA	ATCGACAGTT
101	CCGTCAATTG	TGCGCAGGTT	GCCGCAATTC	GTGCGGAAAA	CAGCCGTGCC
151	GAAAGCAAGG	CGCAACTGCG	CCCAATCCCT	CTGGAAAAAC	AGGTGGTCAA
201	CACCGTGGTC	GCACAGGAAG	TGAAACGCCT	GAAATCTCAG	CAGTCGGCAG
251	AGTTTAAAAA	TGCGCTTGCC	AAATTGCGTG	CCGAAGCGAA	AAAGTCGGCG
301	GACCAACAAGA	AACCGTCTTT	CAAAACCGTT	TGGCAGGCGG	TAAATATGGA
351	CTTGAACGGC	GAGGCATACG	CGCTGCATAT	CGCCAAAACC	CAACCGGTTT
401	CCGAGCAGGA	AGTAAAGGCC	CGATATGACA	ATATCAGCGG	TTTTTACAAA
451	GGTACGCAGG	AAGTCCAGTT	GGGCGAAATC	CTGACCGACA	AGGAAGAAAA
501	TGCAAAAAAA	CGCGTTGCCG	ACTTGAAGCA	GAAAAAAGGT	TTCGATGCCG
551	TCTTTAAAAA	ATATTCCCTC	AACGACCGTA	CCAAACAGAC	CGGTGCCGCC
601	GTCCGATATG	TGCCGCTGAA	AGATTTGGA	CAGGGTGTTT	CGCCGCTTTA
651	TCAGGCAATT	AAGGACTTGA	AAAAAGGCGA	ATTTACGGCA	AGCCCGCTGA

1130

701 AAAACGGCGA TTTCTACGGC GTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep
 1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGVVPLKDL E QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
 251 KVPSFDEMKG QIAGNLQAE R IDRAGGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

	10	20	30	40	50	60
m703.pep	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	LENEVVNTVVAAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVVNTVVAAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
a703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	FDAVLKQYSLNDRTKQTGAPVGVPLKDLQGVPPYQAIKDLKKGEFTAATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGVPLKDLQGVPPYQAIKDLKKGEFTAATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	VYYVNSREVKVPSFDEMKGQIAGNLQAE R IDRAGGALLGKANIKPAKX					
a703	VYYVNSREVKVPSFDEMKGQIAGNLQAE R IDRAGGALLGKANIKPAKX					
	250	260	270	280	289	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq
 1 ATGAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
 101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
 151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCCAAGAAAT
 201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
 251 TGGAAACCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
 301 ACCTGCGCGC CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
 351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
 401 TCTGGGACGA CGCAAAATC CGCCTTTCCG ACATTCTGTT GAAATCAGG
 451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
 501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
 551 TGGGGATGAT GCAGACGATG ATGTTGCGCG TGCCGACCTA CCTTTACGGC
 601 GGCGACATCG AACCCGATTT CCTGCAATC CTCCATTGGG GCGGCTTTTT
 651 AATGGTGCTG CCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
 701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
 751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA


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801 TGGGGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGGCG ACCTTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCCGCCGAGA GGCTGGTGAA GCTGATTCCT GCGTTTGTCC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCCTTGAC
1051 GGCACGGTGC TGGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGA AAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGCGGGC
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTCGACCGCG CTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCCTGC GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GGCGCGCGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCTCG CCCAAACCAC CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCCAAGGC AAACCGCGCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCGCG GTGGCGCAGG CTTAGAACA ACAGTCCGAA
1651 CATCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTCAG ACGGCAGCGT
1701 CCCCGACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAA CAGAAGCGG
1851 CGGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGCGCGT GCGGCAAGTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAAACTG GAATACGTC AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTGGC
2151 GCAGGCAGAC GTATCCGCGC CGCAGCGGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCCCA
2251 CTGCTCGATC AGGCGCGCGC CACCGGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTACAAA CGGGGAAAA TGCACTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

a704.pep

```

1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS IIDAGLSYY
51 KQRTADAQKT ELPPQELDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIE QQLLRDGI V RIDLNYSTHR CRVWDDGKI RLS DILLKTR
151 QIGYTAAPYD AQKIEANQK ERKQYIVRLA VAGLGMQTM MFALPTYLYG
201 GDIEPDLQI LHWGGFLMVL PVVFYCAVPF YQALRDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGREF EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSsav NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEALQYAS SFIFGELL A VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSQSGFQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHLI SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIQDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

      10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLSYYKQRTADAQKT
a704      MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLSYYKQRTADAQKT
      10      20      30      40      50      60

      70      80      90     100     110     120
m704.pep ELPPQELDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRDGI
a704      ELPPQELDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRDGI

```


1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	790	800	810	820		

RIDLNYSTHRCRVVWDDGKIRLSDILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA
RIDLNYSTHRCRVVWDDGKIRLSDILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA
VAGLGMMQTMFALPTYLYGGDIEPDLQILHWGGFLMVLPPVVFYCAVPFYQGALRDLKN
VAGLGMMQTMFALPTYLYGGDIEPDLQILHWGGFLMVLPPVVFYCAVPFYQGALRDLKN
RRVGMPTPITVAIIMTFIAGVYSLATNAGQGMYFESIAMLFFLLGGRFMEHIARRKAGD
RRVGMPTPITVAIIMTFIAGVYSLATNAGQGMYFESIAMLFFLLGGRFMEHIARRKAGD
AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLKAGDIVLVKPGETIPVDGTVLEGSSAV
AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLKAGDIVLVKPGETIPVDGTVLEGSSAV
NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRGTTGGRFRLSHIVRLDRALAQKPR
NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRGTTGGRFRLSHIVRLDRALAQKPR
TAEAEQYASSFIFGELLAVPVFIGWTLYADAHTALWITVALLVITCPCALSATPTAL
TAEAEQYASSFIFGELLAVPVFIGWTLYADAHTALWITVALLVITCPCALSATPTAL
AASGTGLAREGILIGGKQAIETLAQTTDIIIFDKTGTLTQGKPAVRRISLLRGTDFAEFLA
AASGTGLAREGILIGGKQAIETLAQTTDIIIFDKTGTLTQGKPAVRRISLLRGTDFAEFLA
VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR
VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR
ASYVAEISGKEPQTEGGGSAVYLGSGGFAVYFYLDPKDSAAEAVRQLAGKNLTLHL
ASYVAEISGKEPQTEGGGSAVYLGSGGFAVYFYLDPKDSAAEAVRQLAGKNLTLHL
SGDRETAETAARALGVAHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD
SGDRETAETAARALGVAHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD
VSAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHIIRQNLIWAGAYNIIAVPLA
VSAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHIIRQNLIWAGAYNIIAVPLA
VLGYVPWIAALGMSFSSLAVLGNALRLHKGKMQSEKMPSEQX
VLGYVPWIAALGMSFSSLAVLGNALRLHKGKMQSEKMPSEQX

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

m705/g705 95.0% identity in 238 aa overlap

```
m705.pep      10          20          30          40          50          60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g705          VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIA VAVALVRIMP
              10          20          30          40          50          60

              70          80          90         100         110         120
m705.pep      AGGIVRKILLKLVFEFYISVIRGTPLLVLVIVFYGLPSVGVIYIDPIPAAIIGFSLNVGAY
: || | : | |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```


1134

```

g705      SGGIFQKCLLKLVEFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIAAIIGFSLNVGAY
           70      80      90      100     110     120
m705.pep  130      140      150      160      170      180
           ASETIRAAILSVPRGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
g705      ASETIRAAILSVPRGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130      140      150      160      170      180
m705.pep  190      200      210      220      230      239
           AAVVTVTLEFRVAQETANRTYDPLVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
           |||
g705      AAVVTVTLEFRVAQETANRTYDPLVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
           190      200      210      220      230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
51 CGATATGATT GTCAGCGCGT TTTGCCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGGC GATTATGCCG GCCGGCGGCA TCGTGCGGAA
201 AATCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTTGCT TCAGCTTGTG ATGTGTTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTC
651 TTGTAAAGTG CTGTTCTCTGA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51 VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVQLV IVFYGLPSVG
101 IYIDPIPAAI IGFSLNVGAY ASETIRAIL SVPRGQWEAG FSIQMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTLEF RVAQETANRT
201 YDFLEPVYIEA ALVYWCFCVKV LFLIARLEK RFDRYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

a705.pep  10      20      30      40      50      60
           VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           |||
m705      VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           10      20      30      40      50      60
a705.pep  70      80      90      100     110     120
           AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIAAIIGFSLNVGAY
           |||
m705      AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIAAIIGFSLNVGAY
           70      80      90      100     110     120
a705.pep  130      140      150      160      170      180
           ASETIRAAILSVPRGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
m705      ASETIRAAILSVPRGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130      140      150      160      170      180
a705.pep  190      200      210      220      230      239
           AAVVTVTLEFRVAQETANRTYDPLVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
           |||
m705      AAVVTVTLEFRVAQETANRTYDPLVYIEAALVYWCFCVKVLFLLIARLEKRFDRYVAKX
           190      200      210      220      230

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```

1 ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCGgaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCCgGc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAtgaCCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCGcgatt tActccaacg cggtgGAacg taTgctcggt acggtcatcg
251 ggctgGGCGC GGGTTTGGGc gTTTATGGC TGAACcAGCA TTAttteccac
301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATGCGCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
1101 CTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```

1 MNSSQRRLS GRWLNSYERY RHRRLIHAVR LGGTVLFATA LARLLHLQHG
51 EWIGMTVFVV LGMLQFQGA IYNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPHL AGLTMCMLIG DNGSEWLD SG
151 LMRAMNVLLG AAIATAAAL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEQ NMVKMRQINA RMVKSRSHLA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTAAALING
301 RHARRIRIDT ANPELEALA EHLHYQWQGF LWLSTNMREQ ISALVILLQR
351 TRRWLDAHE RQHLRQSLLE TREHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```

1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCTCTGT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGc GTTTATGGC TGAACcAGCA TTATTTCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC CCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGCGAAGC CCTCGAGGAG AACATGGCGA AATATGCGCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCG CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
1101 CTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```

1 MNTSQRRLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51 EWIGMTVFVV LGMLQFQGA IYKAVRMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLPYLTVG TASALAGWAA VGKNGYVPHL AGLTMCMLIG DNGSEWLD SG
151 LMRAMNVLLG AAIATAAAL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMAMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING

```


301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQNRNLVSRWLSYERYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	MNTSQNRNLVSRWLSYERYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
m706.pep	LGMLQFQGAIIYKSAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTGTASALAGWAA					
g706	LGMLQFQGAIIYKSAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTGTASALAGWAA					
	70	80	90	100	110	120
m706.pep	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
g706	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
m706.pep	FMLADNLADCSKMI AEISNGRRMTREERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
g706	FMLADNLADCSKMI AEISNGRRMTREERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
m706.pep	AMMEAMQHAHRKIVNTTELLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLOQTVALING					
g706	AMMEAMQHAHRKIVNTTELLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLOQTVALING					
	250	260	270	280	290	300
m706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMROEISALVILLQTRRKWLDAHE					
g706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMROEISALVILLQTRRKWLDAHE					
	310	320	330	340	350	360
m706.pep	RQHLRQSLE TREHG*					
g706	RQHLRQSLE TREHG*					
	370					
m706.pep	RQHLRQSLE TREHG*					
g706	RQHLRQSLE TREHG*					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCCTGTT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGCGC	GTTTATGCGC	TGAACCAGCA	TTATTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCGG
351	CTGGGCGGCG	GTGGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGCGCGATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCCCA
751	CGTAAATTTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTCGCCCT	TATCAACGGC

1137

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
 951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
 1001 GCACCAATAT GCCTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
 1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
 1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

a706.pep
 1 MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWIGMTVFVV LGMLQFQGA IYKKAVERMLG TVIGLGAGLG VLWLNQHYFH
 101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFD SG
 151 LMRAMNVLIG AAIATAA AKL LPLKSTLMWR FMLADNLTD C SKMIAEISNG
 201 RRMTREERLEE NMAKMRQINA RMVKSRS HLA ATSGESRISP AMMEAMQHAH
 251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
 301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNM RQE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHS*

a706/m706 99.5% identity in 374 aa overlap

	10	20	30	40	50	60
a706.pep	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
m706	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
a706.pep	LGMLQFQGA IYKKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
m706	LGMLQFQGA IYKKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
	70	80	90	100	110	120
a706.pep	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLIGAAIATAA AKLLPLKSTLMWR					
m706	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLIGAAIATAA AKLLPLKSTLMWR					
	130	140	150	160	170	180
a706.pep	FMLADNLTD C SKMIAEISNGRRMTREERLEENMAKMRQINARMVKSRS HLA ATSGESRISP					
m706	FMLADNLTD C SKMIAEISNGRRMTREERLEENMAKMRQINARMVKSRS HLA ATSGESRISP					
	190	200	210	220	230	240
a706.pep	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTD LQQTVALING					
	250	260	270	280	290	300
a706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNM RQE ISALVILLQRTRRKWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNM RQE ISALVILLQRTRRKWLDAHE					
	310	320	330	340	350	360
a706.pep	RQHLRQSLLE TREHSX					
m706	RQHLRQSLLE TREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```

1  ATGGAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51  GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTA
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGAATCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TCGGGGCGGC AAAACGACCG GCAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGTT TTTATGTTTC ATATGGACGC
751 GGTTCGGCGC ACAAACGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCAATTA TTCGGTGCCC GTAAAAAAT
851 GGCCTGTTTC TTTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCATTCCCG TCAATTACGA TTACAACGCG AAACAATATC AGAGCAGCCT
951 GGCCGCGCAG CGCATGCTTT GCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCG CTCTGCAGCG TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGG CATGCGCCAA AGTATGCCTG CACCGGAAGA AAACGCGCGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGG
1251 GCAGCGCGCC CCAATTTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTCGAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTCAGAGGA GGCATAAAG TAGGCGGTAT GTTTCGTTAT GATCTGTTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1  MEIINDAELI RSMQRQOHID AELLTDANVR FEQPLEKNNY VLSEDETPCT
51  RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSQL IIQPNMDSG ILKLRSVAGE IGDIRYEKRR DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQUIP SEEEKGSDLQ
201 IKWQONKPIR FSIQIDDAGG KTTGKYQGNV ALSFDNPLGL SDLFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKRWLFSENH NGHRYHEATE
301 GYSVNYDYNG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTGMRO SMPAPEENG
401 DILPGTSRMK IITASLDAAA PFILGKQOFF YATAIQAWN KPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHRVGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1  NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51  GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACCTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCAATC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAGAAC TGCGTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NTTAAGCGAT TNGTTTTATG TTTTATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAG CTGAAAGCGG ATCCAGAAGT
601 TACACGCTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

```



```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
  1 XKETAFTKGM CLGSNNLSRL QKAAQILIV RGYLTSQAI QPQNMDSGIL
  51 KLRVSAGEIG DIRYEEKRD KSAEGSISAF NNXPLYRNK IINLRDVEQG
 101 LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
 151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
 201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ YQSSLAERM
 251 LWXXXFXXTS VXMKLWTRQT KYIDDAEIE VQRRRSAGWE AELRHAYLX
 301 RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPXXSRMKII TAGLDAAAPX
 351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
 401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
 451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep
10 20 30
XKETAFTKGMCLGSNNLSRLQKAAQILIVR
|||||
m707
50 60 70 80 90 100
EDETPTCRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQILIVR

a707.pep
40 50 60 70 80 90
GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDKSAEGSISAFNNKXPLYRNKI
|||||
m707
110 120 130 140 150 160
GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKXPLYRNKI

a707.pep
100 110 120 130 140 150
LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
|||||
m707
170 180 190 200 210 220
LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT

a707.pep
160 170 180 190 200 210
GKYQGNVALSXDNPGLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
|||||
m707
230 240 250 260 270 280
GKYQGNVALSFDNPLGLSLDFYVSYGRGLAHTDLTDATGTETESGSRYSVHYSVPVKK

a707.pep
220 230 240 250 260 270
WLFNFHNGHRYHEATEGYSVNYDYNKGQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
|||||
m707
290 300 310 320 330 340
WLFNFHNGHRYHEATEGYSVNYDYNKGQYQSSLAERMLWRNRLHKTSGVMKLWTRQTY

a707.pep
280 290 300 310 320 330
KYIDDAEIEVQRRRSAGWEAELRHAYLXRWQLDGKLSYKRGTGMRQSMPEENGSGGTI
|||||
m707
350 360 370 380 390 400
KYIDDAEIEVQRRRSAGWEAELRHAYLXRNWQLDGKLSYKRGTGMRQSMPEENGSGDIL

```


1140

	340	350	360	370	380	390
a707.pep	PXXSRMKIITAGLDAAAPXMLGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG					
m707	PGTSRMKIITASLDAAAPFILGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG					
	410	420	430	440	450	460
	400	410	420	430	440	450
a707.pep	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
m707	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
	470	480	490	500	510	520
	460	470	480			
a707.pep	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
m707	VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX					
	530	540	550	560		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

g708.seq

```

1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCACT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAGACA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

g708.pep

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLKVNDRQAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRILNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SARQGQFGLA EAYLKRSLLA QPQFPFAFKE LARTEMLAGQ LGDADYYFRK
201 YQSRVEVLQA DDLILGWKIA KALGNVQAAY EYEAQLQANF PYSEELQTVL
251 TGG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

m708.seq

```

1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGTTGGTTCC TATGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCACT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAGACA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.pep

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLKVNDAQ ESFRQALSIK
101 PDSAEINNYY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLLVLAGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              |||||
g708           MPFKPSKRISLLLVLAGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90      100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLKVNDAQESFRQALSIKPDSDAEINNYYGWFLCGRLNR
              |||||
g708           DALKSNPKNELAWLVRAEIYQYLKVNDAQESFRQALSIKPDSDAEINNYYGWFLCGRLNR
              70      80      90      100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPFAFKE
              |||||
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPFAFKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF
              |||||
g708           LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
              |||||
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51 GGGCGCGTGC AGCACTTCCT ACCGCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACTAC NGCTGTTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCGGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTGC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLKVNDAQ ESFRQXLSIK
101 PDSAEINNYY XWFLCGRLNR PAESMAYFDK ALADPTYXPX YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIIYQYLVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRINR					
m708	DALKSDPKNELAWLVRAEIIYQYLVNDKAQESFRQALSIPDSAEINNXYGWFLCGRINR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT TCAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51  CGTCGCTGCT GCTCTGATTG CCGCAATGGG CTATACCATC ATTTCAATTG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGG CAGGGATGAT
201 AGGCGCGTTG AATCAGGGTA TGGCGCGGTT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGGCTGAT TTCCCGGACT TATTTTATT TTTCGGCCTT
351 CGCGCTGTGT TCCGTATCG GCGTGTCAT CCGCAGCAGC CTGACCGCCT
401 GCGCCACTGT CCGCGTGTCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGgcggy cgcgattgTT tccggTGTGT TTTTCGGCGA
501 TAAAATGTCC CCGCTTTCCG ACACCACGGG CATTTCGCGG TCCATCGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAAACA TGATGTACAC CACCATCCCT
601 GCGTGGCTTA TCAGCGCGGC ACTGATGCTT TGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTGGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCACT GTTGGTCGTT
751 TTGGCATTGA TCGCGCTCAA TGCCGTGGTC GCCATGCTCT TTACCGTCAT
801 TGCCGCGGTT GCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTATGGC GGCTACAAAC TCGAAGCGCA AGCGTTTAAA
901 GACATTGCCA AACTGATTTT CCGCGCGCGC TTGGAGAGTA TGTTCTTTAC
951 GCAGACCATC GTTATCCTCG GTATGAGTTT GGGCGGGCTG CTGTTTGCGC
1001 TCGGTGTGAT TCCTTCCTTG CTGGAGGCGG TCCGTACCTT CTTGACGAAT
1051 GCCGGACGCG CGACGTTTCA GATTGCCATG ACTTCGGTCG GGGTCAATTT
1101 CCTGATTGGA GAGCAATATT TGAGCATCCT GCTTTCGGGA GAAACGTTCA
1151 AACCCTTTTA CGACAAACTC GGCCTGCATT CGTGCAACCT GTCGCGGACT
1201 CTGGAAGATG CGGGACGCTT GATTAAACCG CTCGTGCCGT GGAGCGTGTG
1251 CGGCGTATTT ATCAGCCACG CCCTTGGCGT ACCCGTTTGG GAATATCTGC
1301 CTTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTAACCTT GTTATTCGGC
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQAGMIGAL NOGMGAVYLE FFIGLMVSAL MMSGAIPTLM
101 YYGFGGISPT YFYFSAFALC SVIGVSIGSS LTACATVGVA FMGMAAFQA
151 DMAMTAGAIV SGVFFGDRMS PLSDTTGISA SIVGIDLFEH IKNMYYTIP
201 AWLISAALML WLLPSVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVV
251 LALMRVNAVV AMLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DIAKLISRGG LESMFFTQTI VILGMSLGL LFALGVIPSL LEAVRTFLTN

```


351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFGL
451 WTGLTSLSKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
1 ATGTTTCGCTT TCAATCCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTCAATTGG
101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGCGCGCAT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTCTCTCCTT
351 CCGCGTGTGT TCCGTCATCG CGGTGTCCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CGGCGTTGCC TTTATGGGGA TGGCGCGGCG GTTTCAGGCC
451 GATATGGCGA TGACGCGGG CCGGATTGTT TCGGCGCAT TTTTGGCGA
501 CAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG
551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
601 GCGTGGCTCA TTAGTGGCGC ACTGATGCTT TGGCTTTTGC CGAATGTCCG
651 CCGCGAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGGCCT GTTGGTCATT
751 TTGGCATTGA TCGGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
801 GGTTGCCGTT GCTGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGCGA AGCGTTTAAA
901 GATGTTGTCA AACTGATTTC GCGCGCGGT TTGGAAGTA TGTTTTTCAC
951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGGC
1001 TCGGTGTGAT TCCTTCCCTG TTGAGGCGCA TCCGTACCTT CTTGACGAAT
1051 GCCCGACGCG CGACGTTTCA GCTTGCCATG ACTTCGCTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTCA
1151 AACCCTGTTA CGATAAGCTC GGTCTGCATT CCGCAATCT GTCCGCGACG
1201 CTGGAAGATG CGGGACGGT GATTAAACCG CTCGTACCGT GGAGCGTATG
1251 CCGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGCG TGACTTTGAG CAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51 YGLARGLKYN DMQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQA
151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFH IKNMYYTTIP
201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DVVKLISRGG LESMFFTTQI VILGMSLGLL LFALGVIPSL LEAIRFTLTN
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFGL
451 WTGLTSLSKR*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQGMIGALNQGMGAIYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQAGMIGALNQGMGAVYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFH IKNMYYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFH IKNMYYTTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLFTVMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
g709	SLIPFALLVVLALMRVNAVVMLEFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMTFTQIVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM					
g709	DIARLISRGGLESMTFTQIVILGMSLGGLLFALGVIPSLLEAVRTLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEYQYLSILLSGETFKPVYDKLGLHSRNLSTLTEDAGTVINPLVPWSVCGVF					
g709	TSVGVNFLIGEYQYLSILLSGETFKPVYDKLGLHSCNLSRTLTEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLSKXX					
g709	ISHALGVVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLSKXX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCCGTCAATG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGGN CNNGATTGTN NNGGNCGCAT TNTTNGGCGN
501 CAAATGTCN CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCTG
551 GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGGCT GTTGGTCGTT
751 TTGGCATTGA TGGCGGTCAA TGGCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGGCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGCGGCT TTGGAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATCTTGT GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGCGCGCAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTGAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCTGGT GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTC ATCANCCAG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQOGMIGAL NOGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYFAFALC SVIGVSIGSS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXIV XXAXXGKXMS PLSDTXGXA SIVGIDLFH IKNMYYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAV VAMLEFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIARLISRGG LESMTFTQTI VILGMSLGG L FALGAIPSL LDAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```


401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTSLKK*

a709/m709 91.1% identity in 459 aa overlap

a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTIIXLEWLPHMSIIAAIVVLILYGLARGLKYN
m709	MFAFKSLDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN
a709.pep	DMQQGMIGALNQGMAIYLFFFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSAFALC
m709	DMQQGMIGALNQGMAIYLFFFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSSFALC
a709.pep	SVIGVSIGSSLTTCATVGVA XMGXAXMXXXXXIVXXAXXGKMSPLSDTXGXSA
m709	SVIGVSIGSSLTTCATVGVA FMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA
a709.pep	SIVGIDLFEHIKNMYYTIPAWLISXXLMXLXLLPSVAAQDLNSVESFERSQLEATGLVHCY
m709	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFERSQLEATGLVHGY
a709.pep	SLIPFALLVIALMRVNAVVA MLFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAXX
m709	SLIPFALLVIALMRINAVVA MLFTVMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK
a709.pep	DIAKLISRGGLESMTFTQIVILGMSLGGLLFALGAIPSLDAVRSFLTNA GRXTFSVAM
m709	DVVKLISRGGLESMTFTQIVILGMSLGGLLFALGVIPSLL EAI RTFLTNA GRATFSVAM
a709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNL SRTLEDAGTVINPLVPWSVCGVF
m709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNL SRTLEDAGTVINPLVPWSVCGVF
a709.pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX
m709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAAACCC	ACGAAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGGCGGAAA	AGCTGGCGAT	GTCGGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCCGCGTTT	GGAGCAGTTG
151	GCTCAGATTT	TCAAAATCGA	TATGTGGGAC	TTGCTCAAAT	CGGGCGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGGC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTTT	AAAAATGGAG

m710.pep

1 METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
51 AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
101 LKHCKEMLEQ KDKEIELLRK LTETV*

a710.seq

```

1  ATGGAACCC  ACGAAAAAT  CCGCTGATG  CGCGAATTGA  ATAAATGGTC
51  CCAGGAGGAT  ATGGCGGAAA  AGCTGGCGAT  GTCGGCAGGC  GGGTATGCCA
101 AAATCGAACG  AGGCGAAACG  CAGTTGAATA  TCCCGCGTTT  GAGGACGTTG
151 CGCGCAGATT  TCAAAATTGA  TATGTGGAC  TTGCTCAAT  CGGCGGCGCG
201 CGGGATGGTG  TTGCAGATTA  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251 CAATCTATAC  CGCTCAGGAT  GCATCNGGTA  AAGCTGGATT  TGTTAAATG
301 GAATTAAAC  ACTGTAAAGA  AATGTGGAA  CACAAAGACA  AAGAAATCGA
351 GCTGCTCCGC  AAGCTGACCG  AAACCGTTTA  A

```

a710.pep

1 METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
51 AQIFKIDMWD LLKSGGGGMV LQINDVDNTS GEFAIYTAQD ASGKAGFVKM
101 ELKHCKEMLE HKDKEIELLR KLTETV*

	10	20	30	40	50	60
a710.pep	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
m710	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a710.pep	LLKSGGGGMVLQINDVDVNTSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKEIELLR					
m710	LLKSGGGGMVLFQINEGDSG-GDIALYASGDVSMKIEFLKMKELKHCKEMLEQKDKEIELLR					
	70	80	90	100	110	

```

a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

```


g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCCGCGC CTGATTGCGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCTT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTGG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATT TAAAACAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEA KVTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTADNL VETHKIYNKK GDTYLTLYAK APDGSLYTTD RGFYDYNAGR
251 NYRPDLDKYD RALAHQFAKA EMGGADFSTS FKQLEKEFYE VKQLDIDGK
301 PDKEQIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYIAFLPDM LQNEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCCGCGC CTGATTGCGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGTCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTGCGGC AAAGCACGTC GGACAATCTT GTTGAAGACC ATAAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCTT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTGG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCCTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATT TAAAACAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
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1148

```

901 CCGGATAAAG AGCAGAAAAAT CAAAATC0GA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```

1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	10	20	30	40	50	60
	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
	MQTAYNAGQYQGYMANIDARPYWYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEYVKQRLDIDGK					
m711	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEYVKQRLDIDGK					
	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

1149

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

m712.seq

```
1  ATGATGCCCC ATATTGATT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGTTGTCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTTCGA CAAGGCTCGC TGGCGCATT GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACGCG AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCAGGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GGCGGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTCCT AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG CGGTATTGGG TATGAGTGGC GCCTTGAGCA CGGCCACCAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCGT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGCGTGTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTAATCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGAGCGT TAAAGAGCGC ATTGCCCTGC GTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCCGCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTGA
1401 TTTGATTTG TAA
```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

m712.pep

```
1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKVL MVAPMLTAGI
51  QPALEPVQLF SDAEAADLFG QGSLAHLMVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDEPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLKLD QAEIIEAEAE NKGKLVVARA QNDPNRVNAI
451 IPADVNVGLH VFAGRIDLIL *
```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```
m713.seq
1  ATGCAAAATA ATTACATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCGCTTTG GGCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGAGCG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGCGGCGCG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GCGGTGTTT GAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```
m713.pep
1  MQNNSYGYAV SVRVGGEHR HWERYDIDS FLIPADSFDF VIGRLGPEAA
51  IPDLSEGECE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVVGAD YSSPPVATLC WSRDTSRCNI
201 ERMIDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLKWVYKD PTMTLHRPKT
251 VVVSADADNLA ALQKQAKQL ADWRLEGFTL TITVGGHKTR DGVWLQPGLR
301 VHVIDDEHGI DAVFFLMGRR FMSLRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGKKG GKKQAEAVF E*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```
a713.seq
1  ATGCAAAATA ATTACATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCGCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGAGCG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGCGGCGCG TTTATGCTAT CTCGCATGGA TGGCAGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
```


1152

1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLGSECE VVIDGQIVMT GIIGSORHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTLVDAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGLTVVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVFLA QSHGRSGDSA KHDWKVYKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKKQAETAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

a713.pep	10	20	30	40	50	60
	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLGSECE					
m713	10	20	30	40	50	60
	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLGSECE					
a713.pep	70	80	90	100	110	120
	VVIDGQIVMTGIIGSORHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAKKL					
m713	70	80	90	100	110	120
	VVIDGQIVMTGIIGSORHGKSKGSRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAKKL					
a713.pep	130	140	150	160	170	180
	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGLTVVGGVD					
m713	130	140	150	160	170	180
	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGLTVVGGAD					
a713.pep	190	200	210	220	230	240
	YSSPPVATLCWSRTDSRRNIERMDIEWDTDNRFSEVFLAQSHGRSGDSAKHDLKWVYKD					
m713	190	200	210	220	230	240
	YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVFLAQSHGRSGDSAKHDLKWVYKD					
a713.pep	250	260	270	280	290	300
	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGQR					
m713	250	260	270	280	290	300
	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGLR					
a713.pep	310	320	330	340	350	360
	VHVIDDEHGI DAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
m713	310	320	330	340	350	360
	VHVIDDEHGI DAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
a713.pep	370	380				
	KGVS HKGKKGKKQAETAVFEX					
m713	370	380				
	KGVS HKGKKGKKQAETAVFEX					

1153

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGCTG TTGCCCCCG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CGGTACGGGC AAAAACCGCC AGCACCGTGT GTTGCCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGCGGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGC GGCAACAACC GCATTACCCG ATTCGCGGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CGGTACGGGC AAAAACCGCC AGCGCCGTGT GTTGCCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGCGGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGC GGCAACAACC GCATTACCCG ATTCGCGGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPRSAGQMLADW					
	10	20	30	40	50	60
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAGVNR					
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAGVNR					
	70	80	90	100	110	120
a714.pep	AGDRLAPQEIIMWVWHVNVRGNNRITRFRAAGDRLTDYSDAVIESLFNRLKPAHTA					
	130	140	150	160	170	180
a714.pep	AGDRLAPQEIIMWVWHVNVRGNNRITRFRAAGDRLTDYSDAVIESLFNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTG
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCCGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLLDD DKQALMDDVQ DYFSGLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTG
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCCGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLLDD DKQALMDDVQ DYFSGLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
 51 GCGCGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAT GCGGCGAAG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

1155

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq
 1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50	
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----					
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCASKSAEGSCGASKSAEG					
	10	20	30	40	50	60
	60	70	80	90	100	
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
g716	SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq
 1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCCCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC


```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGCGCGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTCT  CCGCCGCTGC
251  TGTCTGCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCTTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCATTTCCT
501  GCGCAACACC  TCCGTCCTGA  CCGCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCGGG
601  CGCGCGCGCT  TTTGCCCGCC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGCGCTGG  AACAGCTCGG  CGTTTATTCT
751  ATGGGTATT  CGTTCGGCGG  GCGGCAATTA  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCTCCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGCTC  GGTTTACCGT  CGTATCGTGT  ATGCTGccgc
1001  cgtGTTTGA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGCGGCGCAG  CGCGGCGCGG
1151  CGGTTGCCCT  TGCCGCTCA  TTCTGGTTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTT  TGCTgGCCT  CCTCGCGGCG  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCcctgttt  gccggcgat  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AAATTGCAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MOTKEILGYA AGSIGSAVLA VIIPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYAAAD KDTLFTLFL PPLLSAATA ALLSRPSLP
101  SEILFSLDDA AAGIGLVLE LSFPIRELL LVLMEGRAL AFSSAQLVPE
151  LAILLPLPT VGLRHFPANT SVLTAVYALA NLAAAFLLF QNRCLKAVR
201  RAFFSPAVLH RGLRYGIPLA LSSLAYWGLA SADRLFLKY AGLEQLGVYS
251  MGISFGGAAL LLOSIFSTVW TPYIFRAIEE NATPARLSAT AESAALLAS
301  ALCLTGIFFP LASILLPENY AAVRFTVWSC MLPLFYTLT EISGIGLNVV
351  RKTRPIALAT LGALANLLL LGLAVPSGGT RGAAVACAAS FWLFFVFKTE
401  SSCRLWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAAYLAG
451  CILRHRLNLH KLFHYLKKQG FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

n717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCGCCGCGG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGCGCGCGGG  GCTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTCT  CCGCCGCTGC
251  TGTCTGCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCTTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCATTTCCT
501  AGCGAACACC  GCCGTCCTGA  CCGCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCGGG
601  CACGCACCGT  TTTGCCCGCC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGCGCTGG  AACAGCTCGG  CGTTTATTCT
751  ATGGGTATT  CGTTCGGCGG  GCGGCAATTA  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCGCGC  AATCGAAGAA  AACGCCCGCG
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCCTCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGCTC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTGA  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGCGGCGCGG  CGCGGCGCGG
1151  CGGTTGCCCT  TGCCGCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTT  TGCTGACCT  CCTCGCGGCG  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCCTGTT  GCCGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AGATTGCAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```


This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep

```

1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCGLDQA YVREYYATAD KDTLFKTLFL PPLLSAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVPE
151 LAIILLLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLE QNRCRLKAVR
201 HAPFSPAVLH RGLRYGPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RPLYLHTLF CLTSSAAYTC FGTTPANYPLF AGVWAAAYLAG
451 CILHRKDLH KLFHYLKKQG FPL*

```

m717/g717 96.4% identity in 473 aa overlap

	10	20	30	40	50	60
m717.pep	MDTKEILGYAAGSIGSAVLA VIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCGLDQA					
g717	MDTKEILGYAAGSIGSAVLA VIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCGLDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m717.pep	YVREYYATADKDTLFKTLFLPPLLSAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
g717	YVREYYAAADKDTLFKTLFLPPLLSAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVPEKLA ILLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVPEKLA ILLPLTVGLLHFPANTSVLTAVALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m717.pep	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGPIALSSIAYWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGPIALSSAYWGLASADRLFLKKY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m717.pep	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENATPARLSATAESAAALLAS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m717.pep	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLA EISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLA EISGIGLNVVRKTRPIALAT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m717.pep	LGALANLLL LGLAVPSGGARGA AVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALANLLL LGLAVPSGGTRGA AVACAASFWLFFAFKTESSCRLWQPLKRLPLYMHTLF					
	370	380	390	400	410	420
	430	440	450	460	470	
m717.pep	CLTSSAAYTCFGTTPANYPLFAGVWAAAYLAGCILHRKDLHKLHLYLKKQGFPLX					
g717	CLASSAAYTCFGTTPANYPLFAGVWAAAYLAGCILHRKDLHKLHLYLKKQGFPLX					
	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGCGGCGGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTCAAAAC CCTGTTCTG CCGCCGCTGC

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1158

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTGC
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
501 GCGGAACACC GCCGTCTGA CCGCCGTTTA CGCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGTCTGAA GGCCGTCCGG
601 CGCGCACCGT TTTCATCCGC CGTCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCTT GAAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTTC
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTCCGCGC AATCGAAGCA AACGCCCCGC
851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTTGCCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCCTCCC TCCTGCTGCC
951 GGAAAACTAC GCGGCCGTCC GGTATTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CTGCTGCTG CTGGGGCTTG CCGTACCCTG CGCGCGCGCG CGCGGCGCGG
1151 CGGTTGCTG TGCCGCTCA TTTGGCTGT TTTTGT TTTT CAAGACCGAA
1201 AGCTCTGCC GCCTGTGCA GCCGCTCAA CGCTGCCG TTTATATGCA
1251 CACATTGTT TGCCTGGCT CCTCGGCGG CTACACCTG TTCGGCACTC
1301 CGGCAACTA CCCCTGTTT GCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCTGC GCCACCGAA AGATTGCAC AACTGTTT ATTATTTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

a717.pep

```

1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51 SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLSAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFPIRELL LVRMEGRAL AFSSAQLVSK
151 LAIIIIPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFVFKTE
401 SSCRLWQPLK RPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILHRKDLH KLFHYLKKQG FPL*

```

a717/m717 97.9% identity in 473 aa overlap

a717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
m717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
a717.pep	YVREYYAAADKDTLFKTLFLPPLLSAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE
m717	YVREYYATADKDTLFKTLFLPPLLSAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE
a717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAIIIIPLTVGLLHFPANTAVLTAVYALA
m717	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAIIIIPLTVGLLHFPANTAVLTAVYALA
a717.pep	NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAWGLASADRLFLKKY
m717	NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAWGLASADRLFLKKY
a717.pep	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

1159

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|||||
m717  AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
      250      260      270      280      290      300

      310      320      330      340      350      360
a717.pep ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
|||||
m717  ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
      310      320      330      340      350      360

      370      380      390      400      410      420
a717.pep LGALAAANLLLLGLAVPSGGARGA AVACAASFVLFVFKTESSCRLWQPLKRLPLYMHTLF
|||||
m717  LGALAAANLLLLGLAVPSGGARGA AVACAASFVLFVFKTESSCRLWQPLKRLPLYLHTLF
      370      380      390      400      410      420

      430      440      450      460      470
a717.pep CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHLKLFHYLKKQGFPLX
||:|||||
m717  CLTSSAAYTCFGTPANYPLFAGVWAAVYLAGCILRHRKDLHLKLFHYLKKQGFPLX
      430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTGTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCTT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGTTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TCGGAAAAAT CGGCGGCGCG GCTGATTTG GGGCAAACGC TGACCGAGCG
501 TCGCGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCGGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGTTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPOSWFKW DKDNGLLLR TRENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFTLSWLYM FKHYAVHDFE EFLEYGMPI RIGKYGAGAT
101 KEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTAT SNPFLOMADW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVDVGVO
251 IPESWVRDKL VIPDVQEGEA VLVQRQVDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGCGAAATC GGTCACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACCGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CCGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGCTTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCGG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEELSD QAYEMDSL P TLEDLIMDL M DAVGHGFSAL EVEVWFS DGL
151 YLPRNFIHRP QSWFKWDKDN GLLLR TRENP EGEALWPLGW VVHTQKRSV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMA DWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVKPF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAV AAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS					
m718	SDGLYLPRNFIHRPQSWFKWDKDNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKRSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKRSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFQMA DW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFQMA DW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ					
m718	160	170	180	190	200	210
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ					
a718.pep	360	370	380	390	400	410
	INYPHADPNRVKFEFDTREPKDIAVFADAIPKLVGVQIPESWVRDKLVIPDVQEGEA					
m718	220	230	240	250	260	270
	INYPHADPNRVKFEFDTREPKDIAVFADAIPKLVGVQIPESWVRDKLVIPDVQEGEA					
a718.pep	420	430	440	450	460	470
	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	280	290	300	310	320	330
	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	340	350	360	370	380	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATCGGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCCG GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCCGGAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCGC CAAAGCTGGT TCAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGGCTACCCG CGAAATCCG GAAGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGCGCG GCAACGGGCT TTTCCGCAGC CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCGCTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCTGCT TTCGAGCGGT GCGGAAATC GGTCAACAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGTCCCA CAACGCGGCA AACGATACGA
851 CGGCAACGAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCCGGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC CGGTCCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGGCG CAGGTACCGG ACAATCCGGT AACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAAGCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKEAA LQDVQAITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDSIAAN MGRKRALLT LNWRVAPPRN
101 ATPEEKLSD QAYEMMDSLP TLEDLMDLM DAVGHGFSAL EVEWVFSDDL
151 YLPRNFIHRP QSWFKWDKN GLLRTREN PEGEALWPLGW VVHTQKRSRV
201 QQARNLGFR LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLLRAVAEI GHNAAGIMPE GMEIELHNA NGTTATSNPF LOMADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLVSDAK QVAQTITSQI

```


351 IGPFLQINYP HADPNRVKPF EFDTREPKDI AVFADAIPKL VDVGVQIPES
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
 501 DNAKLRTYMQ QALFISDILG QDHARA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq
 1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
 51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
 101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCGGCAAAA GATGCGCGCC
 151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
 201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
 251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCCGGAAAT
 301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
 351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGGTAG
 401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
 451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAATGGGA
 501 CAAAGACAAC GGGCTGCTGC TCGTACCCG CGAAATCCG GAAGGCGAAG
 551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
 601 CAGCAGGCGC GCAACGGGCT TTTCCGACG CTTTCCTGGC TGTATATGTT
 651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
 701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
 751 AACACCCCTG TTCGAGCGGT GCGGAAATC GTTCACAACG CGGCAGGCAT
 801 CATGCCAGAA GGTATGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
 851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
 901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
 951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
 1001 TGCTGGTGTG GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
 1051 ATCGGACCGT TCCTGCAAA CAACTATCCC CATGCCGACC CAAACCGCGT
 1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC CGCGTCTTTG
 1151 CCGACGCTAT CCCGAAACTG GTGGATGTG GCGTACAAAT CCCCAGAAAGC
 1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
 1251 GTTGGTGGCG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
 1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
 1351 ATATTGGACG CGCGGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
 1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
 1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
 1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
 1551 TATTTTGGGA CAAAGCCATG CCCGCGCCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep
 1 MEPIMAKNN KTKIQPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
 51 LFEDAESGDI RAQHELFIADI EERDSIAAN MGRKRALLT LNWRVAPPRN
 101 ATPEEEKLSQ QAYEMMDSLP TLEDLIMDL DAVGHGFSAL EWEVWFSDDL
 151 YLPRNFIHRP QSWFKWDKN GLLLRTRNP EGEALWPLG VVHTQKRSV
 201 QQARNGLFRT LSWLYMFHY AVHDAEFLE LYGMPIRIG YGAGATKEEK
 251 NTLRAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMAWCEKS
 301 AARLILQTL TSGADGKST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
 351 IGPFLQINYP HADPNRVKPF EFDTREPKDI AVFADAIPKL VDVGVQIPES
 401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
 451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
 501 DNAKLRTYMQ QALFISDILG QDHARA*

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKNNKTKIQPEAAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
m718-1	MEPIMAKNNKTKIQPEAAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
	10	20	30	40	50	60
a718.pep	RAQHELFIADIEERDSIAANMGRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
m718-1	RAQHELFIADIEERDSIAANMGRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
	70	80	90	100	110	120
a718.pep	RAQHELFIADIEERDSIAANMGRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
m718-1	RAQHELFIADIEERDSIAANMGRKRALLTLNWRVAPPRNATPEEEKLSQAYEMMDSLP					
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVWVSDGLYLPNFIHRPQSWFKWDKNGLLLRTRNP					
m718-1	TLEDLIMDLMDAVGHGFSALEVWVSDGLYLPNFIHRPQSWFKWDKNGLLLRTRNP					
	130	140	150	160	170	180

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	190	200	210	220	230	240
a718.pep	EGEALWPLGWVVHTQKSRSVQQAARNGLFRTLSWLYMFKHYAVHDFAEFLEYGMPPIRIGK					
m718-1	EGEALWPLGWVVHTQKSRSVQQAARNGLFRTLSWLYMFKHYAVHDFAEFLEYGMPPIRIGK					
	190	200	210	220	230	240
	250	260	270	280	290	300
a718.pep	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMAWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMAWCEKS					
	250	260	270	280	290	300
	310	320	330	340	350	360
a718.pep	AARLILGQTLTSGADGKSSTNALGNIHNEIRDLLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
	370	380	390	400	410	420
a718.pep	HADPNRPVKFEFDTREPKDIAVFADAIPKLVGVQIPESWVRDKLVIPDVQEGEAVLVR					
m718-1	HADPNRPVKFEFDTREPKDIAVFADAIPKLVGVQIPESWVRDKLVIPDVQEGEAVLVR					
	370	380	390	400	410	420
	430	440	450	460	470	480
a718.pep	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAAAL					
m718-1	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAAAL					
	430	440	450	460	470	480
	490	500	510	520		
a718.pep	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1  ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCCGAGATGA
51  CCGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAAATCGCG GCGCAACTT GAACGGCAA GCCATACTTA TGCGTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TGCGTTTAAC CGTTTGCGCG GCAGCGGCAA GGCATCACAA AATGATTGCG
251 CACGGCGCGC GGTGCGTACG CGTAACCGAA TTCGCGAGCT GAACGCGGAA
301 CTGAAACAGG GCACGGGATT TGCGGACAAG ATGGGAAAAA TCGGAAGATT
351 CCGTGCAGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCAGCGT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTGGC ACTTGAACCT GTGAGAAAAA
551 ATGGCGGGAC CCACGATAAG GCTTTGGATT TAATCAGCGG CATGATGACC
601 ACCGGTCTGA ATTTTGCCCA AACCAAGAAT GAAGCGCAGG CGGCATATGC
651 TTTTGCACCT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AAACCTGATTA
701 AAACCTGAA AGATGCGCGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGTCT TGCAATCGGG TTTAGACGGC ACTTTCGAGG TGCGGGATAT
801 GGTTCGGGAG CTGCCGAGCC TGCTCTGTC CGCGCAACAG GCAGGGATGA
851 ATGGTGTGCG CGGTTTGGAC TACCTGCTCT CACTCTTACA ATCTGCGGCG
901 AATAAATCGG GCAGTCTGCG CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAAACT CTGTCGCTCG ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCCGAATGA CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTGTCGCAA
1051 GGCAGCAAAA ACGGCGAAAA CGCAGTGCAG GTGTTGTCCC GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTGAGGCGCA TAAGACGGCG GCGGAGCAGG CAAATATGCT TAAGGGCGCG
1201 CTTTGGCGC AACTGCTGCC TGATTGTCAG GCAAAACAAG GTTTGCTGGC
1251 TGCAACGGAT ATGACGCAAA TCCGTGAATA TATGGCTTCG TTGGCTGGCG

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1301 TAACGTTGGA TAACGGA AAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTCGGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCGCGCAGG CGCGGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAAGTTG
1651 CTGTTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTCGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTCCTAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGAC GCGGCGTATC AGGCAGCATT
2001 GGCGCAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CGGCCGTGGA GCGGTCAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

m719.pep

```

1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51 GIRSEKQIQR EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIREINAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPMADNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDDG MSGKDLQLGL
251 EHVLSGLDGF TFEVRDMVRE LPSLLSAAQ AGMNGVGGLD YLLSLLQSAA
301 NKSGSPAEEA TNVNLLSKT LSPDTIGRLK KMANPNDPK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKOGLLAATD MTQIREYMAS LAGVTLDNKG IAKNNEARML
451 SAAAOQEQQE SLAMLRESLT GTLVDNETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNPNALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTP
601 MINRLKNNGI RFEPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLESTQTA
651 AYQAAIQOQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMEFRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

m720.seq

```

1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCGG
51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TCGCGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGGTGC
251 TGGTGCACCC TGTTCGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTTT GAAAACGCCT
401 TTTTGGTTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTGTA TCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCAGCA TCGGGTACGT
551 TTGGCGCGGT GCGCGGTTTG TTTGATTGAG ACAAATTGCT CTTTCCCGAT
601 GCGGCGCGAT ACAGTGCAGC GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TCGCGATATA TCGGTCATGG TAGATACTGG CACACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTCCGCCCG ACAGCGGTTT
751 GACGGGGCTG CCGCTGTTGC CGACCGCGCC GCCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCTGCA AAACCGCCTG AACCGGTAA

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTGCGTGGC AACGGCATT AATCGAGGCG ATGGCGAAGA
951 GATGACCGCG CCCGATTGA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGCGG CAGGCCGTCT GAATGCGTTG GTTGGCGCGG
1151 TCATCAACCA AAAGCCCGCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GGCATATAG CCCGCGCAGC
1251 AGAGCTGGT CCGCTCAATC CCCATATCCA CCACCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAQEIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLEADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAADVADRA AAIPDNLLTG RFSDDLQNLRL NRTAKQVQP VAQAVRLLST
301 SSLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAATAE
351 SGGLTANAVY TEAYQTAESL RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPPIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GCGGAAGAGA TGACCGCGCC CGATTGATT
151 GAGGTTAACC GCGCCATCGC CCGCCGTATG CAGGCCGAGA TTGCCGCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GCGCGTCTGA ATGCGTTGGT TCGGGCGGTC ATCAACCAA AGCCGCGGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCACG
401 AGTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGGC GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACCTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNLRLNLT AKQVQVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAESGGL TANAVYTEAY QTAESLRAAA
101 GRNALVAAV INQKPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HIHHPAFIKR GTLVNSYAK*

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m720 / a720 100.0% identity in 169 aa overlap

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250 260 270 280 290 300
m720.pep SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNLRLNLTAKQVQVQAQAVRLLSTSSLL
a720 GLQNLRLNLTAKQVQVQAQAVRLLSTSSLL
10 20 30

310 320 330 340 350 360
m720.pep SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
a720 SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
40 50 60 70 80 90

370 380 390 400 410 420
m720.pep QTAESLRAAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIARAAELVRLNP
a720 QTAESLRAAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIARAAELVRLNP
100 110 120 130 140 150

430 440
m720.pep HIHHPAFIKRGTLVNSYAKX

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a720 |||||
 HIHHPAFIKRGTLVNSYAKX
 160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
 1 ATGTCCAAAA ATGCACAAAA AACCCCTACTT GCCGTGTGCA GTTTCGAGGT
 51 GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTTCCGG
 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
 151 AACGGTCATG ATGTCGCGTT GTTGCCCAAC AGCTCGCGCA ATCAGTTGGT
 201 TGTGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
 251 CACCTGCCCG CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
 351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
 401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT
 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
 501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCGCGGCT CGTGAAGGCC
 601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCCGCG AGCTGGCGGA
 651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
 701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
 751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
 801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
 851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTGTAC CGGCTTTATT
 901 GAAAACGCCC AGCCGGTCCG TGCACTGGCA GGCTCGCAAA CGGGCGGCAA
 951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG
 1001 CAAAAATGCT GGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC
 1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep
 1 MSKNAQRTLL AVCSFEVQPK DGRIQLLPYG EFRVADGRPT DVPAYWLTTEE
 51 NGHVDALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAAAGWM RWLEFTPKGM
 101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
 151 MDEVLAASA QILKPETEON PMKELLQOLF DLPDAGEEEL KAALSALVEA
 201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTRYAPI SVVQELQSKV
 251 AALTARQEAD KGNELITAAL TSGKLLPAOK EWAKGVLPQ GGLAFLTGFI
 301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
 351 EGR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
 1 ATGTCCAAAA ATGCACAAAA AACCCCTACTT GCCGTGTGCA GTTTCGAGGT
 51 GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTTCCGG
 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
 151 AACGGTCATG ATGTCGCGTT GTTGCCCAAC AGCTCGCGCA ATCAGTTGGT
 201 TGTGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
 251 CACCTGCCCG CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
 351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
 401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT
 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
 501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCGCGGCT CGTGAAGGCC
 601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCCGCG AGCTGGCGGA
 651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
 701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
 751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
 801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
 851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTGTAC CGGCTTTATT
 901 GAAAACGCCC AGCCGGTCCG TGCACTGGCA GGCTCGCAAA CGGGCGGTAA
 951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG
 1001 CAAAAATGCT GGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

a721.pep
 1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
 101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
 151 MDEVLAASA QILKPETEON PMKELLQLF GLPDAGEEEL KAALSALVEA
 201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
 251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
 301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
 351 EGK*

a721/m721 99.2% identity in 353 aa overlap

	10	20	30	40	50	60
a721.pep	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a721.pep	SSRNQLVVDYEHXTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHQTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a721.pep	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQLF					
	130	140	150	160	170	180
	190	200	210	220	230	240
a721.pep	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a721.pep	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGVLKQPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAKGVKQPGGLAFLTGFI					
	250	260	270	280	290	300
	310	320	330	340	350	
a721.pep	ENAQPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKMLGMSGEEFVKIKESGKX					
m721	ENAQPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKMLGMSGEEFVKIKESGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

m722.seq
 1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
 51 TACCAAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
 101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
 151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
 201 TTGGAGCGG CATGCCTCCA TGCGCGGCTT GAGCCGCCG AATCCTACCA
 251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
 301 GACGACCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
 351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

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```

401 AGCCGGGCGC GCGCGCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GCGCGCCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GCGCGCAAT GTGCGGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 CGCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GCGGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTA CTGACC GCCTTGCGTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTTCGCGCA GCCGCCGCTA AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTTCAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTCGCGG GTTCTGTTT
851 TGTTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1  MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAIIHAQLH
51  FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LVVAVGELQD FOLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGAAVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACTCAAACCTATTAAACCGCTTTTTTTGCGGTGTTTGACGATTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTTCGGGGAAAAATCACGCTGGTGGTGTGCTCCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+-----+-----+ 120
GACGCGCGCCGGAAGCCCTTTTGTAGTGCACACCACAGCAGGCTCGGCTATGTGCGG
a  L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGCCGACGAAACCCTGCAAGACCTTGAACATTGTCAGGAATAC
121  -----+-----+-----+-----+-----+-----+-----+ 180
CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181  -----+-----+-----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCCGCGTTA
a  G F A S H P P D G S E A V V I P L G G N -
```


1170

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241 -----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTTCGTGCCGTCGATGGCGTAGTTTTTGGAAATTC
a      T S H G V I V C S Q H G S Y R I K N L K -
      CCCGGCGAGACGGCGATTATTAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301 -----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCCACGTTTTTAGCTACTAATTCGTTCCGTTT
a      P G E T A I F N H E G A K I V I K Q G K -
      ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361 -----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a      I I E A D C D V Y R V N C K Q Y E V N A -
      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCACTGTTGACGGCGCAA
421 -----+-----+-----+-----+-----+ 480
      CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACCTGCCGCGTT
a      A T D A K F N A P L V E T S A V L T A Q -
      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481 -----+-----+-----+-----+-----+ 540
      CCGGTTTGTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAATCG
a      G Q I N G N G G M A V E G G D G A T F S -
      GGCGATGTTAACCAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541 -----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGCCCGCCGTGCAAAATTGTGGCTGCCGCTGCACCACCGGCCGTTA
a      G D V N Q T G G S F N T D G D V V A G N -
      ATATCGTTGCGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAAACCTTACCGGCGGAA
601 -----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCGTGGGCGTATGGCTGTCTGTAGCCGCGTTTGGAAATGGCCGCGCTT
a      I S L R Q H P H T D S I G G K T L P A E -
      CCGGCATAG
661 ----- 669
      GGCCGTATC
a      P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI
Sali SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

m724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGN TSHGVIVCSQ HGSYRIKLNK
101 PGETAIFNHE GAKIVIKQ GK IIEADCDVYR VNCKQYEVNA ATDAKFNA PL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724.seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGCGAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGTACCGG GTTAACTGCA
401 AACAAATACGA GGTTAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```


1171

```

501 CCGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CCGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
  1 MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
 51 LQDLEHLQEY GFASHPPDGS EAVVIPLGNN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQKG IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADET					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQKG					
m724	GFASHPPDGS EAVVIPLGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQKG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
  1 ATGGTGC GCA CGGTAAAAAG CTACAACGGC GAGGCCGACG ATTTGGCCGGG
 51 GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
101 TTGAGCCTGC CAGCACCGGC GCGTATGCG GACGTTATCA GGATACCGCC
151 GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
201 GCGGCAAGGC GGCATCGACA GCCCGGAAAT CGGCAGCAAC GATTTAATCC
251 GCGCTGTTCC CCGCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351 GCAAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401 ACACCTGCGG GTTGGAAAAT GACCGCTACC CCGAACGCAC CGACAATCCC
451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501 GTGGCTGAT TTCGAGGGGT TGGACGGCAA AATTTACGAC CCGCAATCCG
551 CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
  1 MVRTVKS YNG EADDLAQI H TLPVAVV TYG GSKVEPASTG GVCGRYQDTA
 51 EFVVMVA ARN LRNEQAQR QG GIDSREIGSN DLIRAVRRLL DGQRLGFADS
101 RGLVPKAV RA IANHVLV QNA AVSIYAVE YA IRFNTCGLEN DRYPERTDNP
151 DDPNHIFT KY QGTLSEP WPD FEGLDGKI YD PQSADEIPVN LTLKDKQ*

```


a725.pap not found yet

g726.seq not found yet

g726.pep not found yet

m726.seq

1	ATGACCATCT	ATTTCAAAAA	CGGCTTTTAC	GACGACACAT	TGGCGGGCAT
51	CCCCGAGGC	GCGGTTGCCG	TCCGCGCCGA	AGAATACGCC	GCCCTTTTGG
101	CAGGACGAGC	GCAGGGCGGG	CAGATTGCCG	CAGATTCCGA	CGGCGGCCCC
151	CGTTTAAACC	CGCCGCGCCC	TGCGGATTAC	CAGGAATGGG	ACGGCAAAAA
201	ATGGAATAAT	AGCAAAGCCG	CCGCCGCCGC	CCGTTTCGCG	AAACAAAAAA
251	CCGCTTGGC	ATTCGCGCTC	GCGGAAAAGG	CGGACGAACT	CAAAAACAGC
301	CTCTTGGCGG	GCTATCCCCA	AGTGGAAATC	GACAGCTTTT	ACAGGCGAGA
351	AAAGAAAGCC	CTCGCGCGGC	AGGGCGGCAA	CAACGCCCCG	ACCCCGATTG
401	TGGCGCAAAAT	CGCCGCGCGA	AGGGGCGTGG	AATTGGAGCT	TTTGATTGAA
451	AAAGTTATCG	AAAAATCCGC	CCGCTGGCT	GTTGCCGCCG	GCGCGATTAT
501	CGGAAGCGT	CAGCAGCTCG	AAGACAAATT	GAACACCATC	GAAACCGCGC
551	CCGGAATTGGA	CGCGCTGGAA	AAGGAAATCG	AAGAATGGAC	GCTAAACATC
601	GGCTGA				

m726.pcp

1	MTIYFKNGFY	DDTLGGIPEG	AVAVRAEEYA	ALLAQQAQGG	QIAADSDGRP
51	VLTPPRPSDY	HEWDGKKWKI	SKAAAAARFA	KQKTALAFRL	AEKADELKNS
101	LLAGYQPVEI	DSFYRQEKEA	LARQADNNAF	TPMLAQIAAA	RGVELDLVIE
151	KVIEKSARLA	VAAGAIIGKR	QOLEDKLNIT	ETAPGLDALE	KEIEEWTLNI
201	G*				

a726.seq

1	ATGACCATCT	ATTTCAAAAA	CGGCTTTTAC	GACGACACCT	TGGGCAGCAT
51	CCCCGAAGGC	GCGGTTGCCG	TCCGCGCCGA	AGAATACGCC	GCCCTTTTGG
101	CAGGACAGGC	GCGGGCGGG	CAGATTGCCG	CAGATTCCGA	CGGCCGCCCC
151	GTTTTCACCC	CGCCGCCGCC	CTCCGAATAC	CACGAATGGG	ACCGCAAGAA
201	ATGGGAAATC	GGCGAAGCCG	CTCGCCCGCG	CCGTTTCGCC	GACAACAAAA
251	CCGCCACGGC	ATTCCGCCTC	GCGGCAAAGG	CGGACGAACT	CAAAAACAGC
301	CTCTTGCGCG	GCTATCCCCA	AGTGGAAATC	GACAGCTTTT	ACAGGCAGGA
351	AAAGCAAGCC	CTCGCGCGCG	AGGGCGGCAA	CAACGCCCCG	ACCCCGATGC
401	TGGCGCAAA	CGCCGCCCGA	AGGGCGTGGA	AATTGGAGCT	TTTGATTGAA
451	AAAGTTGTCG	AAAAATCCGC	CCGCCTGGCC	GTTGCCGCCG	GCGGATTAT
501	CGGAAAGCGG	CAGCAGCTCG	AAGACAAATT	GAACACCATC	GAAACCGCGC
551	CAGGATTGGA	CGCGCTGGAA	AAGGAAATCG	AAGAATTGAC	GCTAAACATC
601	GGCTGA				

a726.pwp

```

1  MTIYFKNGFY DDTLGSIEPG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTPRPSEY HEWDGKKWEI GAAAAAARFA EQKTATAFRL AAKADELKNS
101 LLVYQPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KGVEKSARLA VAAGAIIGKR QQLEDKLNIT ETAPGLDALE KEIEEWTLNI
201 G*

```

a726.pep
MTIYFKNGFYDDTLGSIPEGAVAVRAEYYAALLAGQAQGQIAADSDGRPVLTTPRPSEY
|||||
m726
MTIYFKNGFYDDTLGGIPEGAVAVRAEYYAALLAGQAQGQIAADSDGRPVLTTPRPSDY
|||||

1173

```

              70      80      90      100      110      120
a726.pep    HEWDGKKWEIGAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
            |||||:|:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726        HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep    LARQADNNAPT PMLAQIAAARGVELDV LIEKVVEKSARLAVAAGAIIGKRQLEDKLNTI
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726        LARQADNNAPT PMLAQIAAARGVELDV LIEKVIEKSARLAVAAGAIIGKRQLEDKLNTI
              130      140      150      160      170      180

              190      200
a726.pep    ETAPGLDALEKEIEEWTLNIGX
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726        ETAPGLDALEKEIEEWTLNIGX
              190      200

g727.seq    not found yet

g727.pep    not found yet

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAC TATGCGCGCG AACTGGAAC
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1  MNLVKLLANN WQPIAIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEKKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPD SRNPNTGERL FSPQIPPNET QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAC TACGCCCGCG AACTGGAACA
201 GGCGCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCTGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTGTCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1  MNLVKLLANN WQPIAIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEKKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFHGHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep    MNLVKLLANNWQPIAIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```


1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
           10      20      30      40      50      60

           70      80      90      100     110     119
a727.pep   YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAFAAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDSDRNPTGTF
           70      80      90      100     110

           120     130     140
a727.pep   IDGFGHHGLQLYKRALGYGNX

m727      RLFSPQIPPNFTQIPPX
           120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAATAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTCGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGAAC TATCATGCGC AACAGACGTG GTATTGGGAT GGCGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

```

g728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFAV
51  AKLARLFERNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YEHCLGCMYOM AQVYLAKYRD VANDEQKWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS FDNGKKRQSF EYYLKNLNL
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

```

m728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAACT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

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1175

```

501 CGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGT'TTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGACAAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1  MEKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVPKNPNFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGCMQ AQQYLAKYRD VANDEQKVD FRKESNRIAS DSRNSVFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSVVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

m728.pep	10	20	30	40	50	60
	MEKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEV PKNPNFVAKLARLFRNA					
g728	MEKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEV PENPNFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTVHGENYETTGEYRVV					
g728	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPDGSVFDAAGRGKIGEDVYEHCLGCMQ AQQYLAKYRDVANDEQKVD FRKESNRIAS					
g728	WQPDGSVFDAAGRGKIGEDVYEHCLGCMQ AQQYLAKYRDVANDEQKVD FRKESNRIAS					
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSVFYQNMRELMPRGMKANSLVVGIDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGIDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSVVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

1176

```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360
           370
m728.pep  YAEAAARRSGGRRDLSHX
           |||||
g728      YAEAAARRSGGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGAACCGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GCGGAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGCGCA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
601 TGCTCGGGT GTTATCAGAT GGCCAGGTA TATTTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGACTCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

a728 / m728 96.3% identity in 377 aa overlap

```

a728.pep      10      20      30      40      50
MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
|||||
m728          10      20      30      40      50      60
MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
|||||

a728.pep      60      70      80      90      100     110
DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHGEEV
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728          70      80      90      100     110     120
DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV
|||||

a728.pep      120     130     140     150     160     170
WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728          130     140     150     160     170     180
WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
|||||

```


1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKNESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSFYYLKNLGNLF					
m728	DSRNSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSFYYLKNLGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGGRIVREEKQDRLPDFLNLEDEKEVSR					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGGRIVREEKQDRLPDFLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDLSHX					
m728	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA CATTGAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTCTGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTTCCAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTGGGTTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAAGTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACA TACATGATCG AGCGCAACA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCg
351 caaTGTCAGC AGCAGCTACA ATGTGCGACT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CgcgGATGCG GCACATTTGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
551 CTTTGCGCga gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTCGCGT ACAAGGCAGG CGTGATTTCC GCCGTCGCCC TGCGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
701 gcCGGAACA GCGCGCAAT GCCTTGCAA CCTTGATTAA ccGTCCGATA
751 CCCGAgaCC TGCCCGCCGG TTTGCGGTTG GACAagcAGT TTTTGTGA
801 AAAACTGCCT GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCCGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTCCTC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GCGGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATT TTA CTGTTGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCAA CAGGCACAAA TTGTTGCCTA
1101 TGAATCCGCC GTCCAATCCG CTTTCAAGA CGTGGCAAA GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGCGT
1251 ATCCGCGCGC CTCGATTTCG TCGATGCGGA ACGCATCAGC TATTGCGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAA CCTTGCCGAT
1351 TTGTACAAG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEAAALQG
151 YFASVANRDA AHLILIATVA KAYFNERYAE KAMSLAQRVL KTRREETYKLS

```


m729.seq

m729.pap

m729.pap

MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD

g729

MNTTLKTTLTLSVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDYFAD

1179

	70	80	90	100	110	120
m729.pep	PRLQKLIDIALERNSTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNV					
g729	PRLQKLIDIALERNSTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVLGAASYELDLFGRVRSSEAAALQGYFASTANRDAHLSLIATVAKAYFNERYAE					
g729	SSYNVLGAASYELDLFGRVRSNSEAALQGYFASVANRDAHLILIATVAKAYFNERYAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRVLKTRREETYKLSERYKAGVISAVALRQOEALIESAKADYAHAARSREQARN					
g729	KAMSLAQRVLKTRREETYKLSERYKAGVISAVALRQOEALIESAKADYAHAARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTGTGTGSSELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	ARAAFFPSIRLTGTGSVELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS					
g729	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS					
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC
51 ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGCGGTC
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAAGTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTGCGCA GCACCGCCAA CGCGATGCG GCACATTGTA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGGCGCA ACGTGTTTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTGCC GCGTCGCCC TACGTAGCA
651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTGCGAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCCGCCGG TTTGCCGTTG GACAAGCAGT TTTTGTGTA
801 GAAGCTGCGG GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACGCGG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTCCC ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GCGTTTGGT
1001 TGTTCCGACC TTCCATTACC CTGCCGATTT TTACCTGGG TACGAACAAG

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1180

```

1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

a729.pep

```

1 MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDYFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRKQ YMIERNNLLP
101 TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RRSSEALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSQA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

```

a729 / m729 98.1% identity in 467 aa overlap

a729.pep	MDTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFKN	DTADSGIRAV	DLGWHDYFAD
m729	MDTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFKN	DTADSGIRAV	DLGWHDYFAD
a729.pep	PRLQKLIDIA	LERNLSLRTA	VLNSEIYRKQ	YMIERNNLLP	TLAANANDSR	QGSLSGGNVS
m729	PRLQKLIDIA	LERNLSLRTA	VLNSEIYRKQ	YMIERNNLLP	TLAANANDSR	QGSLSGGNVS
a729.pep	SSKVGLGAAS	YELDLFGRV	RRSSEALQGY	FASTANRDA	AHLSLIATVA	KAYFNERYAE
m729	SSKVGLGAAS	YELDLFGRV	RRSSEALQGY	FASTANRDA	AHLSLIATVA	KAYFNERYAE
a729.pep	EAMSLAQRVL	KTREETYKLS	ELRYKAGVIS	AVALRQOEAL	IESAKADYAH	AARSREQARN
m729	EAMSLAQRVL	KTREETYKLS	ELRYKAGVIS	AVALRQOEAL	IESAKADYAH	AARSREQARN
a729.pep	ALATLINQPI	PDDLPAGLPL	DKQFFVEKLP	AGLSSEVLLD	RPDIRAAEHA	LKQANANIGA
m729	ALATLINQPI	PDDLPAGLPL	DKQFFVEKLP	AGLSSEVLLD	RPDIRAAEHA	LKQANANIGA
a729.pep	ARAAFFPSIR	LTGSVDTHSA	ELGGLFKSGT	GVWLFAPSIT	LPIFTWGTNK	ANLDVAKLRQ
m729	ARAAFFPSIR	LTGSVDTHSA	ELGGLFKSGT	GVWLFAPSIT	LPIFTWGTNK	ANLDVAKLRQ
a729.pep	QAQIVAYEAA	VQSAFQDVAN	ALTAREQLDK	AYDALSKQSR	ASKEALRLVG	LRYKHGVSQA
m729	QAQIVAYEAA	VQSAFQDVAN	ALTAREQLDK	AYDALSKQSR	ASKEALRLVG	LRYKHGVSQA

1181

	430	440	450	460
a729.pep	LDLLDAERSSSYSAEGAALSAQLTRAENLADLYKALGGGLKRDTQTDKX			
m729	LDLLDAERSSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDTQTDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

```

1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GGCGGTCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC
101 CGTTTCATTAC  CGATAACACC  CAACGGCAGC  ACTACGAACC  CCGCGGCAAA
151 TACCACCTCT  TCGGCGaCCC  GCGCGGCAGC  GTTTCGACCC  GCACCGGCAA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCA  GATGGGCAAC  CTGCTCATCC
251 AACAGCGCGC  AATCCAAGGC  AATCTTGTT  ACACCGTCCG  CTTTCCGGA
301 CACGGACACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 AAGCGAAGAA  AAAGGCAACG  TTGACGACGG  CTTTACCGTG  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCTACGA  CGGCCCGAAG
451 GGCGGCAATT  ACCCCAAACC  TACGGGCGCA  CGAGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCCCGCA  GTATCAAAC  CAATCCGACC  GACACCGGCA
551 GCATCCGGCA  ACGCATATTC  GACAACTACA  ACAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TGTCACGGC  GTCGCGCGCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCGA  TGC GCAACAT
801 CGCCCCCTTA  CCCGCCGAGG  GCAAATTCGC  CGCCATCGGC  GGCTTGGGCA
851 GCGCGCGCGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGA  CCGGTGGATA
901 CAGGAAAAAC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCGGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  TGGGGATTTT  TCTAAATCCT  ACACCTGCTC  CTTCCACGGC
1051 AGCACCTTGG  TCAAAACGGC  AGACGGCTAC  AAAGCCATTG  CCCATATTCA
1101 AGCGGAGAC  CGCGTCCTTT  CCAAGGACGA  GGCAAGCGGA  GAAACGGGAT
1151 ACAAACCCGT  TACCGCCCGA  TACGGCAATC  CGTATCAAGA  AACCGTTTAC
1201 ATTGAAGTTT  CAGACGGCAT  CGGCAACAGC  CAAACCTGA  TTTCCAACCG
1251 CATCCACCCG  TTTTATTCGG  ACGGCAATG  GATTAAGGCG  GAAGATTTAA
1301 AAGCGGGAAG  CCGGCTGTTA  TCCGAAAGCG  GCAAAACCCA  AACCCTCCGC
1351 AACATCGTTG  TCAAACCAAA  ACCGCTCAAA  GCCTACAATC  TGACCGTTGC
1401 CGATTGGCAT  ACCTACTTCG  TCAAGGGTAA  TCAGGCGGAA  ACGGAAGGGG
1451 TTTGGGTTCA  TAATGATTGT  CCGCCTAAAC  CAAAACCAAC  CAATCATGCC
1501 CAACAAAGAA  AAGAAGAAGC  TAAAAACGAT  TCTCATCGAA  GTGTGGGAGA
1551 TTCCAATCGT  GTCGTTTCGG  AAGGAAAGCA  ATATTTAGAT  TCCGACACAG
1601 GAAACCATGT  TTATGTAAAA  GGAGATAAAG  TGGTTATTCT  AACTCCTGAT
1651 GGAAGACAGG  TAACTCAATT  TAAGAACTCG  AAAGCCAATA  CGTCAAAAAG
1701 GGTAAAAAAT  GGGAAATGGA  CACCAAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

```

1  VKPLRLRLTNL  LAACAVAAVA  LIQPALAADL  AQDPFITDNT  QRQHYERGGK
51  YHLFGDPRGS  VSDRTGKINV  IQDYTHQMG  LLIQQAIIQG  NLGYTVRFSG
101 HGHEEHAPFD  NHAADSASEE  KGNVDDGFTV  YRLNWEGHEH  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIF  DNYNNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNMEEFVNG  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAAIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVKNLTKAAK  PGKAAVSGDF  SKSYTCSFHG
351 STLVKTADGY  KAIAHIQAGD  RVLSKDEASG  ETGYKPV TAR  YGNPYQETVY
401 IEVSDGIGNS  QTLISNRIHP  FYSDGKWIKA  EDLKAGSRL  SESGKTQTVR
451 NIVVKPKPLK  AYNLTVADWH  TYFVKGNQAE  TEGVWVHND  C  PKPKPTNHA
501 QQRKEEAKND  SHRSVGDSNR  VVREGKQYLD  SDTGNHVYVK  GDKVVILTPD
551 GRQVTQFKNS  KANTSKRVKN  GKWTPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

```

1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GGCGGCCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC

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1182

```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCGGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCAACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCGAAG
451 GGCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAACTGAT GGTTTCATCAA
1151 AATTATTATA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1  VKPLRLRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMG NLLIQQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADEANRK MFEHNAKLDR WGNSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFLNQKN RKQIKATIEA ANQQKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

```

g730.pep      10      20      30      40      50      60
                VKPLRLRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
m730           10      20      30      40      50      60
                VKPLRLRLTNLLAACAVAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS

g730.pep      70      80      90      100     110     120
                VSDRTGKINVIQDYTHQMG NLLIQQAIIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
m730           70      80      90      100     110     120
                VSDRTGKINVIQDYTHQMG NLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE

g730.pep     130     140     150     160     170     180
                KGNVDDGFTVYRLNWEGHEHHPADAYDGP KGGNYPKPTGARDEYTYHVNGTARSIKLNPT
m730          130     140     150     160     170     180
                KGNVDEGFTVYRLNWEGHEHHPADAYDGP KGGNYPKPTGARDEYTYHVNGTARSIKLNPT

g730.pep     190     200     210     220     230     240
                DTRSIRQRIFDNYNNLGSNFS SDRADEANRKMFEHNAKLDRWGNSEFVNGVAAGALNPFI
m730          190     200     210     220     230     240
                DTRSIRQRISDNYSNLGSNFS SDRADEANRKMFEHNAKLDRWGNSEFINGVAAGALNPFI

```


1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAKPGKAAVSGDFSYSYTCSEFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAKPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVTRYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

a730.seq

1	GTGAAACCGC	TGCGAAGACT	CATCAAGCTC	CTTGCCGCCT	GTGCCGTAGC
51	GGCGGCCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTTG	GCGCAAGACC
101	CGTTCATTAC	CGATAACGCC	CAACGGCAGC	ACTACGAACC	CGGAGGCAAA
151	TACCACCTCT	TCGGCGACCC	GCGCGGCAGC	GTCTCCGACC	GCACCGGTCA
201	AATCAACGTC	ATCCAAGACT	ATACCCACCG	GATGGGCAAC	CTGCTCATCC
251	AGCAGGCAAA	CATCAACGGC	ACAATCGGCT	ACCACACCCG	CTTTTCCGGA
301	CACGGATACG	AAGAACACGC	CCCCTTCGAC	AACCACGCCG	CCGACAGCGC
351	GAGCGAAGAA	AAAGGCAACG	TTGACGAAGG	CTTTACCGTA	TACCGGCTCA
401	ACTGGGAAGG	ACACGAACAT	CATCCCGCCG	ATGCCTACGA	CGGCCCGAAG
451	GGCGGCAATT	ACCCCAAACC	TACGGGTGCA	CGCGACGAAT	ACACCTATCA
501	CGTCAACGGC	ACAGCACGCA	GCAATCAAACT	CAATCCGACC	GACACCCGCA
551	GCATCCGGCA	ACGCATATCC	GACAATTACA	GCAACCTCGG	CAGCAATTTT
601	TCCGACCCGG	CCGATGAAGC	CAACAGAAAA	ATGTTGAGC	ACAATGCCAA
651	GCTCGACCGC	TGGGGCAACA	GCAATGGAGT	TATCAACGGC	GTCCGCCGCC
701	GCGCGCTCAA	CCCCTTTATC	AGCGCGGGCG	AAGCCTTGGG	CATAGGCGAC
751	ATACTGTACG	GAACGCGCTA	TGCCATAGAC	AAAGCCGCAA	TGCGCAACAT
801	CGCCCCCTTG	CCGCCCAGAG	GCAAATTCGC	CGTCATCGGC	GGCTTGGGCA
851	GCGTGGCGGG	CTTTGAAAAA	AATACGCGCG	AAGCCGTTGA	CCGGTGGATA
901	CAGGAAAAAC	CCAATGCCGC	CGAAACCGTC	GAAGCCCTGG	TCAACGTCCT
951	GCCGTTTGCC	AAAGTCAAAA	ACCTGACAAA	GGCGGCAAAA	CCGGGAAGG
1001	CTGCGGTTAG	CGGGGATTTT	TCTGCTGCAT	ACAATACAAG	AACAACCTAGA
1051	AAAGTTACTA	CAGAAACAGA	GGGGTTAAAT	AGAATCAGAC	AGAACCAGAA
1101	AAATAGTAAT	ATACATGAGA	AAAATTATGG	AAGAGATAAT	CCTAATCATA
1151	TTAATGTTT	ATCTGGAAAT	TCTATACAAC	ATATACTGTA	TGGAGATGAA
1201	GCAGGAGGTG	GGCATCTTTT	TCCTGGCAAA	CCTGGTAAGA	CAACATTCCC
1251	CCAACATTGG	TCAGCCAGTA	AAATAACTCA	TGAAATTAGT	GATATCGTTA
1301	CATCCCCAAA	AACGCAATGG	TATGCACAGA	CTGGAACAGG	CGGCAATAT
1351	ATTGCTAAAG	GAAGACCAGC	TAGGTGGGTA	TCATATGAAA	CGAGAGATGG
1401	AATTCGTATC	AGAACAGTTT	ATGAACCTGC	AACAGGAAAA	GTGGTAACTG
1451	CATTCCCCGA	TAGAACCTCT	AATCCCAAAT	ATAACCCTGT	AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

a730.pep

1	VKPLRLRIKL	LAACAVAAAA	LIQFALAADL	AQDPFITDNA	QRQHYEPGGK
51	YHLFGDPRGS	VSDRTGQINV	IQDYTHRMGN	LLIQQANING	TIGYHTRFSG
101	HGYEEHAPFD	NHAADSASEE	KGNVDEGFTV	YRLNWEGHEH	HPADAYDGP
151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTRSIRQRIS	DNYSNLGNSF
201	SDRADEANRK	MFEHNAKLDR	WGNMSEFING	VAAGALNPFI	SAGEALGIGD
251	ILYGTRYAID	KAAMRNIAPL	PAEGKFAVIG	GLGSVAGFEK	NREAVDRWI
301	QENPNAAETV	EALVNVLPFA	KVKNLTAAK	PGKAAVSGDF	SAAYNTRTTR
351	KVTTETEGLN	RIRQNQKNSN	IHEKNYGRDN	PNHINVLSGN	SIQHILYGDE
401	AGGGHLFPKG	PGKTTFFQHW	SASKITHEIS	DIVTSPKTQW	YAQTGTGGKY
451	IAKGRPARWV	SYETRDGIRI	RTVYEPATGK	VVTAFFPDRS	NPKNVPK*

1184

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRRLIKLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQOANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQOANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730.pep	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAPGKAASVSGDFSAAAYNTRTRKVTTETEGLN					
m730	QENPNAAETVEAVENVAAAKVAKLAKAAPGKAASVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730.pep	RIRONQKNSNIHEKNYGRDNPNHINVLSGNSIQHILYGEAGGGHLFPKPGKTTTFPQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gattttcgag  cgttttcacg  CGAGAACGGT  TTGTCTGTGC  GCGTCCGCAA
51  TTTGGACGGC  GGCAAAATCG  CGTTGCGGCT  GGACGGCAGG  CGTGCCGTCC
101 TCTCTTCCGA  CGTTGCCGCA  TCCGGCGAAC  GCTATACCGC  CGAACACGGT
151 TTGTTCGGAA  ACGGAACCGA  GTGGCACCAG  AAAGCGGGCG  AAGCCTTTT
201 CGGCTTTACC  GATGCCTACG  GCAATTCGGT  CGAAACTTCC  TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG  LSVVRNLDG  GKIALRLDGR  RAVLSSDVAA  SGERYTAEHG
51  LFGNGTEWHQ  KGGEAFFGFT  DAYGNSVETS  CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA  GGTTTTTCGC  GCTGACCGTA  CCGGTTTTGT  CTTTGGCGGC
51  CTGTGCCGTG  CCGGAGGCGT  ATGATGACGG  CGGACGCGGG  CATATGCCGC
101 CCGTTCAAAA  CCAAGCCGGC  ACGGACGATT  TTCGGGCGTT  TTCCTGCGAG
151 AACGGTTTGT  CTGTGCGCGT  CCGCCATTG  GACAGCGGCA  AAGTCGCGTT
201 GCGGCTGGAC  GGCAGGCGTG  CCGTCCTCTC  TTCCGACGTT  GCCGCATCCG

```


251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
301 CACCAGAAAG GCGGCGAAGC CTTTTTCGCG TTTACCGATG CCTACGGCAA
351 TTCGTCGAA ACTTCTGCC GCGCCCGTTA A

m731.pep

1	<u>MNIRFFALTV</u>	<u>PVLSLAACAV</u>	PEAYDDGGRG	HMPFPVQNQAG	TDDFRAFSC
51	<u>NGLSVRVRHL</u>	<u>DSGKVALRLD</u>	GRRAVLSSDV	AASGERYTAE	HGLFGNATEW
101	HQKGGEAFFG	FTDAYGNSVE	TSCRAR*		

```

g731.pep      10          20          30
               DFRAFSCENGLSVRVNRNLGGKIALRLDGR
m731          |||||:|||:|||:|||:|||
LSLAACAVPEAYDDGGRGHMPPVQNAQTDDFRAFSCENGLSVRVRHLDSGKVALRLDGR
              20        30        40        50        60        70

g731.pep      40        50        60        70        80
RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX
m731          |||||:|||:|||:|||:|||:|||:|||
RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX
              80        90       100       110       120

```

```

a731.seq
1  ATGAATATCA  GGTTTTTCGC  GCTGACCGTA  CCGGTTTTGT  CTTTGGCGGC
51  CTGTGCCGTG  CCGGAGGCGT  ATGATGACGG  CGGACGAGGG  CATATGCCGC
101 CCGTTCAAAA  CCAAGCCCGT  ACGGCAGATT  TTCGGGCATT  TTCCTGCGAG
151 AACGGTTTGT  CTGTGCACGT  CGCCCGTTTG  GACGGCGGCA  GCAATCGCGTT
201 GCGGTTGGAC  GGCAGGCGTG  CCGTCCTCTC  TTCCGACGTT  GCCGCATCCG
251 GCAACGCTA  TACCGCCGAA  CACGGTTTGT  TCGGAAACGG  AACCGAGTGG
301 CATCAGAAAG  GCGCGGAAG  CTTTTTCGGC  TTTAACGATG  CTAACGGCAA
351 TTCGTCGAA  ACCTCTGCC  GCGCCCGCTA  A

```

a731.pep

1	<u>MNIRFFALTV</u>	<u>PVLSLAACAV</u>	PEAYDDGGRG	HMPPVQNOAG	TADFRAFSCE
51	<u>NGLSVHVRL</u>	<u>DGGRIALRLD</u>	GRRVLSDDV	AASGERYTAE	HGLFNGTEW
101	HQKGGEAFFG	FTDAYGNSVE	TSCRAR*		

```

      10      20      30      40      50      60
a731.pep  MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNOAGTADFRAFSCENGLSVHVRRL
          |||||
m731      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNOAGTDDFRAFSCENGLSVVRHL
          |||||

      70      80      90      100     110     120
a731.pep  DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE
          |:::|
m731      DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE
          |||||

      70      80      90      100     110     120
a731.pep  TSCRARX
          |||||
m731      TSCRARX

```

g732.seq
1 ATGTCGAAAC CTGTTTTTAA GAAATCGCA CTTTACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCgagaagg
101 ACGGgcgGGA TAACGAagtC CTGCCGGTGC AATCCATCCG TACGATGGCG

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151 GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTTCG GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CCGTCGTACG ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCGCCG GATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCCTGCCG AGTTGAAAAC GATTCCGATG ACGgtATTGG TcaaATTCCG
951 TTCggttCC GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTTCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTACGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGCGACCTG
1201 CTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CCTtgcCGTA CCGTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAGGAC GAGGATTGT CTTCAAGCGG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732.pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGF AAEKDRDNEV LPVQSIRTMA
51 EVYQGQIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEPGGLGME IGQEDGFVKV VSPIEDTPEE RAEVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGRPGTKITL TLRKNADKP IVVNLTRAIL KVKSVRHHLI
201 EPDYGIVRSV QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSAF FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YGMGGDPLAG
301 IPAEIKTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNNKDKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732.seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGTTTTGCCG GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGCTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCTG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTTCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCTGTACG ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCATTCTCTG AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTGCGCAG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTTCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

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1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTG
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAG ACGACCACTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51 EVYQGIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEGGLGME IGQEDGFVKV VSPIDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDGYIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEYDV YMGGDSLAG
301 IPAEIKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGSVQT
351 LIPLNSGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAACK PVSNDKKDKD KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

m732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGF					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGF					
m732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKG					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKG					
m732.pep	130	140	150	160	170	180
	VSPIDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
g732	VSPIDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
m732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKKGKPLKGLV					
m732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVVS					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVVS					
m732.pep	310	320	330	340	350	360
	IPAEIKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGSVQTLIPLNSGSAV					
g732	IPAEIKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGSVQTLIPLNSGSAV					

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	370	380	390	400	410	420
m732.pep	KLTTALYYTTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
g732	KLTTALYYTTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAARK					
g732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAARK					
	430	440	450	460	470	480
	490					
m732.pep	PVSNDKKDKDKKX					
g732	PVSNDKKDKDKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTGGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGCTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTGTGTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTGC CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAGGAA AATAAAGGAA
701 AACCCTCAAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCTGCGC AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTGCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT CTATTACAGC GCAGGGGATT GTTCCCAGTG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GCGCGATTG
1201 GTCGGACACA TCGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAATT GCGGAAAGCT TTGGATTAGT TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 AATAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EYVQGIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFFGLGME IGQEDGFVKV VSPIDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAUGVSAA FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YGMGGDSLGA
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFQKGSVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDIVKSPEQW QKSLGLAARK PVSNDKKDKD KDKK*

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a732/m732 99.6% identity in 494 aa overlap

	10	20	30	40	50	60
a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYQGQIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYQGQIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a732.pep	VSPIEDTPAERAGVKS GDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	VSPIEDTPAERAGVKS GDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
a732.pep	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
a732.pep	LDLRDDPGGLLTGAVGVSA AFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
m732	LDLRDDPGGLLTGAVGVSA AFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
	250	260	270	280	290	300
	310	320	330	340	350	360
a732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
m732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360
	370	380	390	400	410	420
a732.pep	KLTTALYYTPNDRSIAQAGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	KLTTALYYTPNDRSIAQAGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
m732	PLEKDADKPAVKEKGKKKKDEDLSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
	430	440	450	460	470	480
	490					
a732.pep	PVSNDKDKDKDKKX					
m732	PVSNDKDKDKDKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGA AAAACGg cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCC CCGGTGCGCA CGCCATTG GACTGCTGC

```


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251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDTTS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGC GCGCCATCTG GGAAGTCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDTTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDTSLGKQTEKMEK					
g733	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDTSLGKQTEKMEK					
	10	20	30	40	50	60
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
g733	YFAEAANKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
g733	YFAEAANKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGC GCGCCATCTG GGAAGTCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

```

1  MNPKTSLRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDSTS
51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLSRSGDK EGAFRQFEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

          10      20      30      40      50      60
a733.pep  MNPKTSLRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDSTS LGKQTEKMEK
          |||||
m733      MNPKTSLRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDSTS LGKQTEKMEK
          10      20      30      40      50      60

          70      80      90      100     110     120
a733.pep  YFVEAGNKKMNAAPGAHAHLGLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
          |||||
m733      YFVEAGNKKMNAAPGAHAHLGLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
          70      80      90      100     110     120

a733.pep  GKRX
          |||
m733      GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCCGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGGCC TTTTGCAAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGATATAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
451 GCTGTTGCTT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
1  MMKILAVSA LCLMTAAQA ADTYGYLAVW QNPDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHGV ALNQCIKKYG AQGCGLQTV YCTSSSYGG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTGCGT
51  GAACAATACC TGTGTCGCGC TGGCATACCC GAAAGCCTTG GGCGCGCTGC
101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCACTG CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGGA ACAGTGATT GCACATCTTC TTCTTATTAC GCGGGAAGTG
251 TCGGCTCTTT GATTCAAAAT CTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSLNNT CVALAYPKAL GALRVDNAVV ITS PRFTSVH
51  QVALNQCIKK YGVQGCGLQ TVYCTSSSY GGTVRSLIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

          10      20      30
m734.pep  SGIAEDEPTGCRSVVSLNNTCVALAYPKAL
          :|||
g734      VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL

```


	40	50	60	70	80	90
m734.pep	GALRVDNAVVITSPRFTSVHQVALNQCIKKYGVQGQCGLETVYCTSSSYGGTVRSLIQN					
g734	GAMRVENAVVITSPRFTSVHQVALNQCIKKYGAGQCGLETVYCTSSSYGGAVRSLIQH					
	100	110	120	130	140	150
m734.pep	LKX					
g734	LKX					
	160					

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTTC CAGGTTAAAA CCACAAAAGA AGATTCCAGC
151 AAAAGCGAAG CBTGTGCCGA GTTGAAGACT TTCTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATCGCCG TCGGTCTGTG
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAACAGTG TATTGCACGT CTTCTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AATCTCAAA TAA
```

a734.pep

1	<u>MMKKILAVSA</u>	<u>LCLMTAAARA</u>	ADTYGYLAVW	QNPQNANDVL	QVKTTKEDST
51	KSEAFAELEA	FCKGQDTLAG	IAEDEPTGCR	SVVSLNNTCV	ALAYPKALGA
101	MRVENAVVIT	SPRFTSVYQV	ALNQCIKKYG	AQGQCGLETV	YCTSSSYYGG
151	TVRSLIONLK	*			

```

      10      20      30      40      50      60
a734.pep MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA
          |||
g734      MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA
          |||
      10      20      30      40      50      60

      70      80      90      100     110     120
a734.pep FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVALAYPKALGAMRVENAVVITSPRFTSVYQV
          |||
g734      FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV
          |||
      70      80      90      100     110     120

      130     140     150     160
a734.pep ALNQCICKYGAQGQCGLTGYCTSSSYGGTVRSLIQNLKX
          |||
g734      ALNQCICKYGAQGQCGLTGYCTSSSYGGGAVRSLIQHLKX
          |||
      130     140     150     160

```

m735.seq

```
1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGCGATTTCG GAAGCAGCAG CGCGTCAATG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAC TATGCGCGCG AACTGGAACT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGCGGCAC GCTGTCGGCA
251 TGCGTTTGCG GAAAAACAGC GCGGAAGTCA GCCGTCTGAA AACGGAAAAA
301 AAAAAGGAAA TCGAAATGT CCTTACTCAA ACGCGTAAAA ATGCAAGCGG
```


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351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQO AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DGFSGHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCC GCG AACTGGAACA
201 GCGCGGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGCTGAA AACGGAAAT
301 AAAAAGGAAA TCGAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQO AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGCI DGFHGHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQOAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQOAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFHGHGLQLYKRALGYGNX					
m735	DGFSGHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCCGGCAGT ATCACGCTGT TTCTGCTGAA CATTGTGGCG AAATCCGGCA
101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCC TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTGGGCTA TATGTCGCG GCTTCTCTGT TGC CGGAAC TGGTCCCGTG
301 TTGCGGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCACGCA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCG CGCGTTTTTG GCGGGCGGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT

601 TTGATCAAAT CGCCGCGCTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep
 1 MNFIRSVGAK TLGLIQSFGS ITLFLLNILA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPMQNN ITIHYDVI
 201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq
 1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
 101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGA TTTTGCCGGC
 151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTTC TCGGTATGGT
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGC CGCAACT GGGTCCCCTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGCGTGCGA TGACCAAGCA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCACCC CGTCGCCCGC GTGGTTGCCG CGCGTTTTCG GCGGGGCGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTGCGCG GCATTTTCGG
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTGGACAGC GGTATTTTCT
 551 GGCCGAGAT GCAGAACAC ATTACGATAC ATTACGATGT AATCAACGGT
 601 TTGATCAAAT CGCCGCGCTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep
 1 MNFIRSVGAK TLGLIQSLGS ITLFLLNILA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSPMLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMNN ITIHYDVI
 201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNILAKSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
g736	MKTGQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
	130	140	150	160	170	180

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
g736	GIFWPQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

```

1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCACGCTGT TTCTGCTGAA TATTCTGGCG AAATCCGGTA
101 CGGCTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGTGTATTGT TGCCGTTTCA GGGCTGTTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TCGCGGAACT GGGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGCTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGGCGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTTG GTCGGTGTA A CCTGGCTGGG CTGGACAGC GGTATTTTCT
551 GGTGCAAAAT GCAGAACAA ATCACGATAC ATTACGATG AATCAACGGT
601 CTGATCAAAT CCGCCCGGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCGTCC CGACCTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGCTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

```

1  MNFIRSVGAK TLGLIQSLGS ITLFLNLILA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDVING
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNLILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
m736	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					

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```

m736      GIFWSQMNNTIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep  ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

g737.seq

```

1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

g737.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

m737.seq..

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

m737.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR AQAEKAALAR
           |||||:|||||:|||||
g737      MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKIISR AQAEKAALAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||:|||||:|||||
g737      VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

1197

a737.seq

```

1 ATGAAC TTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTC CGCC CCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep

```

1 MNFKRLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLTA	AATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR	AQAEKAALAR
m737	MNIKHL	LLTSAAT	ALLSIS	APALAH	HDGHG	DDDHGHAHQH
	10	20	30	40	50	60
	70	80	90	100	109	
a737.pep	VGGKITD	IDLEHD	NGRPHYD	VEIVKNG	QYKVVVD	ARTGRVISSRRDDX
m737	VGGKITD	IDLEHD	NGRPHYD	VEIVKNG	QYKVVVD	ARTGRVISSRRDDX
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq

```

1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCGCGCC CCAAAC TGCC
51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCGGCCGCGC TGATTGTCCT GTTGTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAA ATCCCGCCA TCAGCTTCCT CCTGTTGCA ATGGCGGCAT
251 TTGGTGGCT TCAGGCACGC CTGATGAACC TGATTATCC CGGAATGAAC
301 GACATCGCT CTTGGGTTT CATCTGCTC GCCGTCAGCG CGTGGGCTG
351 CAAGAGTTG GTCGCACACT ACGGACAAGA ACGCATcgt ACCCTGTTT
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTT AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCTCTG CTTCAAACA TCATCGTTCA
501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCATA CTCGCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCG CAGCCCTCG CGCAATCTGC CTGATTATGC AGACCGCGT
651 TTTAGGTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCTCATCTT TCCCTTCTG TATTTCCGT CGGACAAATC CAACAGACGG
751 ACGATGCTG GCATAGCCGC AGCCGTATTC CTTACCGCG TGTTCCAATT
801 TTCCATGAAC GCCATTCTG AAACCTTTAC AGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CCGCTGGAAC AGTTTGGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATAA CGACAACCTT CTCAGCACCT TGTTCAACCA TTCCCAAC
1051 ATCATCTCC AACTCCTTGC AGAAATGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTTCTG CTGTGCGCGC TTGCGGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTT GTGGTATGTC TATTTCTCA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGG TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGC CATATTGCA
1351 GGATTGCTGC ACTTGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCC GCCGT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGCAAAC AGCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCGGAATAC CCGAAACCC AGACTTGGG
1551 GGAAGAAGCA ACCCTCAAAG CACTAAATA CCGCCCTAC TCCGCCACCT

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1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
 1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCGGATA
 1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
 1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA
 1801 AAACCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
 51 AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFWWLOAR LMNLIYPGMN
 101 DIASWVFILL AVSAWACKSL VAHYQERIV TLFAWSLLIG SLLQSCIVVI
 151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
 201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
 251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPROS
 301 EWNKALAAFQ SAPIFGHWN SFAQOTFLIN AEQHTIHDNF LSTLFTHSHN
 351 IILQLLAEMG ISGTLIVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAESDG IAFKKAANLG ILTASAAIFA
 451 GLLHLDWYTT RLVSFSPAA DSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALPEY PETQTWAEA TLKALKYRPY SATYRIALYL MRQGVAEAK
 551 QWMRATQSYI PYLMPRYADE IRKLPVWAPL LPELLKDCKA FFAAPGHPET
 601 KPCK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
 51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
 101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTACCACGA TGCCGCGGCC
 151 GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAAGTGT
 201 TGATGTCAA ATCCCGCCA TCAGCTTCCT TCTGTTTGA ATGGCGGCGT
 251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
 301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCTG
 351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
 401 CCTGTGCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
 451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATCGTTTA
 501 CAGCGGGCAA GCGTAAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
 601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCGCCATCG
 701 CCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
 751 ACGATGCTCG GCATAGCCGC AGCCGTATT CTTACCGCGC GTTCCAATT
 801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAACTG
 851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
 951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
 1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCACCCA TCCCCACAAC
 1051 ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
 1151 CCCCCGCATC GCTTTTCCTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTTCGG
 1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
 1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCA
 1351 GGATTGCTGC ACTTGGAAGT GACATACACC CGGCTGGTTA ACGCCTTTTC
 1401 CCCCGCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
 1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
 1501 TCCCTCGTAA ACTTCGCCCT GCCGAATAC CCCGAAACCC AGACTTGGGC
 1551 GGAAGAAGCA ACCCTCAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
 1601 AACCGCATCG CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
 1651 CAATGGATGC GGGGACACA GTCCTATTAC CcGTACCTGA TGCCCGGATA
 1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCCGCTG CTACCCGAAC
 1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
 1801 AAACCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA


```

51  AAGLIVLLFL TAGKKLFDVK IPAISFLFA MAAFWYLOAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGORN NLGHYLMWGI LAAAYLNGQR
201 KIPAAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFO SAPIFGHGWNSFAQQTFLIN AEQHNIYDNL LSNLFTSHHN
351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMSFYADF
501 SLVNEALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

m738.pep	10	20	30	40	50	60
	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	10	20	30	40	50	60
	MSAETTVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
m738.pep	70	80	90	100	110	120
	TAGKKLFDVKIPAISFLFAMAAFWYLOARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	70	80	90	100	110	120
	TAGKKLFDVKIPAISFLFAMAAFWLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL					
m738.pep	130	140	150	160	170	180
	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGORN					
g738	130	140	150	160	170	180
	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGORN					
m738.pep	190	200	210	220	230	240
	NLGHYLMWGILAAAYLNGQRKIPAAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	190	200	210	220	230	240
	NLGHYLMWGILASAYLNGQRKIPAAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738.pep	250	260	270	280	290	300
	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
g738	250	260	270	280	290	300
	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNAILETFTGIRYETAVERVANGGFTDLPRQS					
m738.pep	310	320	330	340	350	360
	EWNKALAAFO SAPIFGHGWNSFAQQTFLINAEQHNIYDNL LSNLFTSHHNIVLQLLAEMG					
g738	310	320	330	340	350	360
	EWNKALAAFO SAPIFGHGWNSFAQQTFLINAEQHTIHDNFLTSTLFTSHHNIIQLLAEMG					
m738.pep	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRSITPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
m738.pep	430	440	450	460	470	480
	FLSPAASDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
g738	FLSPAASDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPLSFYADFSLVNFALPEYPETQTWAEATLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPLSFYADFSLVNFALPEYPETQTWAEATLKALKYRYPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQGKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQGKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEP					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738.seq
1  ATGCCCCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCGGCC
151 GCAGCCGGCC TGATTGTCTT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCTTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTCAAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGC CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCGAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCGCA TATTGCGGCA
951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTACCCCA TTCCCAACAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCTCTGA
1151 CCCCCGCATC GCTTTTCCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTCCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738.pep
1  MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAG
51  AAGLIVLLEFL TAGKKLEFVK IPPISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSQGV VIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```


1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TILGIAAAVF LTALFQFSMN TILEFTTGIR YETAVERVAN GGFTDLPRQI
301 EWRKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

a738.pep	10	20	30	40	50	60
m738	10	20	30	40	50	60
a738.pep	70	80	90	100	110	120
m738	70	80	90	100	110	120
a738.pep	130	140	150	160	170	180
m738	130	140	150	160	170	180
a738.pep	190	200	210	220	230	240
m738	190	200	210	220	230	240
a738.pep	250	260	270	280	290	300
m738	250	260	270	280	290	300
a738.pep	310	320	330	340	350	360
m738	310	320	330	340	350	360
a738.pep	370	380	390	400	410	420
m738	370	380	390	400	410	420
a738.pep	430	440	450	460	470	480
m738	430	440	450	460	470	480
a738.pep	490	500	510	520	530	540
m738	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738.pep	MRQ GK VAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
m738	MRQ GK VAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
	550	560	570	580	590	600
a738.pep	KPKCKX					
m738	KPKCKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CCGCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1  MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSGLP
101 SPAAPKKNRVKPRPSDAARAADSLTGTGTQAENTLKETPVLPNTNAPHPEP
151 RKETPEKQAAKPKETPKENHTKPDTPKNTPAKPHKEILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CGCCAAAGA
501 AAACCATACC AAACCGGACA CCCCAGAAA CACGCGGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1  MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTEESGSGLP
101 SPAAPKKNRVKQPADTAQTDROPDDAGTQAENTLKETPVLPNTNVRPEP
151 RKETPEKQAAKPKETPKENHTKPDTPKNTPKPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET					
	: : : : :					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	: : : : :					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPNTNVRPEPRKETPEKQAQPKETPKE-----NHTKPDT					
	: : : : : :					
g739	ADSLTGTGTAENTLKETPVLPNTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPDT					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPEKPHKEILDKLF					
	:					
g739	PKNTPEKPHKEILDNLF					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPF LTPKLLIRAV LLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSGLP
101 SPAAPKKNRV KQPADTAQT DRQPDAGAQ AENTLKETPV LPTNVRPEP
151 RKETPEKQAQ PKETPKEKET PKNHTKPDT PKNTPEKPHK EILDNLF*

```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTE PQHTDSPRET					
	: : : : :					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	: : : : :					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDAGAQ AENTLKETPVLPNTNVRPEPRKETPEKQAQPKETPKEKETPKENHTKPDT					
	: : : : :					
m739	DRQPDAGTQAENTLKETPVLPNTNVRPEPRKETPEKQAQPKETPK-----ENHTKPDT					
	130	140	150	160	170	

1204

```

                190
a739.pep      PKNTPPKPKHKEILDNLFX
                |||||
m739          PKNTPPKPKHKEILDKLF
                180      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATT
201 GAAACgtcaa ACCATGTTTC TGTATTATCC GATTGTTTGT CTGTTGTGT
251 ATTTGTTCCA CTATTTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFETIKHH LKQGFDLKRQ TMELFIPIVL LVVYLPHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCGTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KQHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LVVYLPHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

                10      20      30      40      50      60
m740.pep      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKQHLINGIILACEATFLFKFVLFDTIKHH
                |||||
g740          MSRNLLVRWLAVCLIPLATLAVFAANPPEDKPQHLINGIILACEATFLFKFVLFETIKHH
                10      20      30      40      50      60

                70      80      90
m740.pep      LKQEFDLKRQTMLLFIPILLIVYLPHYFGAEX
                ||| |||||:||||:|||||
g740          LKQGFDLKRQTMELFIPIVLLVVYLPHYFGAEX
                70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LVVYLPHYFG AF*

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a740/m740 97.8% identity in 92 aa overlap

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                10      20      30      40      50      60

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1205

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a740.pep  MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
          |||||
m740      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
          10      20      30      40      50      60

          70      80      90
a740.pep  LKQEFDLKRQTMLLFPIILLIVLYLFHYFGAFX
          |||||
m740      LKQEFDLKRQTMLLFPIILLIVLYLFHYFGAFX
          70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1  GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTG
51  TGACCGCCTG CAGCAGCGGA GGGCGGAGG CGGTGGTGTG GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCTG CGATTTGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 CCGACACGCG CTACGGCGGC GAAGAGAAAG GCATTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1  VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNTLTL SAQGAETFK AGGKDNSLNT GLKNDKISR
101 FDFVQKIEVD GQTITLASGE FQIYQDHSA VVALRIEKN NPDKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAQ
201 GHGKIEHLKT PEQVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGKEV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1  GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACCTAAC GCACCGCTCG ACCATAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GGGGCGACAA GGTGCGGAAA AACTTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAGGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAC ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1  VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHDKGL
51  QSLTLDQSVR KNEKLKLAQ GAERTYGNQ SLNTGKLKND KVSRFDFIRO
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSK KMAKQRFRI

```

seq ID 3

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQGNNGKI
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLT---	ALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQ			
	: :	:	:	:	:
g741	VNRTTFCCLSLTAGPDS	DRLOQRRGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEA			
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAQA	EKTY---GNGDSLNTGKLKNDKVS	RFD	FIRQIEVDGQLITLES	GE
	: :	:	:	:	:
g741	SIPQNGTLT	LSAQGAETFKAGGKD	NSLNTGKLKNDKIS	RFD	VFQKIEVDGQTITLAS
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQ	TEQIQDSEHSGK	MMVAKRQFRIGD	IAGEHTSF	DKLPEGGRATYRGT
	:	:	:	:	:
g741	FQIYKQDHS	AVVALRIE	KINNPDKIDSL	INQSR	FLVSDLGGEHTAFNQLPDG-KAEYHGK
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLT	YTIDFAAKQGNNGKIEHLKSP	ELNVDLAAADIKPD	GKRHAVISGS	SVLYN
	:	:	:	:	:
g741	AFSSDDADGKLT	YTIDFAAKQGHGKIEHLK	TPEQNV	ELASAE	LKADEKSHAVILGDTRYG
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYS	SLGIFGGKAQ	EVAGSAEVK	TVNGIRHIGL	AAKQX
	:	:	:	:	:
g741	GEEKGTYRL	ALFGDRAQ	EIAGSATV	KIGEKV	HEIGIADKQX
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq
 1 GTGAACCGAA CTGCCTTCTG CTGCCTTCTT TTAGCCGCCG CCCTGATTCT
 51 GACCGCCTGC AGCAGCGGAG GCGGCGGTGT CGCCGCCGAC ATCGGCGCGG
 101 TGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAAGTTTG
 151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
 201 GCGGCGACAA GGTGCGGAAA AAACCTTATGG AAACGCGGAC AGCCTCAATA
 251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GCTTCGACTT TATCCGTCAA
 301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGCGGAG AGTTCCAAGT
 351 GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC
 401 AAGATTCCGA GCATTAGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
 451 GCGGATATAG CGGGTGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
 501 CAGGGCGACA TATCGCGGGA CGGCATTCCG TTCAGACGAT GCCAGTGGAA
 551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGACA CGGCAAAATC
 601 GAACATTTGA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT
 651 CAAGCCGGAT AAAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
 701 ACCAAGCCGA GAAAGGCAGT TACTCTCTAG GCATCTTTGG CGGGCAAGCC
 751 CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAAACG GCATACGCCA
 801 TATCGGTCTT GCCGCCAAGC AGTAA

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep
 1 VNRTAFCCLS LTAALILTAC SSGGGGVAAD IGAVLADALT APLDHDKSL
 51 QSLTLDQSVR KNEKLKLAQA GAETTYGNGD SLNTGKLKND KVSREFDRIQ
 101 IEVDGQLITL ESGEFQVYQ SHSALTALQT EQVQDSEHSG KMKVAKRQFRI
 151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD ASGKLTYTID FAAKQGHGKI
 201 EHLKSPELNV DLAAADIKPD KKRHAVISGS VLYNQAEKGS YSLGIFGGQA
 251 QEVAGSAEVE TANGIRHIGL AAKQ*

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQGAEKTYGNGDSLNTGKLKNDKVSREFDQIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQGAEKTYGNGDSLNTGKLKNDKVSREFDQIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSD					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLYTITDFAAKQGHGKIEHLKSPELNVDLAASDIKPKKRHAVISGSVLYNQAEGKS					
m741	AGGKLYTITDFAAKQGNKGKIEHLKSPELNVDLAADIKPDGKRHAVISGSVLYNQAEGKS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAAKQX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAAKQX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATGGTTTACG	GCATTGCCGA	AGCCGATGCG	GGCGACAGCA	GTGTGCTTAC
51	TTTGGGCGGC	ATGTATCAGA	AGAGTAGGGA	GGTTCCTGAT	TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAT	CAGAAACTG	CCCCGTTTCA	TTCAACGCCT
151	GCCTGCAACC	GGCCTTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TAAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAC
251	ATGTGTTTGA	CAACGGTTGG	CAGCTCAATG	CCGAAGTGTC	TTATACCAAG
301	AATGAATCCG	ATGCGAAGGT	GGGGCAGTTT	TTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG	TCGGGTGAGG	ATGCGGTAGG	CTTTTGTACT	GAAAAAACG
401	AAGTCATCCC	GTTTCGAGCCG	AAAGATAAGG	CATTGGAGAA	ACTGAAAGCA
451	TATCGTGATG	AAACCGCCAA	GGAATACCGG	GAGCGCAAAG	ACGATTTTGT
501	TAAAAACCGT	TTCGATAATA	CTGCTTTCGA	ACAGTATCGC	AGCCGCCGTG
551	CCGCAGAACG	CAAAGCCGGT	TTTGACAAGT	GTATGAGTGA	CCCTTTCGCG
601	CTGGACTTTA	TCTGTCAAGG	TTCTTGGGGG	GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA	TTTGTGATA	AAGCCCTTGC	GAAAGAGGGC	ATCTTTAATA
701	ATGCCGCACA	ACGTTTTC	AACAGCCTGT	ATGACTCTTC	CTTTAATCGG
751	AAGGCTACCG	CCAACCGACG	ATACAGTTAT	ATGCCGTTGC	GGCATAACCA
801	AGACGACCGC	CAATGGGGAA	TTAACTTGA	CCTGACCGGC	ACATATGGGC
851	TGTTCCGGCG	GGAGCATGAT	TTCTTTGTCG	GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT	CGGAATATCT	AGAAATCTAC	GAACGCCGCT	ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGGACGG	CGATTGTGCG	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG	CGTACGATGA	AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT	GACGAATACA	GCGGCAGCCG	GACACCGGTA
1201	TATGTCGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAC
1251	CAATCCCGAC	GGCACGCCTG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCGG
1301	TTTGGAAAAC	CGTCAAAGTG	GCAGACGACC	ATGTTCTCTG	GCTGTATAAC
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTCCGCTGA	CTGCCAGCAC
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTGCACTACA


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1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTCGGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTGAGATT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGGTGACCG TCGGCGGCGG CGTGTCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACCTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

m742.pep

```

1  M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L P C E N Q K T A P F S S T P
51  A C N R P L Q L P R N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K
101 N E S D A K V G Q F F L K N E Y A A G L S G E D A V G F L T E K N E V I P F E P K D K A L E K L K A
151 Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R S R R A A E R K A G F D K C M S D P F A
201 L D F I C Q G S W G D P G V D A D K A E F V D K A L A K E G I F N N A A Q R F P N S L Y D S S F N R
251 K A T A N R R Y S Y M P L R H T K D D R Q W G I K L D L T G T Y G L F G R E H D F F V G Y A Y G D E
301 K I R S E Y L E I Y E R R Y R V R P N T G A T H G V Y A G S C Q E E P D G D L S S P L V R G H K E P
351 D W Q A Y D E K G N R T V Y A E E C R N A K K I K T E P K L D A E G K Q V Y Y Y D E Y S G S R T P V
401 Y V D V Y E L D E K G N K I Q E T N P D G T P A F T G F S G T V P V W K T V K V A D D H V P A L Y N
451 Y A K Y L N T N K T H S L T A S T R E N V T G R L H L L G G L H Y T R Y E T S Q T K D M P V R Y G Q
501 P A S D F Q T A S S I R A D Q D H Y T A K M Q G H K L T P Y A G I T Y D L T P Q Q S I Y G S Y T K I
551 F K Q Q D N V D V S A K T V L P P L V G T N Y E V G W K G A F L Q G R L N A S F A L F Y L E Q K N R
601 T V V D F G Y V P G A G G K Q G S F Q T V A K P I G K V V S R G A E F E L S G E L N E D W K V F A G
651 Y T Y N K S R Y K N A A E V N A E R L A K N S S A D P Y N F S N F T P V H I F R F G T S F H I P N T
701 G L T V G G G V S A Q S G T S S L Y N I R Q G G Y G L I D G F V R Y E L G K H A K L S L I G T N L N
751 G R T Y F E N N Y N R T R G A N N F Y G E P R T V S M K L D W Q F *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

a742.seq

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1  A T G G T T T A C G G C A T T G C C G A A G C C G A T G C G G G C A C A G C A G T G T G C T T A C
51  T T T G G G C G C G A T G T A T C A G A A G A T A G G G A G G T T C C T G A T T T T C G G G C A
101 T T A T T T G T C C T G T G A A A T C A G A A A C T G C C C G T T C A G T T C A A C G C C T
151 G C C T G C A A C C G G C C T T T G C A A C T G C C G C G A A C A C T T A T T G G G G G A G G A
201 T T G G T C G C G G T T G A G T G C T G A C A A T A C A A C C T T T T C T C A G G T T C A A A C
251 A T G T G T T T G A C A A C G G T T G G C A G C T C A A T G C C G A A G T G T C T T A T A C C A A G
301 A A T G A A T C C G A T G C G A A G G T G G G C A G T T T T T C T G A A A A C G A A A A A A C G
351 G G C G G G T T T G T C A G A T G A G G A T G C G G T A G G C T T T T T G A C C G A A A A A A C G
401 A A G T C A T C C C G T T C G A G C C G A A A G A T A A G G C A T T G G A G A A A C T G A A A G C A
451 T A T C G T G A C G A A A C C G C C A A G G A A T A C C G T G A G C G C A A A G A C G A T T T T G T
501 T A A A A A C C G T T T C G A T A A T A C T G C T T T C G A C G A T A C C G C A G C C G C G T G
551 C C G C A G A A C G C A A A G C C G G T T T G A C G A G T G T A T G A G T G C C C T T T T G C G
601 C T G G A C T T T A T C T G T C A A G G T T C T T G G G G G A T C C G G G T G T T G A T G C C G A
651 C A A G T C G G A A T T T G T C G A T A A G C C C T T G C G A A G G A A G G C A T C T T T A A T A
701 A T G C G G C A C A C G T T T T C C A A A C A G C T G T A T G A C T C T T C C T T A A T C G G
751 A A G G C T A C C G C C A A C C G A C G A T A C A G T T A T A T G C C G T T G C G G C A T A C C A A
801 A G A C G A C C G C C A A T G G G G A A T T A A A C T G A C C T G A C C G C G C A C A T A T G G G C
851 T G T T C G G G C G G G A G A C A T G A T T T C T T T G T C G G C T A T G C C T A C G G C G A T G A A
901 A A G A T A C G T T C C G A A T A T C T G G A A T C T A C G A A C G C C G C C A C A G A G T A C G
951 T C C G A A T A C A G G G G C A A C G C A C G G C G T G T A T G C G G G A A G T G T C A G G G G G
1001 A G C C G G A C G G T G A T T T G T C T T C T C T T T G G T C A G G G G G C A T A A G A A C C C
1051 G A T T G C A G G C G T A C G A T G A A A A G G C A A C G T A C C G T T T A T G C C G A A G A
1101 A T G C A G G A A T G C C A A G A A A T A A A A C C G A G C C A A G C T C G A T G C C G A A G
1151 G C A A G C A G G T G T A T T A C T A T G A C G A A T A C A G C G G C A G C C G A G T A

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a742.pcp

1	MVYGIAEADA	GDSSVLTGG	MYQKSREVPD	FSGIILSCEN	QKTAPFSSTP
51	ACNRPLQLQPR	NTLKEDEWSR	LSADKYNFES	GFKHVFDNGW	QLNAEVSYTK
101	NESDAKVGQF	FLKNEHAAGL	SDEDAVGFLE	EKNEVIFPEP	KDKALEKLKA
151	YRDETAKKEYR	ERKDDFVKNR	FDNTAFGEYR	SRRAERKAG	FDECMASPPA
201	LDFICQGSWG	DPGVDADKSE	FVDKALAKEG	IFNNAAQRF	NSLYDSSFNr
251	KATANRRYSY	MPLRHKTDDR	QWGIKLDLTG	TYGLFGREHD	FFVGYAYGDE
301	KIRSEYLEIY	ERRHRVRPNT	GATHGVYAGS	CQGEPPGDLS	SPLVRGHKEP
351	DWQAYDEKGN	RTVYAEECRN	AKKIKTEPKL	DAEGKQVYVY	DEYSGSRTPV
401	YVDVYELDEK	GNKIQETNPD	GTPAFTGFSG	TVPVWKTVKV	ADHDVPAALN
451	YAKYLNTNKT	HSLTAGTRFN	VTGRHLHLPY	LHYTRYETSQ	TKDMPVRYGQ
501	PASDFQTKASS	IKADQDHYTA	KMQGHLKLTPY	AGITYTDLNPQ	QSIYGSYTKI
551	EKQDNVDVDS	AKTVLPPPLVG	NTYEVGWKGA	FLQGRNLASF	ALFYLEQKNR
601	TVVDFGYVPG	AGGKQGSFQT	VAKPIGVVVS	RGAEFELSGE	LNEDKWFVAG
651	YTYNKSRYKN	AAEVNAERLA	KNTGADPPNF	SNFTPVHIFR	FGTSFHIPNT
701	GLTVGGSVYA	QSGTSSLYNI	RQGGYGLIDG	FVRYELGKHA	KLSLIGTNLN
751	GRTYFENNYN	RTRGANNFYG	EPTRVSMKLD	WQF*	

		10	20	30	40	50	60
a742.pep		MVYGIAEADAGDSSVLT	LGGMYQKSREVP	PDFSGIILSCENQ	KTAPFSSSTPACN	RPLQLPR	
m742		MVYGIAEADAGDSSVLT	LGGMYQKSREVP	PDFSGIILPCENQ	KTAPFSSSTPACN	RPLQLPR	
		10	20	30	40	50	60
		70	80	90	100	110	120
a742.pep		NTYLGEDWSRLSADKYN	LFSGFKHVF	DNGWQLNAEVS	YTKNESDAKVGQ	FFLKNEHAAGL	
m742		NTYLGEDWSRLSADKYN	LFSGFKHVF	DNGWQLNAEVS	YTKNESDAKVGQ	FFLKNEYAAGL	
		70	80	90	100	110	120
		130	140	150	160	170	180
a742.pep		SDEDAVGFLTEKNEVI	PFEFPKDKALEK	LKAYRDETAKEYR	RERKDDFVKNR	FDNTAFEQYR	
m742		SGEDAVGFLTEKNEVI	PFEFPKDKALEK	LKAYRDETAKEYR	RERKDDFVKNR	FDNTAFEQYR	
		130	140	150	160	170	180
		190	200	210	220	230	240
a742.pep		SRRAAERKAGFDECM	SAPFALDFICQ	SGSWGDP	GVADADKSEFV	DKALAKEGI	FNNAAORF

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|||||:|||||:|||||:|||||:|||||:|||||:
m742      SRRAAERKAGFDKMSDPFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
          190      200      210      220      230      240
          250      260      270      280      290      300
a742.pep   NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGRHDFVGYAYGDE
          |||||||:|||||:|||||:|||||:|||||:|||||:
m742      NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGRHDFVGYAYGDE
          250      260      270      280      290      300
          310      320      330      340      350      360
a742.pep   KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGE PDGDLSSPLVRGHKEPDWQAYDEKGN
          |||||||:|||||:|||||:|||||:|||||:|||||:
m742      KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQEE PDGDLSSPLVRGHKEPDWQAYDEKGN
          310      320      330      340      350      360
          370      380      390      400      410      420
a742.pep   RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD
          |||||||:|||||:|||||:|||||:|||||:|||||:
m742      RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD
          370      380      390      400      410      420
          430      440      450      460      470      480
a742.pep   GTPAETGFGSTVPVWKTVKVADHDHPALYNYAKYLNTNKTHTSLTAGTRFNVTRGLHLGG
          |||||||:|||||:|||||:|||||:|||||:|||||:
m742      GTPAETGFGSTVPVWKTVKVADHDHPALYNYAKYLNTNKTHTSLTAGTRFNVTRGLHLGG
          430      440      450      460      470      480
          490      500      510      520      530      540
a742.pep   LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQ
          |||||||:|||||:|||||:|||||:|||||:|||||:
m742      LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTPYAGITYDLTPQ
          490      500      510      520      530      540
          550      560      570      580      590      600
a742.pep   QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNR
          |||||||:|||||:|||||:|||||:|||||:|||||:
m742      QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNR
          550      560      570      580      590      600
          610      620      630      640      650      660
a742.pep   TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN
          |||||||:|||||:|||||:|||||:|||||:|||||:
m742      TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN
          610      620      630      640      650      660
          670      680      690      700      710      720
a742.pep   AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          |||||||:|||||:|||||:|||||:|||||:|||||:
m742      AAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          670      680      690      700      710      720
          730      740      750      760      770      780
a742.pep   RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          |||||||:|||||:|||||:|||||:|||||:|||||:
m742      RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          730      740      750      760      770      780
a742.pep   WQFX
          |||
m742      WQFX
```

a742/ p25184

sp|P25184|PUPA_PSEPU

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

>gi|94923|pir||S15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)
 pseudobactin uptake protein [*Pseudomonas putida*] Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADHDV-PALYNYAKYLNTNKTSLTAGTRFNVTGRLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y

Sbjct: 511 QTPKPGDDEIIPGI-----QYNISNRQSGYFVASRFLNLTDDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q

Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLQGRNLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG

Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMKRDNLAESTNEVVPDSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + ++G + ELSGE+ W VF GY++ ++

Sbjct: 669 IAS-----RAVDGAETRGVDVELSGEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +

Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWKLTLLGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F

Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTT CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGGC GGTATTGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCCAAT CCAATTGAGA GCCGGGAGGA ACCGTCAATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRSTATGM RIAGKDT PQS VSVITRSLD DKAVHTLEEA
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTT CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTGCG
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTTGGC GGTTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPOS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

```

a743.pep      10      20      30      40      50      60
MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT
|||||
m743          10      20      30      40      50      60
MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT
|||||

a743.pep      70      80      90     100     110     120
IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSSLQTRFL
|||||
m743          70      80      90     100     110     120
IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSSLQTRFL
|||||

a743.pep     130     140     150     160     170     180
SRGFYIDQIGEDGITVNVAGRSYGTAKIDVSPSTDLAVYDHIIEVVRGATGLTQSNSEPGG
|||||
m743         130     140     150     160     170     180
SRGFYIDQIGEDGMTVNVAGRSYGTAKIDVSPSTDLAVYDHIIEVVRGATGLTQSNSEPGG
|||||

a743.pep      TVNLIRKR
|||||
m743          TVNLIRKX

```

g744.seq not found yet

g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAGAAGA GAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTGGA TGAATTATGT GAACCAAATA TTTCGTTTTT AATCGGAGAA
151 AAGGGAACTG GAAAGACAGC ATATGCTGTT TATTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTC AGATTTTACA
301 AGTATTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AATGAATAT TATTATGGCG CTTTGATCC GGAATTTGTA
451 CAAGCAATAA CTTTAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAAATTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTA
551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTATTATGA
651 TGGGATAGAT ATTAGACCAT CACAGATTEC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CCTTCATTAA AGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAT ACCAACTTC
851 AAGATAATTC AGTATTTTAA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTCCAT
1001 GGAATGCTCC TAATTTACAT GATGAGTATA AAAATTTAAC TTCATTTATT
1051 AGCTTCCTAA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTTACTT
1201 GGTGAATCA AAGATCATCT TTTGTTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTCCTG AAATTTTTTG AATTTTTTAA CGGGAAGAT AGATTTAAAT

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1301 ATAGTGATTT TTTAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAC TGAAGCTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAGCC CTGATGTTG GTACTCCATT TAAGACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

```

m744.pep
1 MKPLKTLFEG FVDAANYRRR ENKDLFNRIK VKGEYLDELK EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEEESQO ITFTESKFOA NLGFIERKFK
201 DALSQLKLD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVLLIRPDI FDSLGLQONQ TKLQDNSVEL DWRTDYKSYR
301 SSKIFGVFDH LLRTQOEKQD SLERGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLFY YSQSDYQNFL KFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKFS TANEFLQFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTFFRNK Q*

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g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

```

m745.seq
1 ATGTTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAACCTCATA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTTGCGCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGCG ACGAGTTTTA TGGGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTGT TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTGGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

```

m745.pep
1 MEWQLTVVSV TAVIALGTIF INKKTSKOKA TLDVILNDYQ DAQFVEADNH
51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDELK FKRLHCTNFI KLWNAVSPV MKIREERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

```

g746.seq
1 ATGTCCGAAA ACAACAAAA CGAAGTCCTG ACCGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCGCAACCGC AGGCCGGCGA AACC GGCGCA AGGGAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAAATCCGC CGCCGAAAAC GGGGAAACCG
251 CCGCCGACAA ACCGACGAC TTGGCAGCGG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACACGTA GCGCGCCCGC TGGTGCTGAT
351 TAACGACCGG CTGGAAGACA GCAACATCAA AGGTTTGGA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACC GAAGCA GGCAAAACAA
451 CGCGTGCCTG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAAC TGCTGCCGAA AAACCAAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAACG

```


g746.pap

1	MSENKQNEVL	TCYEQLKRRN	RRRLVTASSL	VAASCILLAA	ALSSDPADSN
51	PAPAQGETGA	TESQTANTAQ	TPALKSAEN	GETAADKQPD	LAGEDKPSAA
101	DSEISEPENV	GAPLVILNDR	LEDNSIAGEL	ESEKLQFAO	AKTEPKQAKQ
151	RAAEKVSATA	DSTDVTAVEK	PKRTAEPKPQ	KAERTAAEAK	KAETKTKAEK
201	VADPKPTAAE	KTRPDTAKSD	SAVKEAKKD	KAEGKKTAEK	DRSDGKRHET
251	AQRTDRAKDT	KTAEEKSGK	AGSKAAIQAG	YAEKERALS	QRKMKAGAGD
301	STITEIMTDN	GKYVRVKSSN	YKNARDAERD	LNKLRVHGIA	GQVTNE*

m746.seq

1	ATGTCGGA	ACAAACAAA	CGAAGTCTG	AGCGGTTACG	AACAACCTCA
51	ACCGGCAAC	CGCCCGCGCC	TCGTAACGCG	AAGTTGCCTG	GTTCGCGCCT
101	CTCGCATCT	GTGGCGAGC	CGCCTCAGTT	CGCGCCCTGC	CGAACAGACT
151	CGCGGCGAAA	CAAGCGGCGT	AGAAAAACAAA	CGCGCAGGTG	CGGCACAAAC
201	CCCTGCTCTG	AAATCGCGCG	CCGACAAACG	GCAGGACTTG	GCAGCGCAAG
251	ACAAGCCTTC	TGCTCCGCGC	AGCGAAATCA	CGCAGCTTGA	AAACGTATGGC
301	CGCCGCTCTG	TGCTGATTAA	CGAGCGCCTC	GAAAGACAGA	ACATCAAAGG
351	TTTGGAAAGCA	TCCGAGAAAC	TGCAACAGGC	AGAAATCGCC	AAAACCGCAC
401	CGAAGCAGCG	AAAAACAACG	GCTGCCGAAA	AAGTCCGCGG	ACGATCGCCAC
451	AGTACGGATA	CGTAGCGCGT	TGAAAAACCG	AAACGCACGT	CCGAAACAAC
501	ACCGCAAAAA	CGGGAACAGC	CTGCCAAAGC	CAAGCCCAAA	GCCAAAGAAA
551	CCAAAACCCG	CGAAAACAGT	GCGCAACAAAC	CGAAAACCTG	CGCCCGAAAA
601	ACCAAACCGG	ATACGCGAAA	ATCCGACAGC	CGCGTAAAGC	AAGCGAAAAA
651	AGCCGACAAG	GCTGAAAGCA	AAAAAACAGC	CGAAAAGAGC	CGTTCCGACG
701	GCAAAACAGCA	GCAAAACGCGA	CAAAAACCGG	ACAAAGCCGA	CAAGACCCAA
751	ACCGCCGAGA	AGGAAACAAATC	CGGTAAAAAC	GCGCCACTTC	AGGCAGGTTA
801	TGCCGAAAAA	GAACGCGCCT	TAAAGCTTCA	GCCCAAAATG	AAGCGCGCGG
851	GTATCGATT	GACCATCACC	GAAATATGCA	CCGACACCGG	CAAAGTTTAC
901	CGCGTCAAT	CAAGCAACTA	TAATAACGCA	AGGGATGCCG	AACCGGATT
951	GAACAATAATG	CGCGTACACG	GTATCGCGCG	TCAGGTAACG	AATGAATATG

m746.psp

1	MSENKQNEVL	SGYEQLKRRN	RRRLVTASCL	VAASCILIAA	ALSSGPAEQT
51	AGETSGVNEK	AAGAAQTPAL	KSAADRPQDL	AGEDKPSAAD	SEISEPENVG
101	APLVILNERL	EENASIGLEA	SEKLQAAETA	KATPKQAQOR	AAEKVVPATAD
151	SDTVAVEKP	KRTAETKPKQ	AERTAKAPKP	AKETKTAEKV	ADPKPTAAEK
201	TKPDTKASDS	AVKEAKKADK	AESKKTAEKM	RSDGKKHETA	QKTDKADKTK
251	TAEKERSGKK	AAIQAGYAE	ERALSQRMK	KAGIDSTIT	EIMTDNGKGY
301	RVKSSNYKNA	DAERDLNKL	RVHGIAGQVT	NE*	

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

m746/g746 89.9% identity in 346 aa overlap

[illegible]

1215

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      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQ
g746      LEDSNIKGLEESEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPKQ
              130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK
              190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKHETAQKTDKADTKTAEKEKSGK---KAAIQAGYAEKERALSQRKMKAAAGID
g746      DRSDGKKHETAQKTDKADTKTAEKEKSGKAGKAAIQAGYAEKERALSQRKMKAAAGID
              250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
              310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1   ATGTCCGAAA  ACAAACAAAA  CGAAGTCTTG  AGCGGTTACG  AACAACTCAA
51  ACGGCGCAAC  CGCGCGCGCC  TCGTAACGGC  AAGTTGCCTG  GTTGCCGCCT
101 CCTGCATCCT  GCTGGCAGCC  GCCCTCAGTT  CCGGCCCTGC  CGAACAGACT
151 GCCGGCGAAA  CAAGCGGCGT  AGAAAAACAA  GCGGCAGGTG  CGGCACAAAC
201 CCCTGCCTTG  AATCCGCGG  CCGACAAACC  GCAGGACTTG  GCAGGCGAAG
251 ACAAGCCTTC  TGCCGCCGAC  AGCGAAATCA  GCGAGCCTGA  AAACGTAGGC
301 GCGCCGCTGG  TGCTGATTAA  CGACCGCCTC  GAAGACAGCA  ACATCAAAGG
351 TTTGGAAGCA  TCCGAGAAAC  TGCAACAGGC  AGAAACCGCC  AAAACCGCAC
401 CGAAGCAGGC  AAAACAACGC  GCTGCCGAAA  AAGTGCCGGC  AACTGCCGAC
451 AGTACGGATA  CGGTAGCGGT  TGAAAAACCG  AAACGCACTG  CCGAAACAAA
501 ACCGCAAAAA  GCGGAACGCA  CTGCCAAAGC  CAAGCCCAAA  GCCAAAGAAA
551 CCAAAACCGC  CGAAAAAGTT  GCCGACAAAC  CGAAACTGCG  CGCCGAAAAA
601 ACCAAACCGC  ATACGGCAAA  ATCCGACAGC  GCGGTAAAAG  AAGCGAAAAA
651 AGCCGACAAG  GGTGAAAGCA  AAAAAACAGC  CGAAAAAGAC  CGTTCGGACG
701 GCAAAAAACA  CGAAACGGCA  CAAAAAACCG  ACAAGCGGGA  CAAGACCAAA
751 ACCGCCGAGA  AGGAAAAATC  CGGTAAAAAA  GCCGCCATTC  AGGCAGGTTA
801 TGCCGAAAAA  GAACGCGCCT  TAAGCCTCCA  GCGCAAAATG  AAGGCGGCGG
851 GTATCGATTG  GACCATCACC  GAAATTATGA  CCGACAACGG  CAAAGTTTAC
901 CGCGTCAAAT  CAAGCAACTA  TAAAAACGCA  AGGGATGCCG  AACGCGATTT
951 GAACAAATTG  CGCGTACACG  GTATCGCCGG  TCAGGTAACG  AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1   MSENKQNEVL  SGYEQLKRRN  RRLVTASCL  VAASCILLAA  ALSSGPAEQT
51  AGETSGVENK  AAGAAQTPAL  KSAADKPQDL  AGEDKPSAAD  SEISEPENVG
101 APLVLINDRL  EDSNIKGLEA  SEKLQQAETA  RTAPKQAKQR  AAEKVPATAD
151 STDTVAVEKP  KRTAETKPKQ  AERTAKAKPK  AKETKTAEKV  ADKPKTAAEK
201 TKPDTAKSDS  AVKEAKKADK  AESKKTAEKD  RSDGKKHETA  QKTDKADTK
251 TAEKEKSGKK  AAIQAGYAEK  ERALSQRKM  KAAGIDSTIT  EIMTDNGKVV
301 RVKSSNYKNA  RDAERDLNKL  RVHGIAGQVT  NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
m746      MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
              10      20      30      40      50      60

```


1216

	70	80	90	100	110	120
a746.pep	AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA					
m746	AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA					
	70	80	90	100	110	120
a746.pep	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPQKAERTAKAKPK					
m746	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPQKAERTAKAKPK					
	130	140	150	160	170	180
a746.pep	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
a746.pep	QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
m746	QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
a746.pep	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
	310	320	330			

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

m747.seq

```

1 CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51 GATGACGACC CAGATGGGTG CTCCCGCGA TGTCAGCAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGGACG GTGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

m747.pep

```

1 LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51 VGLEFDPYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

a747.seq

```

1 CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51 GATGACGACC CAGATGTGTG CTCCCGCGA TGTCAGCAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAAACC
201 CCGTGAGATT GTTTTGGACG GCGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

a747.pep

```

1 LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51 VGLEFDPYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

	10	20	30	40	50	60
a747.pep	LTPWADAYADLRGKTKVMTTQMCASRDVSKSAGWSVGIGLVGKQLTDSVGLFDPYYR					
m747	LTPWADAYADLRGKTKVMTTQMGASRDVSKSAGWSVGIGLVGKQLTDSVGLFDPYYR					
	10	20	30	40	50	60
	70	80	90	100		
a747.pep	HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX					
m747	HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX					
	70	80	90	100		

a747/m80195

gi150271 (M80195) outer membrane protein [Neisseria meningitidis] Length = 272
Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAGWSVGIGLVGKQLTDSVGLFDPYYR 60
+ PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+
Sbjct: 174 INFWSEVKFDLNSRYKLNTGVNLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
+T + E + GD ++ EYG RV F
Sbjct: 234 QRTYKESGEFSVTTKSGDVSILTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

1	ATGAGTCAAA	ACCAACCCGC	ACAACCGACC	AAACGCAATC	TGTTCAAAAC
51	CGCCCTTGCC	GTCGGCGCAA	TCGGCGCAAT	CGGAGGTAT	TTCGGCGGCA
101	AAAACACGGG	CGAAACCGCC	GAACGCACCG	CCGAAAGCCA	ACACTCGCCC
151	CAAGCCTATC	CCTGCTACGG	CGAACATCAG	GCAGGTATCG	TTACGCCCGC
201	GCAGCGGTTT	TCCATTATGT	GCGCCTTCGA	CGTAACCGCG	CAAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTC	CGCACACTGA	CCGCCCGCAT	CGAGTTTCTC
301	ACCCAAGGCG	GAGAATACCA	AGACGGCGAC	GACAAATCC	CGTCAGCCCG
351	CAGCGGCATT	TTGGGTAAG	CCTTCAACCC	CGACGGATTG	ACCGTTACCG
401	TGGGGTGGG	CAGCAGCCTG	TTTGACGGCC	GGTTCGGACT	CAAAGACAAA
451	AAAACGGTTC	ATTGTCAGGA	AATGCGCGAC	TTCCCAACG	ATAAGCTGCA
501	AAAAGCTGG	TGCGACGGCG	ATTTGAGCCT	GCAATCTGC	GCCTTCACCC
551	CCGAAACCTG	CCAAACCGCC	CTGCGCGACA	TCATCAACA	CACCGCCCAA
601	ACCGCGGTCA	TCCGCTGGAG	TATCGACGGG	TGGCAGCCTA	AATCCGAACC
651	CGGCGCGATG	CGGCGCGCA	ACCTGTTGGG	CTTCCGAGAC	GGCAGGGGCA
701	ACCCAAGGT	TTCCGATCCC	AAAACCGCCG	ACGAGGTTT	ATGGACGGGC
751	GTGGCCGCCA	ACAGCCTCGA	CGAACCGGAG	TGGGCGAAAA	ACGGCAGCTA
801	TCAGGCGATG	CGCCTTATCC	GCCGCTTGT	CGAGTTTGG	GACAGGACGC
851	CGCTTCAAGA	GCAAACCGAC	ATTTTCGGGC	GGCGAAAATA	CAGCGGGGCG
901	CCGATGGACG	GCAAAAAAGA	AGCCGACCAA	CCGGATTTCG	CCAAAGACCC
951	CGAGGGTGAT	ATCAGGCCCA	AAGACAGCCA	TATGCGCCTG	GCGAATCCGC
1001	GCGATCCCGA	ATTCTCTCAA	AAACACTGCC	TCTTCCGCGC	CGCCTACAGC
1051	TATTCTCGCG	GACCCGCTC	AAGCGGACAG	CTTGATGTCG	GGCTGGTGTT
1101	CGTCTGCTAT	CAGGCAAATC	TTGCCGACGG	TTTCATCTTC	GTGCAAAACC
1151	TCCTCAACGG	CGAACCCTG	GAAGAATACA	TCAGCCCTT	CGGCGGCGGC
1201	TATTCTTCG	TCTTCCCGG	CGTGGGAAA	GGCGATTCT	TGGGACAAGG
1251	GCTGCCGGGC	GTATAA			

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

1	MSQNQPAQPT	KRNLFKTALA	VGAIGAIGGY	FGGKKQGETA	ERTAESQHSP
51	QAYPCYGEHQ	AGIVTPRQAF	SIMCAFDVTA	QSAKOLENLF	RTLTAIEFL
101	TQGGYQDGD	DKLPSAGSGI	LKAFNPDGL	TVTGVGSSSL	FDGRFGLDK
151	KTVHLQEMRD	FPNDKLQKSW	CDGDLSLQIC	AFTPETCQTA	LRDIIKHTAQ
201	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP	KTADEVLTWG
251	VAANSLDEPE	WAKNGSYQAV	RLIRRFVEFW	DRTPLQEQTD	IFGRRKYSGA
301	PMDGKKEAD	PDFAKDPEGD	ITPKDSHMLR	ANPRDPEFLK	KHCLFRRAYS
351	YSRGPASSGO	LDVGLVFVCY	QANLADGFIF	VQNLLNGEPL	EEYISPFGGG

1218

401 YFFVLPGVGK GGFLGQGLPG V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq

```

1 ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51 CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATTG ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAACTGG TCGACGGCGG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAACA CACCGTCCAA
601 ACCGCGGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCAGGGAC GGCACGGGCA
701 ACCCCAAAGT TTCCGATCCC AAAACTGCCG ACGAGGTTT GTGGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCAGGAG TGGCGCAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCAATA CAGCGGTGCG
901 CCGATGGAGC GCAAAAAAGA AGCCGACCAA CCGATTGTTG CCAAAGACCC
951 CGAGGGTGAT ATCAGCCCCA AAGACAGCCA TATACGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACCGCC TCTTCGCGG CGCCTACAGC
1051 TATTCCGCGG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAACC TTGCGGACGG ATTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTCTTCG TCTTGCCCGG CGTGAAAAA GCGGCTTTT TGGGGCAAGG
1251 GCTGCTGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep

```

1 MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPQOAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGEYQDGD DLPPAGSGI LGKAFNPDL TTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNDKLQSW CDGDLQLQIC AETPETQQA LRDIIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFARDPEGD ITPKDSHRL ANPRDPEFLK KHLRFRRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VONLLNGEPL EEYISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSPQAYPCYGEHQ					
g748	MSQNQPAQPTKRNLFKTALAVGAIGAIGGYFGGKKQGETAERTAESQHSPQAYPCYGEHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m748.pep	AGIVTPQOAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGEYQDGDKLPPAGSGI					
g748	AGIVTPROAFSIMCAFDVTAQSAKQLENLFRILTARIEFLTQGEYQDGDKLPSAGSGI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m748.pep	LGKAFNPDLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
g748	LGKAFNPDLTVTVGVGSSSLFDGRFGLKDKRTVHLQEMRDFPNDKLQKSWCDGDLQLQIC					
	130	140	150	160	170	180
	190	200	210	220	230	240
m748.pep	AETPETQQAALRDIIKHTVQTAVIRWSIDGWQPKSEPGAMAAARNLLGFRDGTGNPKVSDP					

[illegible]

```

a748.seq
1      ATGAGCAAAA   ACCAACCCGC   ACAACCGACC   AGGCGCACTC   TTTTAAAAAC
51     CGCGATCGCA   CCTGGAGCAG   TCGGCAGCAT   CGGAGGTTAT   CTCCGCGGCC
101    AAAAACCGGG   CGAAACCGCC   GACGCACCCG   CCGAAAGCCA   ACATCGCCCA
151    CAAGCTCATC   CCTGCTACGG   CGAACATACG   GCAGGACATCG   TTACGCGCCA
201    GCAGGCGTTT   TCGATTATGT   CGCCTTCGAG   CGTAACCGCG   CAAAGTGGCA
251    AGCAGCTGGA   ARAACTGTTC   CGCACGCTGA   CGCGCCGATC   CGAGTTCTTC
301    ACCCAAGCGG   GCGCAATACA   AGACGGCGAC   GACAAACTTC   CGCCAGCCGG
351    CAGCGCATT   TTGGGCAAAG   CCTTCAACCC   GCACGGGTG   ACCGTTACCG
401    TGGGGGTGGG   CAGCAGCCTG   TTTTGCAGCC   GGTTCGGATC   CAAAGACAAA
451    AAACCGATT   ATTTGCAAG   AATGCGCGAC   TTCTCCAACG   ATAAGCTGCA
501    AAAACGCTG   TCGCAGCGCG   ATTTGAGCCT   GCAAACTGTG   GCCTTCAACC
551    CCGAAACCTG   CCAAGCGGCC   CTGCGCGACA   TCATCAACA   CACGTCGCAA
601    ACCGCGGTTA   TCGCGTGGAG   TATCGACGGG   TGGCAGCCTA   AATCCGAACC
651    CGCGCGGAT   CGGCGCGCA   CTCGTGTTGG   TCTCCGCGAC   GGCACGGGCA
701    ACCCCAAAGT   TTCCGACCCC   AAAACTCGCG   ACCAGGTTT   GTGACGGGG
751    GTGGCGCGCA   ACAGCCTCGA   CGAACCCGAG   TGGGCGAAAA   ACGGCAGTCA
801    TCAGGCAGTC   CGCCTTATCC   CGCACTTTGT   TGAGTTTTTG   GACAGGACGC
851    CGCTTCAAGA   GCAAACCGAC   ATTTTCGGGC   GCGCGAAATA   CAGCGCGCG
901    CCGATGGACG   GCCAAAAAG   AGCGCAGCAA   CCGGATTTTG   CCAAAGACCC
951    CGAGGGGAAT   ACACAGGCCA   AAGACGCCA   TATACGCTTG   CGGAATCCGC
1001   GCGATCCCGA   GTTCCTTAAA   AAACACCGCC   TCTTCGCGCG   CGCCTACAGC
1051   TATTCGCGCG   GACTCGCCTC   AAGCGGACAG   CTTGATGTGC   GGCTGGTGTT
1101   CGETCTGCTAT   CAGGCCAAAC   TTGCCGACGG   ATTCACTTC   GTGCAAAACC
1151   TCCTCAACGG   CGAACCCTG   GAAGAATACA   TCAGCCCTT   CGGCGCGGCG
1201   TATTTCCTCG   TCTTGGCCGG   CGTGGAAAAA   GGC GGCTTTT   TGGGGCAAGG
1251   GCTGTGGGC   GTATAA

```

```

a748..pep
1      MSKNQPAQPT  RRTLFKTAIA  AGAVGAIGGY  LGGKKRGETA  ERTAESQHSP
51     QAYPCYGEHT  AGIVTPQQA  SIMCAFDVTA  QSAQLENLF  RLTLTARIEF
101    TQGGEYQDGD  DKLPPAGSGI  LGKAFNPDL  TVTVGVGSSL  DFGRGLKDL
151    KPIHLQEMRD  FSNDKLQSW  CDGDLSLQIC  AFTPETCQA  LRDIKHTVQ
201    TAVIRWSIDG  WQKSEPGA  AARNLLGFER  GTGNPKYSVP  KTADEVLTWG
251    VAANSLEDE  WAKNGSYQAV  RLRIHFVEVF  DRTPLEQET  IFGRKYSGA
301    PMDGKKEAGQ  PDFAKDPEGN  TTPKDSHIRL  ANPRDPEFLK  KHRLFRAYS
351    YSRGLASSGQ  LDGVLVFVCY  QANLADGFIF  VQNLNNGEPL  EEYISPFGGG
401    YFVLPGVEK  GVLGOGLLG  V*

```

Computer analysis of this amino acid sequence gave the following results:

1220

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

a748.pep	MSKNQPAQPTRRRLFKTAIAAGAVGAIGGYLGGKKRGETAERTAESQHSFPQAYPCYGEHQ
m748	MSKKQPAQPTRRRLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSFPQAYPCYGEHQ
a748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRITLTARIEFLTQGGYQDGGDKLPPAGSGI
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRITLTARIEFLTQGGYQDGGDKLPPAGSGI
a748.pep	LGKAFNPDGLTVTVGVGSSLFDRGFLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLQIC
m748	LGKAFNPDGLTVTVGVGSSLFDRGFLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLQIC
a748.pep	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
m748	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
a748.pep	KTAEVLWTVGAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA
m748	KTAEVLWTVGAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSGA
a748.pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
m748	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
a748.pep	LDVGLVFVCYQANLADGFIQVQNLNGEPLLEYISPFGGGYFFVLPVGEKGGFLGQGLLG
m748	LDVGLVFVCYQANLADGFIQVQNLNGEPLLEYISPFGGGYFFVLPVGEKGGFLGQGLLG
a748.pep	VX
m748	VX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

1	ATGAGAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTGGGTTT
51	GACCGCGTGC CAGCCGCCGG AGCGGAGAA AGCCGCGCCG GCCGCGTCCG
101	GTGAGACCCA ATCCGCCAAC GAAGCGGTT CGGTCCGTAT CGCCGTCAAC
151	GACAATGCCT GCGAACCGAT GAATCTGACC GTGCCGAGCG GACAGGTTGT
201	GTTCAATATT AAAAAACA CA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251	AGGGCGTGAT GGTGGTGGAC GAACGCGAAA ATATCGCCCC GGGGCTTTCC
301	GACAAAATGA CCGTAACcct GCTGCCGGGC GAATACGAAA TGACCTGCGG
351	CCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAGCCGAC AGCGGCTTTA
401	AAGACACCGC CAACGAAGCG GATTGGAAA AACTGCCCCA ACCGCTCGCC
451	GACTATAAAG CCTACGTTCA AGCGGAGGTT AAAGAGCTGG CGCGGAAAAC
501	CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551	CCCTGTTTGC CGCCACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601	GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATCGGTGTG AAGACGACTT
651	CAAAGACGGT GCGAAAGATG CCGGGTTTAC CGGCTTCCAC CGTATCGAAC
701	ACGCCCTTTG GGTGGAAAAA GACGTATCCG GCGTGAAGGA AACCGCGGCC
751	AAACTGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC

1221

```

801 GttccctCCG GGC AAAAGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 CGGCGGGCAG TAAAATCAGC GCGGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGCGACGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATTGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCATA
1051 GACGGTTTGG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

g749.pep

```

1 MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIADV
51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMMVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLQPLA
151 DYKAYVQGEV KELAARTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSQVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEAAGSKIS GEEDRYSHTD
301 LSDFOANADG SKKIVDLFRP LIEAKNKALL EKDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGLGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

```

1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCACTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCAGT GGAACGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGGCG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCBAAGCAGG CGCATTGAA AAGCGGAAT
551 CCTGTGTTGC CGACACCGCG GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGAT CCGATGTGCA AGCCCTGCAA AAAGAAATCG ACAGATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTGG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCTT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

m749.pep

```

1 MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIADV
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMMVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVARTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSQVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEEVAGSKIS GEEDRYSHTD
301 LSDFOANVDG SKKIVDLFRP LIEAKNKALL EKDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGLGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

          10      20      30      40      50      60
m749.pep  MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIADV NDNACEPMELT
          |||
g749      MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIADV NDNACEPMNLT
          10      20      30      40      50      60

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	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNSGRKLWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVTD SGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAE L FSELD PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATR VHYERIEPIAE L FSELD PVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFOANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDFETYDKLG					
g749	LSDFOANADGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDFETYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

1	ATGAGAAAAT	TCAATTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGCGGTT	CGGTCAGTAT	CGCCGTCAAC
151	GACAAATGCT	GCGAACCAGT	GGAAGTACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCTGA
251	AAGCGGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCACCCT	GTTGCCGGGC	GAATACGAAA	TGACTTGGCG
351	TCITTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTC	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGCGGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCGC	GTCCGAATG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTCGATTT
951	GTTCGCTCCG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTG	GAAAAAACCG
1001	ATACCAACTT	CAACACAGTC	AACGAAATTC	TGGCGAAATA	CCGACTAAA
1051	GACGGTTTTC	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAATAA			

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

1	MRKENLTALS	VMLALGLTAC	QPPEAEKRAAP	AASGEAQTAN	EGGSVSIAVN
51	DNACEPMELT	VPSGQVVFNI	KNNSGRKLWE	EILKGMVVVD	ERENIAPGLS
101	DKMTVTLLPG	EYEMTCGLLT	NPRGKLVVTD	SGFKDTANE	DLERLSQPLA
151	DYKAYVQGEV	KELVAKTKTF	TEAVKAGDIE	KAKSLFADTR	VHYERIEPIA
201	ELFSELDPVI	DAREDDFKDG	AKDAGFTGFH	RIEYALWVEK	DVSGVKEIAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	IEEVAGSKIS	GEEDRYSHTD

1223

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

a749.pep	10	20	30	40	50	60
	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT				
m749	10	20	30	40	50	60
	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT				
a749.pep	70	80	90	100	110	120
	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
m749	70	80	90	100	110	120
	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
a749.pep	130	140	150	160	170	180
	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
m749	130	140	150	160	170	180
	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
a749.pep	190	200	210	220	230	240
	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGA	KDAGFTGFHRIEYALWVEK				
m749	190	200	210	220	230	240
	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGA	KDAGFTGFHRIEYALWVEK				
a749.pep	250	260	270	280	290	300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGA	SELIEEVAGSKISGEEDRYSHTD				
m749	250	260	270	280	290	300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGA	SELIEEVAGSKISGEEDRYSHTD				
a749.pep	310	320	330	340	350	360
	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTK	DGFETYDKLG				
m749	310	320	330	340	350	360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTK	DGFETYDKLG				
a749.pep	370	380	389			
	EADRKALQASINALAEDLAQLRGILGLKX					
m749	370	380				
	EADRKALQASINALAEDLAQLRGILGLKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

```

1  GTGAAACCGC GTTTTATTG GGCAGcctGC GCCGTCCTGC CGGCCGCCCTG
51  TTCGCCCGAA CCTGCCGCCG AAAAACTGT ATccgCCGCA TCCCAAGCCG
101 CATCCACACC TGTCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC
151 GTTGTGCCGA AGAATCCGA ACgcgtcgcc gtgtAcgaCt ggGCGCGGt
201 ggaTACGCTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG
251 TGCGCGTGGA CTATTGCGAG CCTGCATTG ACAAGGCGGC AACGGTGGGG
301 ACGCTGTTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT
351 TGTCATTACC GCGGGGCCGG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
451 GCGGAGAAGC AGATGGAGAC CTTGTGCGGG ATTTTCGGTA AGGAAGCGCG
501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCGCC CAAAGCGCG
551 AAGCCGCCAA AGGCAAGGA CGCGGGCTGG TGCTGTGGGT TACAGGCAAC
601 AAGGTGTCGG CTTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
651 CGACATCGGC CTGCCGCCGG TGGACGAATC TTTACGCAAC GAAGGGCAGC
701 GGCAGCCCGT TTCCTTCGAA TACATCAAAG AGAAAACCC CGGCTGGATT
751 TTCATCATCG ACCGCACCGC CGCCATCGGG CAGGAAGGGC CGGCTGCCGT

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801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGGAAGCGCA
 851 AGCAAATCAT CGTCATGCCT GCCGCGAACT ACATTGTGCG GGGCGGCGCG
 901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGCGGCGCT TTGAAAAGGC
 951 AGAACCCGTT GCGGCGCAGT AG

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

g750.pep
 1 VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
 51 VVPKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLQ PAFDKAATVG
 101 TLFEPDCESL HRHNPQFVIT GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS
 151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKRG RGLVLSVTGN
 201 KVSAGTQSR LASWIHGDIG LPPVDESRLN EGHGQPVSEF YIKEKNPGWI
 251 FIIDRTAAIG QEGPAAEVL DNALVCGTNA WKRRQIIVMP AANYIVAGGA
 301 RQLIOAAEQL KAAFEKAEPV AAQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

m750.seq
 1 GTGAAACCGC GTTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
 51 TTCGCCCGAA CCTGCCGCGG AAAAACTGT ATCCGCCGCA TCCGCATCTG
 101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
 151 AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTGG ATACGCTGAC
 201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
 251 ATTTGCAGCC TGCATTGAC AAGGCGGCAA CGGTGGGGAC GCTGTTCGAG
 301 CCCGATTACG AAGCCCTGCA CCGTACAAT CCTCAGCTTG TCATTACCGG
 351 CGGGCCGGGC GCGGAAGCGT ATGAACAGT AGCGAAAAAC GCGACCACCA
 401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
 451 ATGGAGACCT TGGCGCGGAT TTTCCGCAAG GAAGCGCGCG CGGCGGAATT
 501 GAAGGCGCAG ATTGACGCGC TGTTCGCCCA AACGCGCGAA CCCGCCAAAG
 551 GCAAAAGGACG CGGGCTGGTG CTGTCCGTTA CGGGCAACAA GGTGTCCGCC
 601 TTCGGCACGC AGTCGCGGTT GCGAAGTTGG ATACACGGCG ACATCGGCCT
 651 ACCGCTGTGA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
 701 CCTTCGAATA CATCAAAGAG AAAAACCCTG ATTGGATTTT CATCATCGAC
 751 CGTACCGCCC CCATCGGGCA GGAAGGGCCG GCGGCTGTCG AAGTATTGGA
 801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
 851 TCATGCCTGC CGCGAACTAC ATTGTCCGGG GCGGCGCGCG GCAGTTGATT
 901 CAGGCGGCGG AGCAGTTGAA GCGGCGGTTT AAAAAGGCAG AACCCGTTGC
 951 GCGGGGAAA AAGTAG

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

m750.pep
 1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
 51 NPERVAVYDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
 101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
 151 METLARIIFGK EARAELKAQ IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
 201 FGTQSRLASW IHGDI GLPPV DESLRNEGHE QPVSEFYIKE KNPDWIFIID
 251 RTAAICQEGP AAVEVL DNAL VRGTNAWKRR QIIVMPAANY IVAGGARQLI
 301 QAAEQLKAAF KKAEPVAAGK K*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

	10	20	30	40	50
m750.pep	VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASA----ATLTVP TARGDAVVPKNPERVA				
g750	VKPRFYWAACAVLPAACSPEPAAEKTVSAAASQAASTPVATLTVP TARGDAVVPKNPERVA				
	10	20	30	40	50
	60	70	80	90	100
m750.pep	VYDWAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGT LFE PDYEALHRYNPQLVIT				
g750	VYDWAALDTLTEPGNVNVGATTAPVRVDYLQPAFDKAATVGT LFE PDCESLHRHNPQFVIT				
	70	80	90	100	110
	120	130	140	150	160
m750.pep	GGPGAEEYEQ LAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFA				

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g750      GGGPAAEAYEQLAKNATTIDLTVDNGNIRTSGEKOMETLSRIFGKEARVAELNAQIDALFA
          130      140      150      160      170      180

m750.pep  180      190      200      210      220      230
          QTREAAKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF
          |||||
g750      QKREAAKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF
          190      200      210      220      230      240

m750.pep  240      250      260      270      280      290
          YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNADLVRGTNAWKRKQIIVMPAANYIVAGGA
          |||||
g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNADLVRGTNAWKRKQIIVMPAANYIVAGGA
          250      260      270      280      290      300

m750.pep  300      310      320
          RQLIQAAEQLKAAFKKAEPVAAAGKX
          |||||
g750      RQLIQAAEQLKAAFEKAEPVAAQX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1  GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
51  TTCGCCCGAA CCTGCCGCGG AAAAACTGT ATCCGCCGCA TCCGCATCTG
101 CCGCCACACT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151 AATCCCGAAC GCGTCGCCGT GTACGACTGG CCGCGGTTGG ATACGCTGAC
201 CGAATTGGGT GTGAATGTGG GCGCAACCAC CCGCGCGGTG CGCGTGGATT
251 ATTTGCAGCC TGCATTTGAC AAGGCGGCAA CGGTGGGGAC GCTGTTCGAG
301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT GCGAAAAAC GCGACCACCA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCCGGCAAG GAAGCGCGCG CGGCGGAATT
501 GAAGCGCGAG ATTGACGCGC TGTTCCGCCA AACGCGCGAA GCCGCCAAG
551 GCAAAGGACG CGGGCTGGTG CTGTCCGTTA CGGGCAACAA GGTGTCCGCC
601 TTCGGCAGCG AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCTG ATTGGATTTT CATCATCGAC
751 CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGGCTGTCG AAGTATTGGA
801 TAACGCGCTG GTACGCGGCA CGAAGCCTTG GAAGCGCAAG CAAATCATCG
851 TCATGCCTGC CGCGAACTAC ATTGTGCGCG GCGGCTCGCG GCAGTTGATT
901 CAGGCGCGCG AGCAGTTGAA GGAGGCGTTT GAAAGGCAG AACCCGTTGC
951 GCGGGGAAA GAGTAG

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This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

```

a750.pep
1  VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51  NPERVAVYDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAELKAQ IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
201 FGTQSRLASW IHGDIGLPPV DESLRNEGHG QPVSFYEIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVLNADL VRGTNAWKRK QIIVMPAANY IVAGGSRLI
301 QAAEQLKEAF EKAEPVAAAGK E*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

a750/m750 98.8% identity in 321 aa overlap

```

          10      20      30      40      50      60
a750.pep  VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASAATLTVPPTARGDAVVPKNPERVAVYDW
          |||||
m750      VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASAATLTVPPTARGDAVVPKNPERVAVYDW
          10      20      30      40      50      60

          70      80      90      100     110     120
a750.pep  AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG
          |||||
m750      AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG

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	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNIRTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNIRTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEIKE					
m750	AAKGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRRQIIVMPAANYIVAGGSRQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRRQIIVMPAANYIVAGGARQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQLKEAFEKAEPVAAGKEX					
m750	QAAEQLKAAFKKAEPVAAGKXX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```

1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CGGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTGGTTC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTATTGCA
301 GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTTCGTGAA CTGATGTATG
401 TCGGTTACGA CCAATTAAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTCAG AAAAACTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
501 GGGTAACGGC TGSTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGCTA TTCGCATAGC AGTTATTTTG
851 CGGAGGTGCC AAAAGCAGGT ACAAAGAAT TTGATGACTA TGTAAAAATA
901 TGGGGTGAAG TTGAATATGA CGTCAAGGT AAGCCAATTA ACAAACTTAA
951 ACCCATACTG GTAGAACCBA ACAAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

```

1  MAWSMFATTQ ADRAVRSATA PKEMWPHKKI IDEKTGKVSF DTRQIWSLND
51  LSKKEIASIQ DTNGKVITVS NPGIFNNRED SLSNAARQNR NSTNGSGVIA
101 VMNPPITGKYK SDSNNKIDF LNLGSSLVSE LMYVGYDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVDKMGNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQRNGYT YTGADGKTYN SGSYSIVHDK
251 DFGVGNKNIFF LLGTNDTTQG TCKGLCYSHS SYFAEVPKAG TKRFDDYVVKI
301 NGEVEYDAQG KPINKSKPIL VEPNKTONE KYEKRAF*

```

a751.seq not found yet

a751.pep not found yet

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

m752.seq..

```

1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTGA TGA AAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTGC ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGCGG TGGAAAATCC GTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTGT ATGCGGAAAC TGACGATTA
1051 GATTTAACCT ATTTTCTCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATGCGA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

m752.pep

```

1  MKISRPPEFT LLQEQYMOHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHEDTRM KWRVAKESRK KIQKPIDFFP
101 EHQWFPCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEATTSQALE GAATTRKVK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTIFYIYQC DIIKRAVDL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVFFK
451 SGNALFYVAP QDLLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

m752-1.seq

```

1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTGA TGA AAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTGC ACCGCATTGC

```


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```

651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGCG GGACAGCGCG GGCCTTGTTT TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTGAAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTGG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAATA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQOEYMOHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQRPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSQALE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLYFYIYQC DIKRAVADL EHYISDRQKH QOEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLEKLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGCT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTAAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTCG GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TCGCCAGTT ATTTCTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAI WLWYQSPTHR QVPIVEEMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESD RHLRDNSDWN
101 CGDNWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTGTCACAGT ATTTCCGGA AGGCTTTTGG GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTGA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTAAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCTG CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTTGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MMKSILTVSG NMRKPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRCND PLFNEWIDGL EMKNPRIITE RDLIGINARQ
151 VFOQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSLSE SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDT SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKRTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTAATCCGAT ATTAACCAAC
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAAGTAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTACC
251 GCCTTGAAAG TGATTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```


1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

```
m755.pep..
  1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
 51 REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLESIDL AQFIADGVYQ
101 AKQAFLLQVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

```
m756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGACG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

```
m756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAEQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVPYGAE LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

```
a756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGACG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

```
a756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAEQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVPYGAE LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m756.pep	TLVRFRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADFVQIGRRSYSREDISEANRRAERVYPYGAEIVSDGNFTAV					
a756	RLAESQERITSAILKGARGADFVQIGRRSYSREDISEANRRAERVYPYGAEIVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAATAAAC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAGAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGCGG ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSDGLTI LTVUTDKADK
101 ITAVRVVWNT DAMPQKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGGTGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTGGCGG AAGTCGCTGC TTTCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCGCG
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTGCGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAAGAA GGATTGAGCC
501 ATGA

```


1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1 MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151 LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1 ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51 TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAACCT GGTGGAATTT CCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGAGAAA GGATTGAGCC
501 ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1 MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151 LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

	10	20	30	40	50	60
m758.pep	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPLAEVAAAFHQ					
a758	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPLAEVAAAFHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m758.pep	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAAGSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAAGSVGIGGSQT					
	70	80	90	100	110	120
	130	140	150	160		
m758.pep	GVYPFASPGGWQIIGRTELPFRADLNPPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELPFRADLNPPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1 ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51 TCTTTTGGCC GTTTCCTG CTTACTCATC CATTGTCCGC AACGATGTCG
101 ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTCACCGTA
151 GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201 GGTTCCTCAAC GGCATCCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251 CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301 AACGTCGGCT ACGGTTCCAT ACAATTCCGC AACGACACCC AAAATCCAGA
351 AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401 ACGACTACCA CCTCCCCGC CTCACAAAC TGGTTACCGA AATCTCACCT
```


451 ACCGCACTCA GCAGCGTACC CTGCTTGGA AACGGCCAGC CAAAGGCCAA
501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTGTACGA CTCGGCTCAG
551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGGTACACG AACCGCCCCG
601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA
651 AAACCACGGC TTACTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTTGACAAG
751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGGCTT
801 CGATAATTTC TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC
901 GAACTCATAT GGCGCGACAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
951 CAACGAACGC ATCACCCTGC CCATTGCAAA CCCTTCGCTT GCCCCACAAA
1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
1101 AGGCGCAGGC GCATTGCAGT TCGACAGCAA CTTACCCGTC GTCGGTAAAA
1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC
1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
1251 AGGCACGCTT ATCGCCAAAG GACAAGGCAT CAACCAGGGC GACATCAGCA
1301 TCGGGGAAGG CACTGTCGTA CTCGCCAAA AAGCTGCTTC AGACGGCAGC
1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA
1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC
1501 CGCCATGCGG ACGGCGGCGC GCAATTCGTC AATCACAACC CTGACCAAGC
1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCG
1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGG GGTTCAGAA
1651 TACATCAACC CGCACCAGCA CCGTCGGACC GACTACTTCA TACTCAAACC
1701 CGGCGGCAAC CCGCGCGAAT TTTTCCGTT AAATATGAAA AACTCAACAA
1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC
1801 CAAGCCGAAA ATGCCGCCC CGACCTGATT ACCTTCGGCG GATACTGGG
1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCG CGTATACGGC
1951 CGGCCCGAAT ACCGTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
2001 AGCCACCGAC AGCAGCTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG
2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC
2101 CATGCCCTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCTGCGA AACCATGCCC
2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCGC
2351 TTTTAAAGC CGAAACTAT CGTGCACTAC CTGCAACGCA AGTACGCGGC
2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGCGCG ACTGACGCTT
2551 GACGGCGCAC AAATTACCCT GAACCCCGAT TTCGCCAATA ATACACACAA
2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCGGCA
2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
2701 AAAGTGAAG GGGACAGCCG CGGCGCATTC CAAATCCAGC TCAAAAACAC
2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCACTTGT AGCCTCAATC
2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT
2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAAA AACAACAACG GATACAGCCT
2901 GTACAACCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCGTGCGG
2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
3151 CGTGCCCAA ACCTGTGTGC CGCACAAGGA TACAGTCCG ATATCTGCCG
3201 TCAGGTTGCC AAAGCCGCG ACACGAACGA CCTGACACTC TTCGAAACCG
3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC
3301 AAAGCACGGC AAGGCGGCGA TCGCAAGCC GTCGAAACAG CCGGCACGC
3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAAC GATCAGCCGG
3451 TCGGCCAACA CCGCGTTTC CGAACAGGCC GCCTACAATA CCGCCCGGCA
3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
3551 ACATCTGGCT GGAAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAAC
3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAAAC GATGAGCGCA
3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

1234

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTCCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
1 MRFTHHTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFV
51 GASNSIQDK QGKILGRVLN GIPMPDFRVS NRQTATLV HPOYVNSVKH
101 NVGYGSIQFG NDTQNPEEQ A YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTDREPFYFVR LSGSQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFONHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAV LSTYAGFDNF FNKYIVTQPE FIRSTIROYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNSRHRMP SEDAGKTLIL
351 SSREFDNKTL LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAAGL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGRLDL NGNNLAFTHI
501 RHADGGAQIV NHNPQAATL TLTGNPVLSP EHVEWVQWGN RPOGNAAVYE
551 YINPHNRRT DYFILKPGGN PREFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAYVG
651 RPEYRYNGAL NLHYRPKRTD STLLNGGMN LINGEVLEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLGDGITA
751 YDLSGIDLGF TQGKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDRSEL RLKGAHLYGS IRAGKDTAVR MEADSNWTLS QSSHTGALT
851 DGAQITLNDP FANNTNNRF NTLTVNGTLD GFGTFRFLTG IVRKQNAAPL
901 KLEGDSTRGAF QIHVKNTQGE PQTTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQO AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCQAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEELIS
1151 SANTAVSEQA AYNTGRQOAG RRIDRHLTDF QQQNIWLETG TQQTDYHSGT
1201 HRPYQQTNY AHIGIQGTIT DRLSVGTILT DERTNNRFE GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
1 AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGATGC ATGCAGGCGG TTATGCCACG
301 TCGATGCCA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
1 NNRNTRYAAL GKRVMGVEV EISGAITPKW QIHAGYSYLH SIKTAANPR
51 DDGIFLLVPK HSNLWTTYQ VTPGLTVGG VNAMEGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

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1235

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCCT ACAACGCGAT TGCCACCGAG
151 AAAAAACGGC ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGCGCTGC GCGTGTGTAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCACG CTGCCCAACC TGTTTCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTG AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGTCTC CGCGTCCCGC CGAGAAAAAC AACCGCGCGC
701 AAACCTTCTA CGCGCGGCGG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GGCGCGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGCGCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGCGCGCGA TTGGAACAAA TTTAAATGAC ACAGCCACGA CGTGTTCGCC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAGCCTT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAGCGT CGCTTTAGAT
1201 GGTTTCGCGC CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCTC TGGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAATTTTAC AAGCTAGGCC GCGCGGTTT
1451 ACGATATAGA CCGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCGG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCCTGGACT CAAACAACAA AAAAACCCGT TACGCCGCAT TGGGCAAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CCGCGCGATG ACACCGAAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTGCG GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAAGGAT ACATGCAGGC
1951 GGTATGCGCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAT
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGGTTCCGA GCGCAGCCTG
2101 ACGGCAAAAC TCGGTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51  KNGDYSSFSA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLNDD GRSSVYARGY EYSEYNIDGL PAQMOSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAED
201 VSGSLNSDGS VRCRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQQRK LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSADVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNYTFA GSKLNNTGQA DVAGLGTDIK
351 QKAFVADASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSVALLD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKHI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKTR YAALGKRVM GVEITEISGAM TPKWQIHAGY SYLHSQIKTA
601 GNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLO INADNIFNRH YYARVGSEST FNI PGSERSL
701 TANLRYSF*
```


1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSFYRMKDKNAAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
g760				NNRNRTRYAALGKRVMEGVETEISGAITPKW		
				10	20	30
	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90
	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAYRFTPCLKLQINADNIFNRHYARVGSESTFNIPGSESLTANL					
g760	AGMHAGGYATFDAMAAYRFTPCLKLQINADNIFNRHYARVGTTNTFNIPGSESLTANL					
	100	110	120	130	140	150
	709					
m760.pep	RYSFX					
g760	RYSFX					

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq

1	ATGAAAATAT	CATTTCATTT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTTTCC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGGCGTGCGC	GAAAGCCGGAC
401	AAGTGGCGCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAAACG	TCGCCATCCG	TCTCACCGGC	GAAGTCGGGC	GCGCCAATTC
651	GTTCGCGAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATT
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCCA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACCGCA	TGGGGTTTCG	CCACCGGAAC	GATTTTGTC
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATT
951	TGATCATTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTGTAA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTTC	AGCAGCGCCT
1151	TTTCGGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCGATTTC	AAATTCGTCC
1301	TCGGCGGCGG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACCTCAC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTACGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCTTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTTGAGCAT	CGATACGTTG
1501	TCTTCGCGCG	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGCGGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA

1237

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1701 ATGTGTCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCGGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACCTACGGT TACAACCTCA GAAATAAGA AGTGACTACG
1951 CTTCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 GTTAAACGTT ACCTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGT AATCCGCGC GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m761.pep
1 MKISFHLALL PTLIIASFPV AAADTDNCE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGCVINMVSX YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDREGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLT
351 NGDYITGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTONR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFENSEKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPAPYG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMOA KVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a761.seq
1 ATGAAATAT CATTTCAATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGCGCAA AGCATTTTCC TCGCGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GCGCGCGGTG TCATCAACAT
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTCGTG GGCAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTCACCAGC GAAAGTGGGC GCGCCAATTC
651 TTCCGCGAGC GGCATAGACA GCAAAATGT CATGGTTTCG CCCAGCATT
701 CCGTCAAACT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCGGACTG CCTTACCGCA TGGGTTTCGC CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC GGCACGGCGG CGCAGGATT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAT
1001 ACGCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGGAACACC GCAACCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTCCGCGCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCGATTG AAATTCGTCC
1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCGCGCG TGTTCACGCG CAGCCCGGAG TACACCGGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAAT CGAACGCTTC AATATCCGCT ACCGCCCGCA TCCAAAAAAC
1651 AACCTTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGA
1701 ATGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTAAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1  MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51  KGYINYDEAA VTRNGQLIKE TPQTIPTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVMS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDREGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTD NKTLSNLT
351 NGDYYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KEVLGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NRYRYPDPKN
551 NPYYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMA KVEDKENPD
601 RVGIHLNNTS NVTGNLFERY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAANLENQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

m761.pep	10	20	30	40	50	60
	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
m761.pep	70	80	90	100	110	120
	VTRNGQLIKETPQTIPTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIPTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
m761.pep	130	140	150	160	170	180
	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVSKYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVSKYANFKQSRNI					
	130	140	150	160	170	180
m761.pep	190	200	210	220	230	240
	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
	190	200	210	220	230	240
m761.pep	250	260	270	280	290	300
	LKWTGQYTYDNVERTPDRSPTKSVYDRFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPTKSVYDRFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
	250	260	270	280	290	300
m761.pep	310	320	330	340	350	360
	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTNDKTLSSNLTNGDYYTIGRFE					
a761	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTNDKTLSSNLTNGDYYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

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m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRQLPILTQNRHKADSYGIFV
a761      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRQLPILTQNRHKADSYGIFV
          370      380      390      400      410      420

          430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
a761      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
          430      440      450      460      470      480

          490      500      510      520      530      540
m761.pep  YNKGFAFYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTSLAYQIERF
a761      YNKGFAFYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTSLAYQIERF
          490      500      510      520      530      540

          550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761      NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
          550      560      570      580      590      600

          610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYNSRNKEVTTLPGFARVDAM
a761      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
          610      620      630      640      650      660

          670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761      LGWNHKNVNVTFAAANLFNQKYWRSDSMPGNPRGYTARVNYRFX
          670      680      690      700

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g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTITTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTCCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVOLCTIL FHSQKIYFIT
51  LFLLEIFNEV TKSIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNE ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTITTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
 351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSEF DLLVQLCTIL FHSQKIYFIT
 51 LFLLFIFNFV TKSIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSEFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIINFFSLLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
 201 GCGCGAGCAA CATTCCGCTG ATTTTCAAGC GTCCTATTAC CAGCGTGATG
 251 CAGTGGCGGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
 401 CCAAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAGC CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTGCG CGCTTTATAC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
 1201 TTGGAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
 1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAGAGAG CGGGTTAGGG TTGGAACCG TATTTCGGGA
 1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGCTA TTCCTGTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCACCCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCAAGT GAACGACTAC ACCGCGCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAGACA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCAGCTGG AAGTAATACG GGCGCGGCG AGAGTCGCCC
1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAACCG TATTTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a763      MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60

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	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHVSANASYQRQPPSISSTRETQ					
a763	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHVSANASYQRQPPSISSTRETQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKMSVGVQLNPLPLYTGGEISGKIHEAEA					
a763	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKMSVGVQLNPLPLYTGGEISGKIHEAEA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAEQERVLESSRLKLKSTETGQYQYGR					
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAEQERVLESSRLKLKSTETGQYQYGR					
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVAAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763	NRLEVIRARQEVAAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

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g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```

m764.seq
1  ATGTTTCTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTTCGGCAA AACGGTGTCT GCGGCGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCGGTTTG CCGGCGGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACCGGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CCGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CCGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGCATGTA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGTGCTT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```

m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEEOAFL PAHLELTDTP
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVQKQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLIALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVGAE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSF ADGTVQELAT YTVGVVQAA
351 QRMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEIK
451 TGKRRVLDYL LSPLQTKLDE SFRER*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```

a764.seq (partial)
1  ATGTTTCTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTTCGGCAA AACGGTGTCT GCGGCGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA

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701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACGCGGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CCGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

a764.pep (partial)

```

1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAF LPAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHV KQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSA LRGHQ AELQSAKAE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVINT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMV VAPDD DKMDVEVLVL NKDIGFEVQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

	10	20	30	40	50	60
m764.pep	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
a764	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
	10	20	30	40	50	60
m764.pep	FIMAFALLALLWSWFGKIDIVAAASGKT VSGGRSKTIQPLETAVVVKAVHV RDGQHV KQE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKT VSGGRSKTIQPLETAVVVKAVHV RDGQHV KQE					
	70	80	90	100	110	120
m764.pep	FIMAFALLALLWSWFGKIDIVAAASGKT VSGGRSKTIQPLETAVVVKAVHV RDGQHV KQE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKT VSGGRSKTIQPLETAVVVKAVHV RDGQHV KQE					
	70	80	90	100	110	120
m764.pep	TLAELEAVGTDSDVVQSEQA LQAAQLSKLRYEAVLAALESRTVPHIDMAQARS LGLSDAD					
a764	TLAELEAVGTDSDVVQSEQA LQAAQLSKLRYEAVLAALESRTVPHIDMAQARS LGLSDAD					
	130	140	150	160	170	180
m764.pep	TLAELEAVGTDSDVVQSEQA LQAAQLSKLRYEAVLAALESRTVPHIDMAQARS LGLSDAD					
a764	TLAELEAVGTDSDVVQSEQA LQAAQLSKLRYEAVLAALESRTVPHIDMAQARS LGLSDAD					
	130	140	150	160	170	180
m764.pep	VQSAQVLAQH QYQAWAAQDAQLQSA LRGHQAE LQSAKAE QKLVSVAIE QOKTADYRRL					
a764	VQSAQVLAQH QYQAWAAQDAQLQSA LRGHQAE LQSAKAE QKLVSVAIE QOKTADYRRL					
	190	200	210	220	230	240
m764.pep	VQSAQVLAQH QYQAWAAQDAQLQSA LRGHQAE LQSAKAE QKLVSVAIE QOKTADYRRL					
a764	VQSAQVLAQH QYQAWAAQDAQLQSA LRGHQAE LQSAKAE QKLVSVAIE QOKTADYRRL					
	190	200	210	220	230	240
m764.pep	RADNFISEHAFLEQQSKSVSNWNLESTRG QMRQIQAAIAQAEQNRVINTQNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLESTRG QMRQIQAAIAQAEQNRVINTQNLKRDTLDA					
	250	260	270	280	290	300
m764.pep	RADNFISEHAFLEQQSKSVSNWNLESTRG QMRQIQAAIAQAEQNRVINTQNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLESTRG QMRQIQAAIAQAEQNRVINTQNLKRDTLDA					
	250	260	270	280	290	300
m764.pep	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMV IAPDD					
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMV VAPDD					
	310	320	330	340	350	360
m764.pep	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMV IAPDD					
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMV VAPDD					
	310	320	330	340	350	360
m764.pep	DKMDVEVLVLNKDIGFEVQGQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT					
	370	380	390	400	410	420

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|||||
a764      DKMDVEVLVLNKDIGFVEQGDVAVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
              370      380      390      400      410      420

              430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAETIKTKRRRVLDYLLSPLQTKLDESFRRERX
|||||
a764      AVVSLDKHTLNIDGK
              430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTTACGGT CATGATTCGG CCACAATGAA
201 CGCTGCGGCT GCCAAGATT ATATGAAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATAACCACA TCCAGAACAG CCCGAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGCGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCCG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```

m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVYG HDSATMNAHA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEIAAI MGHEMTHALH EHGRNKGQQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGTYGLTL PYRSLEEEA DEGGMMLMAQ AGYHPAAAVR
251 VWERMNOEND QNGFIYAITS THPTNNARIE NLKRLIPTVM PVYEQSVRNK
301 GRVNRKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTTACGGT CAGGATTCGG CCACAATGAA
201 TGCTGCGGCT GCCGAAGATT ATATGAAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCGG CGGGAATG GCGTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGCGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCCG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```

a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG

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51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEIAAI MGHEMTHALH EHGNKVGQK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILMGYITL PYSRSL EEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT THPTNNARIE NLKRLLPVPM PVYEHSVRNK
301 GRVKNRRRX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

```

          10      20      30      40      50      60
m765.pep  MLRCRPKSVLDSGIFLKFNFLRSKPKEISFLPSFKRILCLSAVISVLGACAVVADVYG
          |||||
a765      MLRCRPKSVLDSGIFLKFNFLRSKPKEISFLPSFKRILCLSAVISVLGACTVVADVYG
          10      20      30      40      50      60

          70      80      90     100     110     120
m765.pep  HDSATMNAAAAKDYMKTVELNKSAGNVDTSRTARRVQAVFRRLPYADAANNTSHKFDW
          :|||
a765      QDSATMNAAAAEDYMKTVELNKSAGNVDTSRTARRVQAVFRRLPYADAANNTGHKFDW
          70      80      90     100     110     120

          130     140     150     160     170     180
m765.pep  KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHEMTHALHEHGKKNKVGQQ
          |||||
a765      KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKKNKVGQK
          130     140     150     160     170     180

          190     200     210     220     230     240
m765.pep  ILTNTAAQIGTQIILDKKPDNTPELVGLGMDILGTGYGLTLPYSRSL EEEA DEGGMMLMAQ
          |||||
a765      ILTNMAAQIGTQIILDKKPDNTPELVGLGMDILMGYITL PYSRSL EEEA DEGGMMLMAQ
          190     200     210     220     230     240

          250     260     270     280     290     300
m765.pep  AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPVMPVYEQSVRNK
          |||||
a765      AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPVMPVYEHSVRNK
          250     260     270     280     290     300

          310
m765.pep  GRVKNKRRRX
          |||||
a765      GRVKNKRRRX
          310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCGG TACATTGCCA TCATTTGAT CCTTTGTAT TGAACCTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGCTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGT TTGAAAACA GGGCTGTTCG CGGGAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AAATGATGC GCGCTATGA TTCCCCGAA
451 GCTGCCGCGG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGC TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
51  YFCVHCHHFD PLLLLGKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANSV FKAIVEQKIR LENRAVAGKW ALSQKGFDDG KLMRAYDSPE
 151 AAVALKMQK LTEQYIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTGCCG
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AGAACAGTCG GGTAAAATTG AGGTTTGTGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTGAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTGTGCG
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGAAAAACA GGTGCGTTGC CGGAAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AAAGTATGCG GCGCCTATGA TTCCCGCGAA
 451 GCTGCCGCGG CCGCATTAAA AATGCAGAAA CTGACGGAAC AATACCGCAT
 501 CGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
 551 ATAACGCTT TGACGGCGGC GTTCATACGA TTAAGAATT GGTTCGCAAA
 601 GTCAGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
 51 YFCVHCHHFD PLLLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
 101 GLKYQANPAV FKAIVEQKIR LENRSVAGKW ALSQKGFDDG KLMRAYDSPE
 151 AAAAAKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQPGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g767.pep	PLLLKLKALPSDYLRTHEHVVRPEMLGLARMAAAVKLSGLKYQANSV FKAIVEQKIR					
m767	PLLLKLKALPSDAYLRTEHVVRPEMLGLARMAAAVNLSGLKYQANPAV FKAIVEQKIR					
	70	80	90	100	110	120
	130	140	150	160	170	180
g767.pep	LENRAVAGKWALSQKGFDDGKLMRAYDSPEAAVAALKMQKLTQYRIDSTPTVIVGGKYR					
m767	LENRSVAGKWALSQKGFDDGKLMRAYDSPEAAAAALKMQKLTQYRIDSTPTVIVGGKYR					
	130	140	150	160	170	180
	190	200	210			
g767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTGCCG
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCTCTCA AAAACAGTCG GGCAAAATTG AGGTTTGTGA ATTTTTCGGC
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAATTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTGAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCAAGAATGG CTGTCGGGT CAAGCTGTCA
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGAAAAACA GGTGCGTTGC CGAAAAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AAAGTATGCG GCGCCTACGA CTCTCCTGCG

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451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
 501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
 551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAGAATT GGTGCCAAA
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

a767.pep
 1 MKLKHLPLLL LSAVLSAQAY ALTEGEDYLV LDKPIPOKQS GKIEVLEFFG
 51 YFCVHCHHFD PLLKLKGLAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
 101 GLKYQANPAV FKAVYEQKIR LENRSVAEKW ALSQKGFQDGK KLMRAYDSPA
 151 AAAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
 201 VREERRKQTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

a767.pep	10	20	30	40	50	60
m767	10	20	30	40	50	60
a767.pep	70	80	90	100	110	120
m767	70	80	90	100	110	120
a767.pep	130	140	150	160	170	180
m767	130	140	150	160	170	180
a767.pep	190	200	210			
m767	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

g768.seq
 1 ATGAATATCA AACAAATGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCACGCGC GCAGCCCGCG AAAAACCGGT ATCCGCGCGC CAAACCGCGC
 101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGTCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
 201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

g768.pep
 1 MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
 51 GHLHNAVNIPI VDQIVRIYE AAPDKDTPVN LYCRSGRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGKMK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

m768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCGC GCAGCCCGCG AAAAACCGGT ATCCGCGCGC CAAACCGCGC
 101 AACATCCGCG CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
 201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNI PVDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAAPQKPVSAQAQHS	AVWIDVRSEQEFSEGLHNAVNI				
m768	MNIKHLITAA LIASAAFAAQ AAPQKPVSAQAQHS	AVWIDVRSEQEFSEGLHNAVNI				
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	V	DQIVRRIE	EAAPDKDTPVNL	YCRSGRRAE	AALQELKKAG	YTNVANHGGYEDLLKKGMMKX
m768	V	DQIVRRIE	EAAPDKDTPVNL	YCRSGRRAE	AALQELKKAG	YTNVANHGGYEDLLKKGMMKX
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCGT ATCCGCGGCC CAACCCGCGC
 101 AACATTGATC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTCG ACAACGCGGT CAACATCCCG GTCGACCAA TCGTCCGCGC
 201 CATAACGAA GCCGCGCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
 51 GHLHNAVNI PVDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAA LIASAAFAAQ AAPQKPVSAQAQHS	AVWIDVRSEQEFSEGLHNAVNI				
m768	MNIKHLITAA LIASAAFAAQ AAPQKPVSAQAQHS	AVWIDVRSEQEFSEGLHNAVNI				
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	V	DQIVRRIE	EAAPDKDTPVNL	YCRSGRRAE	AALQELKKAG	YTNVANHGGYEDLLKKGMMKX
m768	V	DQIVRRIE	EAAPDKDTPVNL	YCRSGRRAE	AALQELKKAG	YTNVANHGGYEDLLKKGMMKX
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq
 1 TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTATGCC
 51 TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
 101 CCGAAGaAAC ACCgtgCGAA CCGGATTGA GAAGCCGTCC CGAGTTCAGG
 151 CTTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
 201 GGTGCGGGAA AAAGGAAAAG TTTTGCAAGT TGACGgcGAA ACCCTGCTGA
 251 AAAATCCCGA ATTGTGTGCG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
 301 AATATTGCCG GTATCCGCGT GATTITGCCG ATTTACCTAC AACAGGCGCG
 351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
 401 AGGGCAGGGT GAAGGAGGCG GTTTCCTTATT ACCGGGAATT GATTGCCGCC
 451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
 501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
 551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
 601 TTGCGCGAAC GCGATGCGTG GAAGGTAAC GGCGGTTTCA GCGTTACCCG
 651 CGAACACAAAT ATCAACCAAG CCCCAGAACG GCAGCAGTAC GGCAATTGGA
 701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
 751 GAGAAAAAAT GGTGCTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
 801 CGTGTCCCGG AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
 851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
 901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
 951 CGCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAAAC CCGAGATGGC
 1001 AAACGCTGTC TTCGGCGGAG TGGGGCGGTT TGAAGAATAC GCGCCGGGCG
 1051 CGTTCCGACA ATACCCATT TCAAAATTTCC AATTGCTGG TGTTTTACCG
 1101 GAATGCGGCG CAATATTGGA CGGGCGGTTT GGATTTTAC CGCGAGCGCA
 1151 ACCCCGCGCA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
 1201 TGGGGGCAAG AATGGGGCGG CAGCGGCCTG TCTTCGCTGT TCCGCTCGG
 1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAGC AGTTTAAAG
 1301 GGGAAAGGCG CAGGATAAAA GAATCGGACA CATCCTTGAG CTTTGGCAC
 1351 CGGCATTGCG ATTTCAAAGG CATCAGCCG CGCCTGACGC TGTGCGACCG
 1401 CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGGCGT
 1451 TTGTCGAGTT TAACAAAACG TTCTGA

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep
 1 LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
 51 LHEAEVKPID REKVPQVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
 101 NIAGIRVILP IYLOQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
 151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPPQL MEQVELYRKA
 201 LRERDAWKVN GGFVTRERN INQAPKQQQY GNWTFPRQVD GTAVNYRFGA
 251 EKKWSLKNW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
 301 LAVFHERRY GNDAYSANG ARLYFNWQT PRWQTLSSAE WGRLNKTRRA
 351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
 401 WGQEWGSGSL SSLFRLGVAK RHYEKPGFSS SFRGERRRDK ESDTSLSLWH
 451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq
 1 TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTA TGCCTGCACG
 51 AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
 101 AAGAAACACC GCGGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
 151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCAGGT
 201 CCGGGAAAAA GAAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
 251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAACAAT
 301 ATTGCCGATA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
 351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
 401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGGAAATTGAT TGCCGCCCAA
 451 CCGGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCAGCAT TGTTTGAAAA
 501 CAGGCAGAAC GAGGCGGCGG CAGACCAATT CGACCGCCTG AAGGCGGAAA
 551 ACCTGCCGCG GCAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG
 601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
 651 ACACAAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
 701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
 751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGG GCGGCGACGT
 801 GTCCGCGCAGG GTTTATCCGG GGAATAAGAA ATCAACGAT ATGACGCGAG
 851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
 901 GCAGTGTTC ACGAACGCGG CACCTACGGC AACGACGCTT ATTCTTACAC
 951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
 1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
 1051 TCCGACAATA CCATTGCA AATTTCCAAT TCGCTGTTGT TTTACGGAA
 1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCAGC GAGCGCAACC
 1151 CCGCGACCG GGGCGACAAT TTCAACCGTT ACGGCGTGG CTTTGCCTGG
 1201 GGGCAGGAAT GGGCGGCAG CGGCTGTCT TCGCTGTTGC GCCTCGGCGC

1251

1251 GCGGAAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTAAAGGGG
 1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
 1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCACGA
 1401 AACCGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGCGCTTGT
 1451 TCGAGTTTAA TAAACGTTT TGA

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

m769.pep
 1 LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
 51 HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
 101 IAGIRVILPI YLQQAQODKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
 151 PDAPAVRMRL AALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
 201 RERDAWKVNG GFSVTRHNI NQAPKQQYG KWTFFKQVDG TAVNYRLGAE
 251 KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
 301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
 351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
 401 GQEWGSGSLS SLLRLGAAR HYEKPGFFSG FKGERRRDE LNTSLSLWHR
 451 ALHFKGITPR LTLSHRETRS NDVFNEYKN RAFVEFNKTF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

	10	20	30	40	50	59
g769.pep	LIMVIFYFCGKTFMPARNRWMLL-PLLASA	AYAETPREPDLRSRPEFRLHEAEVKPI				
m769	LIMVIFY--FCGKTFMPARNRWMLLPLLASA	AYAETPREPDLRSRPEFRLHEAEVKPI				
	10	20	30	40	50	
	60	70	80	90	100	110
g769.pep	DREKVPQGVREKGVQLQVDGETLLKNPELLSR	AMYSAVVSNNIAGIRVILPIYLQQAQOD				
m769	DREKVPQGVREKGVQLQIDGETLLKNPELLSR	AMYSAVVSNNIAGIRVILPIYLQQAQOD				
	60	70	80	90	100	110
	120	130	140	150	160	170
g769.pep	KMLALYAQGILAQAEGRVKEAVSHYRELIAAQ	PDAPAVRMRLAALFEDRQNEAAADQFD				
m769	KMLALYAQGILAQADGRVKEAISHYRELIAAQ	PDAPAVRMRLAALFENRQNEAAADQFD				
	120	130	140	150	160	170
	180	190	200	210	220	230
g769.pep	RLKTEDLPPQLMEQVELYRKALRERDAWKVNG	GFSVTRHNIHQAPKQQYGNWTFPKQV				
m769	RLKAENLPPQLMEQVELYRKALRERDAWKVNG	GFSVTRHNIHQAPKQQYGNWTFPKQV				
	180	190	200	210	220	230
	240	250	260	270	280	290
g769.pep	DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGR	VYPGNKKFNDMTAGVSGGIGFADRRKDV				
m769	DGTAVNYRLGAEEKWSLKNWYTTAGGDVSGR	VYPGNKKFNDMTAGVSGGIGFADRRKDA				
	240	250	260	270	280	290
	300	310	320	330	340	350
g769.pep	GLAVFHERRTYGNDAYSANGARLYFNRWQTP	RWQTLSSAEWGRLKNTRRARSNDNTHLQI				
m769	GLAVFHERRTYGNDAYSYTNGARLYFNRWQTP	KWQTLSSAEWGRLKNTRRARSNDNTHLQI				
	300	310	320	330	340	350
	360	370	380	390	400	410
g769.pep	SNSLVFYRNARQYWTGGLDFYRERNPADRGDN	FNRYGLRFAWGQEWGSGLSLRLGVA				
m769	SNSLVFYRNARQYWMGGLDFYRERNPADRGDN	FNRYGLRFAWGQEWGSGLSLRLGAA				
	360	370	380	390	400	410
	420	430	440	450	460	470
g769.pep	KRHYEKPGFFSSFKGERRRDKESDTSLSLWHR	ALHFKGITPRLTLSHRETWSNDVFNEYE				

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m769      KRHYEKPFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRAFVEFNKTFX
          |||||
m769      KNRAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTSTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGGAAATTGAT TGTGCCCCAA
451 CCCGACGCGC CCGCGTCCG TATGCGTTTG GCGCGGCAT TGTGAAAAA
501 CAGGCAGAAC GAGGCGCGCG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CCGGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAAATAT AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAAAA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
901 GCAGTGTTCG ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAAACCCG AAATGGCAAA
1001 CGTTGTCTTC GCGCGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCGACCGG GGGCGACAAT TTCAACCGTT ACGGCTGCGC CTTTGCCTGG
1201 GGGCAGGAAT GGGCGGCGAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 GCGGAAACGG CATTATGAAA AACC CGGCTT TTCAGCGGT TTAAAGGGG
1301 AAAGCGCAGG GGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACC GG
1351 GCATTGCAAT TCAAAGGCAT CACGCGCGCG CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CCGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NOAPKRQYQ KWTFFPKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRYTG NDAYSYTNGA RLYFNWQTP KWOTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDIFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGSL SLLRLGAAKR HYKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDFVNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

m769/a769 99.8% identity in 490 aa overlap

```

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREKGVKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM

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|||||
m769      EKVPGVQREKGVLDGETLLKNPELLSRAMYSAVVSNINAGIRVILPIYLQQAQQDKM
              70          80          90          100         110         120

              130          140          150          160          170          180
a769.pep   LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
              |||||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
              130          140          150          160          170          180

              190          200          210          220          230          240
a769.pep   KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNINQAPKROQYQKWTFFPKQVDG
              |||||||
m769      KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNINQAPKROQYQKWTFFPKQVDG
              190          200          210          220          230          240

              250          260          270          280          290          300
a769.pep   TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
              |||||||
m769      TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
              250          260          270          280          290          300

              310          320          330          340          350          360
a769.pep   AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQISN
              |||||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQISN
              310          320          330          340          350          360

              370          380          390          400          410          420
a769.pep   SLVFYRNARQYWMGGDLFYRERNPADRGDNFNRYGLRFANGQEWGGSGLSLLRLGAAGR
              |||||||
m769      SLVFYRNARQYWMGGDLFYRERNPADRGDNFNRYGLRFANGQEWGGSGLSLLRLGAAGR
              370          380          390          400          410          420

              430          440          450          460          470          480
a769.pep   HYEKPGFFSGFGERRRDKELNLSLSLWHRALHFKGITPRLTLSHRETRSDNVFNEYEKN
              |||||||
m769      HYEKPGFFSGFGERRRDKELNLSLSLWHRALHFKGITPRLTLSHRETRSDNVFNEYEKN
              430          440          450          460          470          480

              490
a769.pep   RAFVEFNKTFX
              |||||||
m769      RAFVEFNKTFX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGGGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AGCGCGGTAC GGGCTTCGCG TCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCACGGG GTGCAAGCCG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCCGATA AAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACSGSE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKRGTFEA FKSRIQVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FSGGIPQTDG VQADTSGLL AGACIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGGGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCCTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCTCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSRIQVRY DPKRRTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

```

m770/g770 93.5% identity in 186 aa overlap

      10      20      30      40      50      60
g770.pep MNRLLLLSAAVLP TACGSGETDKIGRASTVFNILGKNDR IEVEGFDDPDVQGVACYISYA
          |||||
m770      MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR IEVEGFDDPDVQGVACYISYA
          10      20      30      40      50      60

      70      80      90      100     110     120
g770.pep KKGGLKEMVNL EEDASDASVSCVQTASSISFDETAVRKPK EVFKRGTFAFKSRQIVRY
          |||||
m770      KKGGLKEMVNL EEDASDASVSCVQTASSISFDETAVRKPK EVFKHGASFAFKSRQIVRY
          70      80      90      100     110     120

      130     140     150     160     170     180
g770.pep DPKRKAFAYLVYSDKIVQGS PKNSLSAVSCFGSGIPQTDGVQADTSGKLLAGACIISNPI
          |||||
m770      DPKRRTFAYLVYSDKIIQGS PKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
          130     140     150     160     170     180

g770.pep KNPDKRX
          :| |||
m770      ENLDRKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCCTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSRIQVRY DPKRRTFAYL VYSDKIIQGS PKNSLSAVSC

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1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPKRR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRLLLLSAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
m770	MNRLLLLSAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGASFAFKSRQIVRY					
m770	KKGGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGASFAFKSRQIVRY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRRTFAYLVYSDKIIQGSFKNSLSAVSCFSGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770	DPKRRTFAYLVYSDKIIQGSFKNSLSAVSCFSGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPKRRX					
m770	ENLDRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

```

1  ATGGATTAT  TATCGGTTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTGGC
51  GGTGCTGACG  ATGCTGCTTT  TGGCGGCAGT  CGGGCTGCAC  GCTTCCGTAT
101  ATCGCACCTT  CACGCCCGAA  AACATCCGCA  GCCGCCTCCA  ACAAGCATT
151  GCCATACCC  ACCGAAAT  CTCGTTTGAT  GCGGATATAC  GCGCAGGCT
201  TCTGCCCGCG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCGG
251  ACGCGCGCGG  GGTGCGCGTT  TCCGTCAAAG  AAACCAAAAT  CGGATTGAGC
301  TGGAAAAACC  TGTGGTCGGA  TCGGATACAG  GTTGAAAAAT  GGGTGGTTTC
351  GGTGCGCGAT  CTTGCCCTGA  CGCGCGACAG  AAACGGCGCT  TGGACATCC
401  AAGACCTGTT  CGACGGCGCG  AAACACTCCG  CCTCAGTCAA  CCGCATTATC
451  GTCGAAAAAC  GCACCGTCCG  CCTCAATTTC  CTGCAGCAAC  AGCTTATCCT
501  GAAGGAAATC  AGCCTCAACC  TGCAATCCCC  CGATTCTGTCG  GGGCAGCAGT
551  TTGAAAGTTC  GGGCATACTG  GTTTGGAGAA  AGCTGTCCGT  CCCGTGAAAA
601  AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCG  AAATCTCACC
651  GTTCCATTTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATCACCATT
701  CCACCACCGG  CAGCCCTTCT  GTCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751  GCCGGCCTCG  GCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801  CGCGCAAATC  CCCGCACTGG  CACTCAAAAA  CAACAGCATC  AAAACCGGCA
851  CGGTCAACGG  CACGTTTACC  GCCGGCGGCG  AATATGCCCG  ATGGGACGGT
901  TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951  CAACGCCGAA  ATCTCCGGCA  GCTTCAAAC  ACCGCGCCTT  CAAACCAATT
1001  TCTCCCTCGG  CTCGCCCTTG  GTTTGGAGTC  GGGACAACGG  GCTGGACGCC
1051  CCGCGCCTGC  ACATATCGAC  CTTTCAGGAT  ACCGTCGACC  GCCTGCCGCA
1101  ACCCGTTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCATA  CCGAATCTGC
1151  AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  ACCGTTGCC
1201  GCAAAATTC  AATATACGCG  GGAAGGCGCA  CCGCACCTGG  AAGCCGCGCG
1251  CCGCGCTCAA  AATTAAC  TCGCCCCCTA  TCTTGACGAA  TTTGCGCAAC
1301  AAAACGGCAA  AATATCCCC  GACATCCTCG  GCAGGCTGTC  CGGCAACGTC
1351  GAGGCACACC  TCAAAATCGG  CAGCATCCAA  CTCGCCGGCT  TGCAACTGGA
1401  CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGACCATATC  GCGCTCAGCC
1451  GTTTCAGTC  AGGCTTTAC  GCGCGCCATA  CCGAAGGCGG  CATCAGCATC
1501  GCCAACACCC  GTCGCCGCAC  TTACCGCCTG  CAACAGATG  CAAGCAACAT
1551  CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCAC  AGCTTCAGCG
1601  GCAACGGCGA  TGGCGTCATC  GACCTGACCG  CAAGCGGCGA  AAACCGCAAA
1651  CAGCTTATCC  GCTCGCTGCA  AGGACGCTG  TCGCTGAATA  TTTCCAACGG
1701  CGCGTGGCAC  GGCATCGATA  TGGACAGCAT  TTTAAAAAAC  GGCCTTCCG

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1256

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1751 GGAATTCCTC GGGCAGCACA CCCTTCTACC GATTACGCT CAACAGCGAA
1801 ATTTACAGACG GCATCAGCCG CCACATCGAT ACCGAATCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCCGC CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```

g771.pep
1 MDLLSVFHKY RLKYAVAVLT MLLLAUVGLH ASVYRTFTPE NIRSRLQOSI
51 AHTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRII
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSFS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNNSI KTGTVNGTFT AGGEYARWDG
301 SFKLDRKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNWNAEL NGTFDRQPVA
401 AKFKYTREGA PHLEAAAALQ KLNLPYLDL FRQNGKIFP DILGRLSGNV
451 EAHLLKIGSIQ LPGLQLDDME TYLHADKDH IALSRFKSGLY GGHTGGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTASGENRK
551 QLIRSLQGS LSNISNGAWH GIDMSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHH TELFSDSLYV TSNGYTNLDT QELSEDVLR NAVHPKPKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKPE
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

```

m771.seq
1 ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGTGACG ATACTGCTTT TGGCGGCAGT CGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAGCATT
151 GCACACACAC ACCGAAAAAT CTCGTTGAT GCGGACATTC AGCGCAGGCT
201 CCTGCCCCCG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAT CCGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGGCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAACA GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTGCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGCG TGTTCCTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCGTGA CGGACACGGC ATTACCATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGCGG AGCGGATGCC
751 GCGGCGCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAATC CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTACG GCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCTCAA TCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCGGTTTC ATCAGCCGCG TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACGCCCA AACCGTTGCC
1201 GCGAAATTC GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTCCC GACACCCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGACCC TGAATATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTTC AGGGCTTTAC GCGCGCCATA CCGAAGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCTG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTATC GACCTGACCG CGGCGCGCGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGTAAATA TTTCAAACGG
1701 TGCAATGGAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAACTGCG CGACAATGCC GCACCCAGCA CACCCCTTCA CCGATTACG
1801 CTCAACAGCG AATATTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACAGCAA CGGCTATACC AATCTGGATA
1901 GCGAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGTA AATCACCGGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCG CGCAAGAGA
2051 AACAGAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2101 CCTAAGAACC CGTA

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This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

m771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLAAVGLH ASVYRTFTPE NIRSRLQQSI
 51 AHTRKISFD ADIQRRLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNNWNAEL NGTFDRQTVA
 401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYDD VRQNGKIFP DTLAKLSGDI
 451 EAHLKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTGGISI
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SPSGNGDAVI DLTAGGETRK
 551 ELIRSQGS LSNISNGAWH GIDMDNLIK N GISKATDNA APSTPFHRT
 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
 701 PKEP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap					
	10	20	30	40	50	60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSI AHTRKISFD					
m771	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSI AHTRKISFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g771.pep	ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETIGLSWKNLWSDRIQVEKWVVSAD					
m771	ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETIGLSWKNLWSDRIQVEKWVVSAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g771.pep	LALTRDRNGAWN IQDLFDGAKHSASVNRIIVENSTVRLNLFQQLILKEISNLQSPDSS					
m771	LALTRDRNGAWN IQDLFDGAKHSASVNRIIVENSTVRLNLFQQLILKEISNLQSPDSS					
	130	140	150	160	170	180
	190	200	210	220	230	240
g771.pep	GQPFESSGILVWRKLSVPWKSRLGLFLSDGIGTPEISPFHFEASTSLDGHG ITISTTGSPS					
m771	GQPFESSGILVWRKLSVPWKSRLGLFLSDGIGTPEISPFHFEASTSLDGHG ITISTTGSPS					
	190	200	210	220	230	240
	250	260	270	280	290	300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSLVWSRDNGLDAPRLHISTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSLVWSRDNGLDAPRLHISTLQD					
	310	320	330	340	350	360
	370	380	390	400	410	420
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQNNWNAELNGTFDRQPVAAKFKYTREGAPHLEAAVALQ					
m771	TVDRLPQPRFISRLDGSLSIPNLQNNWNAELNGTFDRQPVAAKFKYTREGAPHLEAAVALQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
g771.pep	KLNLTPLYDDVRQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH					
m771	KLNLTPLYDDVRQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH					

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRRQLIRSLQGSLSLNISNGAWHGIDMDSILKNLSGKISG----STPFYRFT					
m771	DLTAGGETRKLIRSLQGSLSLNISNGAWHGIDMDNILKNISGKTADNAAPSTPFHRT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

1	ATGGATTAT	TATCGGTCTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTAGC
51	CGTGCTGACG	ATACTGCTTT	TGGCGGCAAT	CGGGCTGCAC	GCTTCCGTAT
101	ATCCGATCTT	CACACCTGAA	AACATCCGAA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACGC	ACCGGAAAT	CTCGTTGAT	GCGGATATAC	AGCGCAGGCT
201	TCTGCCCGCG	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	GCGGCGACCG	GACTGCCGTT	TCCGTCCAAG	AAACCAAAAT	CGGATTGAGC
301	TGGA AAAACC	TGTGGTCGGA	TCAGATACAG	ATTGAAAAAT	GGGTGGTTTC
351	GAGTGCGGAA	CTTGCCCTGA	CGCGCGACGG	GAAAGGTGTT	TGGAACATCC
401	AAGACCTGAT	CGACAGCCAA	AAACGCCAAG	CCTCAGTCAA	CGGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTC	CTGCAGGAAC	AGCTTATCCT
501	GAAGGAAATC	AACCTCAACC	TGCAATCCCC	CGATTGCTCG	GGGCAGCCGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGGGGAA	AGCTGTCCGT	CCCGTGAAAA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCAGGCCCA	AAATCTCACC
651	GTTCCATTTC	GAAGCTTCCA	CTTCGTGGA	CGGACACGGC	ATTACCATTT
701	CCACCAACCG	CAGCCCTTCT	GTCGCTTCA	ACGCGGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	GCCCAAAATC	CCTACGCTGG	CACTCAGGAA	CAACAGCATT	AAAATTGAAA
851	CCGTCAACGG	CGCATTACCC	GCCGGCGCGG	AATATGCCCA	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCAC	CAGACCAACT
1001	TCTCCCTCAA	TTCGCGGCTC	GTATGGACGG	AAAACAAAGG	GCTGGACGGG
1051	CCGCGCCTGT	ATGTATCGAC	CCTTCAGGAT	ACCGTCAACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TGACGGTTTC	GCTGTCCGTA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	AACCGTTGCC
1201	GCGAAATCCA	GATACACACA	TGAAGACGCA	CCGCATCTGG	AAGCCGCCGT
1251	CGCACTGCAA	AAATTGAACC	TGACCCCTTA	TCTTGACGAC	GTGCGGCAAC
1301	AAAACGGCAA	AATATTTCCC	GACACCCTCG	CCAAGCTGTC	CGGCACATC
1351	GAGGCGCACC	TGAAAATCGG	AAAAGTCCAA	CTTCCCGGCC	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCGGACAA	AGGCCATATC	GCGCTCAGCC
1451	GTTTCAAATC	AGGGCTTTAC	GCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCGCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	CGCGGTCAATC	GACCTGACCG	CGGGCGGCGA	AACCGAAAAA
1651	GAGCTTATCC	GCTCGCTTCA	GGGACGCTG	TCGCTAAATA	TTTCCAACGG
1701	TGCATGGCAC	GGTATCGACA	TGGACAATAT	CCTGAAAAAC	GGCATTTCCG
1751	GCAAAACTGC	CGACAATGCC	GCACCCAGCA	CACCTTCCCA	CCGATTACAG
1801	CTCAACAGCG	AAATTTGAGA	CGGCATCAGC	CGCCACATCG	ATACCGAACT
1851	CTTCTCCGAC	AGCCTCTATG	TTACAGCAAA	CGGCTATACC	AATCTGGATA
1901	CGCAGGAATT	GCTGGAAGAT	GTCCTTATCC	GCAACGCCGT	CCATCCGAAA
1951	AACAAACCGA	TTCCCTGAA	AATCACCCTG	ACGGTGGACA	AACCGTCCAT
2001	TACCGTCCAT	TACGGCAGGC	TGACCGCGCG	CATCAATTTC	CGCAAAGAGA
2051	AACAGAAAAT	CCTCGAAGAC	ACCCTGCTGG	AACAATGGCA	GTGGCTCAAA
2101	CCTAAAGAAC	CGTAA			

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI
 51 AHTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKVVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQWNNAEL NGTFDRQTVA
 401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLD VROQNGKIFP DTLAKLSGDI
 451 EAHKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
 551 ELIRSLQGS LSNISGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
 601 LNSEISDGI RHIDTELFSD SLYVTSNGYT NLDQQLSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
 701 PREP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPENIRSRLQOSIAHTRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFPENIRSRLQOSIAHTRKISFD
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKVVVSSAE
m771	ADIQRRLPRPTVILKNLTITEPGGDQTAHSVQETKIGLSWKNLWSDQIQIEKVVVSSAE
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNQSPDSS
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNQSPDSS
a771.pep	GQPFESSGILVWGKLSVPWKSRLGLFLSDGIGTPKISPFHFEASTSLDGHGITISTTGSPS
m771	GQPFESSGILVWGKLSVPWKSRLGLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
a771.pep	TVNRLPQPRFISRLDGSLSVNLQWNNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
m771	TVNRLPQPRFISRLDGSLSVNLQWNNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
a771.pep	KNLNTPYLDDVROQNGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGHI
m771	KNLNTPYLDDVROQNGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGHI

1260

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKEILIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKEILIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

```

1  GTGTTCCGCA  CGGTCTTGCG  GACTGATGCC  GACTGCCTGC  AAATCATCGT
51  CGTCGGCAAG  TTCTTTCAGG  TTGTTGCGTA  TGGTTTTCGG  GCGTTGGCGG
101 AAGGCGAGTT  TCACCAAGTT  GCGGAAATGA  TCGAAATCGT  CCGCCTTGCC
151 GATACGGTGT  TTCACCGGAA  TCATGCGCAC  CACTGCGGAA  TCGATTTTCG
201 GCGCGGGATC  GAACGATTCG  GCGGGCACGT  CAATCAGCAG  CTCATATATC
251 AAAAAATATT  GCAGCATCAC  ACCCAAGCGA  CCGTAGTCGT  TGCTTTTCGG
301 CGCGGCAACC  ATGCGCTCGA  CCACTTCTTT  TTGCAACATA  AAGTGCAAT
351 CGGCGACATC  GTCCGCCACC  TCCGCCAGTT  TGAACAAAAG  CGGCGTGGAG
401 ATGTTATACG  GCAGTTGCC  GACGATTTTC  TTTTGCCTG  AGATGCCGTT
451 GAAATCAAA  TGCAACACGT  CGCCTTCGTG  AATCACCAGT  TTATCCGCAA
501 ACGGCAGCGT  TTTAGACGCG  CATAACGATG  CGCGGTCGAT  TTCGACAACG
551 TGCAGGCGGT  TCAGCTTTT  CGCCAAAGGT  TCGGTAATG  CCGCCAAACC
601 CGGGCCGATT  TCAATCACGA  CATCATCCGC  CTGCGGGCGC  ACGGCGTTGA
651 CAATATCGCC  GATAATCCGC  GTGTCCTGCA  AAAAATTCTG  CCCGAAACGC
701 TTGCGGGCTT  TGTGTTCTTT  CATCGTGTG  CCTCTTCGGT  TGAACCCCG
751 CCCTTAGGG  CGGCAGGATC  AGACTCTGTT  TGGCGGGGCG  GTAACCCCTT
801 CCAATCAGG  ACGACACATA  GGGCGGTGCT  TTATGTGTCG  TCCTGTGTGT
851 TGAACATAA  ATGTGTTTAC  AGTATCCGTT  TGATGTCGGC  ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

```

1  VFGTVLRTDA  DCLQIIVVGK  FFQVVAYGFA  ALAEGEFHQF  GEMIEIVRLA
51  DTVFHRNHAH  HCGIDFRRGI  ERFCRHVNOQ  LHIEKILQHH  TQATVVVAFR
101 RGNHALDHEF  LQHKVHIGDI  VRHLRQFEQK  RRGDVIRQVA  DDFLFA*DAV
151 EIKLQHVAFV  NHQFIRKRQR  FQTAYDVAVD  FDNVQAVQLF  RQRFNGCRQT
201 RADFNHDIIR  LRAHGVDNIA  DNPRVLQKIL  PETLAGFVFF  HRVSSSVETP
251 PFRAAGSDSV  WAGRNPFQIR  TTHRAVLVYS  SCVLEHKCVY  SIRLMSAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

```

1  ATGTTCCGCG  CGGTCTTGCG  GATTGATGCC  GACTGCCTGC  AAATCATCGT
51  CGCCTGCAAG  CTCTTTCAGA  TTGTTGCGTA  TGGTTTTCGG  GCGTTGGTGG
101 AAGGCGAGTT  TCACCAAGTT  GGCAAAATGC  TCGAAATCGT  CCGCCTTGCC
151 GATGCGGTGT  TTCACCGGAA  TCATACGGAC  GACGGCGGAA  TCCACTTTCG
201 GCGCAGGTC  GAACGATTCG  GCGGGTACGT  CAATCAGCAT  TTCCATATCG
251 AAAAAATATT  GCAGCATCAC  GCCCAAGCGG  CCGTAGTCGT  TGCTTTTCGG
301 CGCGGCAACC  ATACGCTCGA  CCACTTCTTT  TTGCAACATA  AAGTGCAAT
351 CGACGACATC  GTCCGCCACC  TCCGCCAGTT  TGAACAAAAG  CGGTGTGGAA
401 ATGTTGTACG  GCAGTTGCC  GACGATTTTC  TTTTGCCTG  CGATGCCGTT
451 GAAATCAAA  TGCAATACAT  CGCCTTCGTG  AATCACCAGT  TTATCCGCAA
501 ACGGCAGCGT  TTTAGACGCG  CATAACGATG  CGCGGTCGAT  TTCGACAACG
551 TGCAGGCGGT  TCAGCTTTT  CGCCAAAGGT  TCGGTAATG  CCGCCAAACC
601 CGGGCCGATT  TCAATCACGA  CATCATCCGC  CTGCGGGCGC  ACGGCGTTGA
651 CAATATCGCT  GATAATCCGC  GTGTCCTGCA  AAAAATTCTG  CCCGAAACGC

```


1261

```

701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

m772.pep

```

1 MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GKMLEIVRLA
51 DAVFHRNHTD DGGIHFRRRV ERFGRYVNH FHIEKILQHH AQAAVVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLEACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGRNRQT
201 RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLVVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIVGKFFQVYVAYGFAALAEGEFHFQFGEMIEIVRLADTVFHRNHAH					
m772	: : : : : : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
g772.pep	HCGIDFRRGIERFGRHVNQQLHIEKILQHHTOATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	: : : : : : : :					
	70	80	90	100	110	120
	130	140	150	160	170	180
g772.pep	VRHLRQFEQKRGRDVIRQVADDFLFAFXDAVEIKLQHVAFVNHQFIRKRQRQTAYDVAVD					
m772	: : : : : : :					
	130	140	150	160	170	180
	190	200	210	220	230	240
g772.pep	FDNVQAVQLFRQRFGRNCRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
m772	: : : : : : :					
	190	200	210	220	230	240
	250	260	270	280	290	299
g772.pep	HRVSSSVETPPFRAAGSDSVWAGRNPFIQRTTHRAVLVSSCVLEHKCVYSIRLMSALX					
m772	: : : : : :					
	250	260	270	280	290	299

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

a772.seq

```

1 ATGTTTCGGCG CGGTCTTGGC GATTGATGCC GACTGCCTGC AAATCATCGT
51 CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTCG GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 ACGGCAGCGT GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTGGCC GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCGAGCT TTTCAGACGG CATACGATGT CGCGGTTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCAGCA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCTGCA AAAAATCTG CCGGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```


This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

a772.pep
 1 MFGAVLRIDA DCLQIIVACK LFIQIVAYGFA ALVEGEFHEF GEMLEIVRLA
 51 DTVFHRNHAD DGRIHFRRGV ERFGRHVNH FHIEEILQHH AQAAVVVAFR
 101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
 151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGRNRQT
 201 RTDFNHDII RLAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
 251 PFRAVESDSI WEGRNSFQIR TAHRAVLYVS SCVLKHKCVY SIRLMSAL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

m772/a772 95.6% identity in 298 aa overlap

a772.pep	10	20	30	40	50	60
m772	10	20	30	40	50	60
a772.pep	70	80	90	100	110	120
m772	70	80	90	100	110	120
a772.pep	130	140	150	160	170	180
m772	130	140	150	160	170	180
a772.pep	190	200	210	220	230	240
m772	190	200	210	220	230	240
a772.pep	250	260	270	280	290	299
m772	250	260	270	280	290	

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

m773.seq
 1 ATGGGATTGG GTGCAACGAC TTTGTCTGGT TCGGGTGCTA TAGGCGGAGG
 51 TCTGTGCAGT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
 101 CAGGTATGAC CGGTGGTTAT ACACAGGCCCT CAGAAGGAAG CCGGCAATTG
 151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
 201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
 251 CCGTATGGGG ATTGGAACG CTGATTACGC GCAAATTGGG AAACCTTGCA
 301 ACGGGTGTGA AAACCTTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
 351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
 401 GACAGGGAAT GCCTTGGGAG GATTATGTCC GTAAGGGCTT GTCTGCCAAT
 451 GCAAGGTTAC CTAATAATTT TAAAACATTT GATTATTTTG ATCGTGGTAC
 501 AGGCACGGCA ATCAGTGCCA AAACCTCTGA TACGCAAACT ACGGCAGGCC
 551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAGGGTA CATCGATAAG
 601 ACGGCAAATT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
 651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA
 701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
 751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

m773.pep
 1 MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TOASEGSRQL
 51 FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
 101 TGVKTSITPK TADVQRNLS QSEVGIKWKG GIEGQGPWE DYVGKGLSAN
 151 ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGIDK
 201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYKGSQ
 251 NITVKITEIE *

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

g774.seq
 1 ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
 51 CTGTGCTTCC GTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
 101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
 151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAT
 201 GGAAATGTTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
 251 CTTCGGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
 301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
 351 CGCACAAAAA CTCTACAATC AGGCACTCAA ACATATCAA AACGGCAGGT
 401 TTTCTGCCGC AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
 451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
 501 GGGGAACGTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
 551 TCAAAGACAG CCCAACC GCGCAGTCA TATTCAAAT CGGCGAATGC
 601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT
 651 GATACAGACC TATCCCGGCA GCCCGCGCGC AAAACGCGCC GCCCGAGCCG
 701 TACGCAAAAC ATAG

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

g774.pep
 1 MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
 51 DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRTYV QKLDDRKLKE
 101 HYLNTEGSSA SAHTVETAQN LYNQALKHYQ NGRFSAAL LKGADGGDGG
 151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC
 201 QYRLQQKDIA RATWRSLIQT YPGSPAARKA AAARVRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

m774.seq
 1 ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
 51 CTGTGCTTCC GTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTGCA
 101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
 151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAT
 201 GGAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
 251 CTTCGGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAGAG
 301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC
 351 CGCACAAAAA CTCTACAATC AGGCACTCAA ACATATAAA AGCGGCAAGT
 401 TTTCTGCCGC TGCTCCCTG TTGAAGGGG CGGACGGAGG GCACGGCGGC
 451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
 501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
 551 TCAAAGACAG CCCAACC GCGCAGTCA TGTCAAAT CGGCGAATGC
 601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT
 651 GATACAGACC TATCCCGGCA GCCCGCGGC AAAACGCGCC GCCCGAGCCG
 701 TCGCAAAAC ATAG

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

m774.pep
 1 MKIKLPLFII WLSVSASCAS VSPVPAQSOT EMSTRENASD GIPYPVPTLQ
 51 DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
 101 HYLNTEGSSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
 151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC
 201 QYRLQQKDIA RATWRSLIQT YPGSPAARKA AAARVRR*

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60																																																						
g774.pep	M	K	T	K	L	P	L	F	I	I	W	L	S	V	S	A	S	C	A	S	V	L	P	V	P	E	G	S	R	T	E	M	P	T	Q	E	N	A	S	D	G	I	P	Y	P	V	P	T	L	Q	D	R	L	D	Y	L	E	G	K	I
m774	M	K	I	K	L	P	L	F	I	I	W	L	S	V	S	A	S	C	A	S	V	S	P	V	P	A	G	S	Q	T	E	M	S	T	R	E	N	A	S	D	G	I	P	Y	P	V	P	T	L	Q	D	R	L	D	Y	L	E	G	K	I
	10	20	30	40	50	60																																																						
	70	80	90	100	110	120																																																						
g774.pep	V	R	L	S	N	E	V	E	M	L	N	G	K	V	K	A	L	E	H	T	K	I	H	P	S	G	R	T	Y	V	Q	K	L	D	D	R	K	L	K	E	H	Y	L	N	T	E	G	G	S	A	S	A	H	T	V	E	T	A	Q	N
m774	V	R	L	S	N	E	V	E	T	L	N	G	K	V	K	A	L	E	H	A	K	T	H	S	S	G	R	A	Y	V	Q	K	L	D	D	R	K	L	K	E	H	Y	L	N	T	E	G	G	S	A	S	A	H	T	V	E	T	A	Q	N
	70	80	90	100	110	120																																																						
	130	140	150	160	170	180																																																						
g774.pep	L	Y	N	Q	A	L	K	H	Y	Q	N	G	R	F	S	A	A	A	L	L	K	G	A	D	G	G	D	G	G	S	I	A	Q	R	S	M	Y	L	L	Q	S	R	A	R	M	G	N	C	E	S	V	I	E	I	G	G	R	Y		
m774	L	Y	N	Q	A	L	K	H	Y	K	S	G	K	F	S	A	A	A	S	L	L	K	G	A	D	G	G	D	G	G	S	I	A	Q	R	S	M	Y	L	L	Q	S	R	A	R	M	G	N	C	E	S	V	I	E	I	G	G	R	Y	
	130	140	150	160	170	180																																																						
	190	200	210	220	230																																																							
g774.pep	A	N	R	F	K	D	S	P	T	A	P	E	V	I	F	K	I	G	E	C	Q	Y	R	L	Q	Q	K	D	I	A	R	A	T	W	R	S	L	I	Q	T	Y	P	G	S	P	A	A	K	R	A	A	A	V	R	R	R	X			
m774	A	N	R	F	K	D	S	P	T	A	P	E	A	M	F	K	I	G	E	C	Q	Y	R	L	Q	Q	K	D	I	A	R	A	T	W	R	S	L	I	Q	T	Y	P	G	S	P	A	A	K	R	A	A	A	V	R	R	R	X			
	190	200	210	220	230																																																							

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

```

1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCCG TATCCGCCGC
51 CTGTTCTTCC CCTGTTTCCC GCAATATTCA GGATATGCGG CTCGAACCGC
101 AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACTCTG
151 CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTGGAACGA
201 AGTGGAAACC TTAACGGCA AAGTCAAAGC ACTGGAGCAT GCGAAAACAC
251 ACCCTTCCAG CAGGGCATAC GTCCAAAAAC TCGACGACCG CRAAGTGAAA
301 GAGCATTACG TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCGA
351 AACC GCACAA AACCTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
401 GGTTTTCTGC CGCTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
451 GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGCGCGC
501 TATGGGCAAC TCGGAATCCG TCATCGAAAT CGGAGGGCGT TACGCCAACC
551 GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
601 TGCCAATACA GGCTTCAGCA AAAAGACATT GCAAGGGCGA CTTGGCGCAG
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GCACAAACGC GCCGCCGCGA
701 CCGTGCACAA ACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

```

1  MKTKLPLFII WLSVAACSS PVSRIQDMR LEPQAEAGSS DAIPYPVPTL
51  QDRLDYLEGT LVRLSNEVET LNGKVKALEH AKTHPSSRAY VQKLDRLKLG
101 EHYLNTEGGS ASAHTVETAQ NLYNQALKHY KSGRFSAAAS LLKGADGGDG
151 GSIAQRSMYL LLQSRARMGN CESVIEIGGR YANRFKDSPT APEAMFKIGE
201 CQYRLQQKDI ARATWRS LIQ TYPGSPA AKR AAAAVRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60																																																						
a774.pep	M	K	T	K	L	P	L	F	I	I	W	L	S	V	A	A	C	S	S	P	V	S	R	N	I	Q	D	M	R	L	E	P	Q	A	E	A	G	S	S	D	A	I	P	Y	P	V	P	T	L	Q	D	R	L	D	Y	L	E	G	T	
m774	M	K	I	K	L	P	L	F	I	I	W	L	S	V	S	A	S	C	A	S	-	V	S	P	V	P	A	G	S	Q	T	E	M	S	T	R	E	N	A	S	D	G	I	P	Y	P	V	P	T	L	Q	D	R	L	D	Y	L	E	G	K
	10	20	30	40	50	60																																																						

1265

```

      70      80      90      100     110     120
a774.pep  LVRLSNEVETLNGKVKALEHAKTHPSRAYVQKLDKRLKEHYLNTGGSASAHTVETAQ
          :|||||
m774      IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDKRLKEHYLNTGGSASAHTVETAQ
      60      70      80      90      100     110

      130     140     150     160     170     180
a774.pep  NLYNQALKHYKSGRFSAAASLLKGADGGDGGSIQRSMYLLQSRARMGNCSVIEIGGR
          :|||||
m774      NLYNQALKHYKSGRFSAAASLLKGADGGDGGSIQRSMYLLQSRARMGNCSVIEIGGR
      120     130     140     150     160     170

      190     200     210     220     230     239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARAAA VRRKRX
          :|||||
m774      YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARAAA VRRKRX
      180     190     200     210     220     230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA  GGTCAAAAAC  ATTTGAAGAA  GCTGCTGCTG  AGGTTGAGGA
51  ACGTTTCGGT  CATCGTGGCA  TTAAGTTGGT  CGAGTTTGAG  GGTACAGCCA
101 AGCCGTGTGT  AATCAACTGC  CCTAAACATG  GAAACCAAAC  CTGTTTCGAGG
151 TACTCCAATA  TGTTTCATAGG  AAGTAGCTGG  GGTGCCCCCT  CTTGTGGTAA
201 TGAGCAAGCT  GCAAAGCCG  GTATAGCGAC  CCTTAGGAAG  AATCACATAG
251 CGTTAGAAAT  GCTGAAACAG  GCTGTAACAG  GTATGACCAA  GCAAGAGCCG
301 ATCAGCAGCG  AAGCCTACAA  TGAGATGACC  AAATCCGTGG  CAGGTTCAAA
351 CAGCATAGTC  CTTAACGATG  TCCAAGCCGA  TACGACCATC  AACAAACATC
401 ATACGCATAC  GCACAACCAC  AGCGATGCCG  ATGGCAAAGC  ACTGTCGATG
451 AGGCTCACAC  CCCGTCCTTT  GTTGTCTGAC  CGTCAGGCCG  CGGCTTTTCG
501 CCGTACAGGC  AAATCAGCG  GCAGTTTCGA  CCTGTTTGCT  TCGGTGgTCG
551 CCCCTTCGCA  GTACACGTTT  GCCGTGCGCA  TGCCCGACAC  GTCCATGTCTG
601 CCGGTTATCG  AAAAGGGAGA  CTTGCTGGTG  GTCGAGCCGC  GTATGTGCCC
651 TGCGGACGAA  GACATCGCGC  TGATTGAACT  GTCCGACAAG  CGGCTGGTCG
701 TCAGCGACCT  TGTATCGAT  ATTGCGGGCA  GGATGCTGAT  TTATCAGACG
751 GGCAGGCCGT  CTGAAGCCTT  TGACCTGCCC  GAAGGCAGCA  CGATTTTAGG
801 TGTGGTGTCT  GAGTCAAAA  ACGGTTTATG  TCCGCCGCAC  AGGCAAGAAG
851 GCGTGTGTAT  TCGGATTACC  GCCCTGATG  TGTGGACGGT  TGGTATGATT
901 TCCGCTTCCA  AAACGTCGTG  TACGCGCCCG  ACCGCAGCCC  GGAAATCAGC
951 CGTATGCTTT  CTTGATTTT  GGCAGGCTAC  GCGTGGGATA  CCGAAAACCC
1001 GTTCGTGGCG  AAATCCGAAC  AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE  AAEEVEERFG  HRGIKLVEFE  GTAKPCVINC  PKHGNQTCRS
51  YSNMFIGSSW  GCPSCGNEQA  AKAGIATLRK  NHIALEMLKQ  AVTGMTKQER
101 ITTQAYNEMT  KSVAGSNSIV  LNDVQGDITI  NNHHTHTNH  SDADGKALSM
151 RLTPRPLLS  D RQAAAFARTG  KLTGSFDLFA  SVVAPSQYTF  AVAMPDTSMS
201 PVIEKGDLIV  VEPRMCPADE  DIALIELSDK  RLVVAHLVID  IAGRMLIYQT
251 GRPSEAFDLP  EGSTILGVVL  ESKNGLCPPH  RQEGVLIRIT  APDVWTVGMI
301 SASKTSCTRP  TAARKSAVCF  LRFWQATRGI  PKTRSWRNFN  NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA  GGTCAAAAAC  ATTTGAAGAA  GCTGCTGCTG  AGGTTGAGGA
51  ACGTTTCGGT  CATCGTGGCA  TTAAGTTGGT  CGAGTTTGAG  GGTACAGCCA
101 AGCCGTGTGT  AATCAACTGC  CCTAAACATG  GAAACCAAAC  CTGTTTCGAGG
151 TACTCCAATA  TGTTTCATAGG  AAGTAGCTGG  GGTGCCCCCT  CTTGTGGTAA
201 TGAGCAAGCT  GCAAAGCCG  GTATAGCGAC  CCTTAGGAAG  AATCACATAG
251 CGTTAGAAAT  GCTGAAACAG  GCTGTAACAG  GTATGACCAA  GCAAGAGCCG
301 ATCAGCAGCG  AAGCCTACAA  TGAGATGACC  AAATCCGTGG  CAGGTTCAAA
351 CAGCATATC  CTTAACGATG  TCCAAGCCGA  TACGACCATC  AACAAACATC
401 ATACGCATAC  GCACAACCAC  AGCGATGCCG  ACGGCAAAGC  ACTGTCGATG
451 AGGCTCACAC  CCCGTCCTTT  GTTGTCTGAC  CGTCAGGCCG  CGGCTTTTCG
501 CCGTACAGGC  AAATCAGCG  GCAGTTTCGA  CCTGTTTGCT  TCGGTGgTCG
551 CCCCTTCACA  ATATACGTTT  GCCGTGCGCA  TGCCCGACAC  GTCCATGTCTG
601 CCGGTTATCG  AAAAGGGGGA  TTTGCTGGTG  GTCGAGCCGC  GTATGCGCCC
651 TGCGGACGAA  GACATCGTAC  TGATTGAACT  GTCCGACAAG  CGGCTGGTCG
701 TCAGCGACCT  TGTATCGAT  ATTGCGGGCA  GGATGCTGAT  TTATCAGACG

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1266

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751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGTCTG GAGTCAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTQKER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTNNH SDADGKALSM
151 RLTPRLLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVMTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

a790/m790 98.2% identity in 342 aa overlap

	10	20	30	40	50	60
a790.pep	MARRSKTFEEAAAEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
m790	MARRSKTFEEAAAEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
	10	20	30	40	50	60
a790.pep	70	80	90	100	110	120
	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTQKERITTQAYNEMTKSVAGSNSII					
m790	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTQKERITTQAYNEMTKSVAGSNSIV					
	70	80	90	100	110	120
a790.pep	130	140	150	160	170	180
	LNDVQGDTTINNHHHTHTNNHSDADGKALSMRLTPRLLSDRQAAAFARTGKLTGSFDLFA					
m790	LNDVQGDTTINNHHHTHTNNHSDADGKALSMRLTPRLLSDRQAAAFARTGKLTGSFDLFA					
	130	140	150	160	170	180
a790.pep	190	200	210	220	230	240
	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMPADE DIVLIELSDKRLVVAHLVID					
m790	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMCPADE IALIELSDKRLVVAHLVID					
	190	200	210	220	230	240
a790.pep	250	260	270	280	290	300
	IAGRMLIYQTGRPSEALDLP EGSVILGVVLESKNGLCPPHRQEGVLIRITAPDVMTVGTI					
m790	IAGRMLIYQTGRPSEAFDLP EGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVMTVGTI					
	250	260	270	280	290	300
a790.pep	310	320	330	340		
	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC					
m790	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTACTTGT TT
51  TGGTTTGT TTGTTTGT TTGTTTGT GTGTTTGT AGTGGGTCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCT CTTTGGATTG TTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GAGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GCGCGGAATT TACAAAAATC GGCATTTC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCGG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGTG CCCCAGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

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401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCTTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAAC TGCATTATGAG CGGTTTGTTC GGAATTCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT CGCTCGGGA CTGTATGAGA
851 AATATGTTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCAGATC ATCAGAAGGC GGCACCGGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TGCAGAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTGG ATGTTACTAA
1101 AAAGAAAAAT TCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCCTTG
1151 ACAGGCGCGC CTGGGTTTT GCGGCCGAG CGGTCGATAA TGAGAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCTTGG GCGGTGTTT AAGAGCCGTT GCTGACGGG GCTTGTGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGTGTGTCGG CGGTTATGAT
1351 TTTACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CGCGCTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAA ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCGGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GGCAGGAGCA TATAGTGAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGC ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTGCG CGCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCATATAT ATGTATAAGA
1901 TTATCGAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGCG AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAACG ACAATAAGA
2001 TCGGTGGTTT GTCGGTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG CCGGTACGG CGGTACGATT
2101 CGCGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGG ATGAAATGC CTGAAGGTGT GGTGACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAC GCCGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1 MVNYYSAMIK KILTTFCGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLOH
51 YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWGV ARAAVGNVVS GSVQSGASTI TQOVAKNFYL SSEKTETRFK
151 NEVLAYKIE QLSKDKILE LYFNQIYLQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LKAPSAYNP IVNPERAKLR QKIILNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNF RDSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMVFA VVLDVTRKKN VVIQLPGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGRW AVVQEPLLOQ ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGRG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPVVTA VYIGFDKPKS MGRAGYGGTI
701 AVPVVVDYMR FALKGKQKGG MKMPEGVVSS NGEYYMKERM VTDPLMLDN
751 SGIAPOPSRR AKEDDEAAVE NEQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGTTT TTTGGGTTTT GTGTATTGG AGTGGGTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGGAAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAATC GCGGATTTC
251 CAGAGGTGTT CCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGT CCCCAGCTG CCGTCGGCAA
351 TGTCTGTGCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

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1268

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451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTCA ATCAGATTGA CCTCGGTGAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCATAAAGATGT CCGAGATTG
601 ACTTTGCGCG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAT GCATTACGAG CGGTTGTTC GGAATATCGA
801 TCAGAGTGGG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAAGT GGCACCGGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGGAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGTGCCCGG CGGCAGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTT GCGGCCCGG CGGTCAATA TGAATAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTG TCTATTCCGC GGCATTATCT AAGGGATGA
1451 CGCGGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGT ACGCACAACA GTATATCCGG
1651 CGTTTCCGGT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGCGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTGCG CGCCAAATG CAACCTTGG TGGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATAT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGTGCCTTG
1951 GGAAGAACGG ATATTGCCG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TCGGTGGTTT GTCGGTTTAA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGC CTGAAGGTGT GGTACGACG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGCGGCGGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAC GCCGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

```

m791.pep
1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAMLAG LPKAPSAYNP IVNPERAKLR QKYLNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVROE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNF RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMVA VVLDTVKKKN VVIQLPGRR VTLDRRALGF AARAVNNERM
401 GEDRIRRGAV IRVKNNGRW AVVQEPILLQ ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRLAQM QPLVAGQNAF QAIDPRNAYI MYKIMQDVVR VGTARGAAL
651 GRDIAAGTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMEGVVSS NGEYMKERM VTDPLTLN
751 SGIAPQPSRR AKEDDGAEE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

g791/m791 97.3% identity in 805 aa overlap

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          10      20      30      40      50      60
g791.pep  MVNYYSAMIKKILTTFCGLFEGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          |||
m791      MVNYYSAMIKKILTTFCGLFEGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90     100     110     120
g791.pep  SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
          |||
m791      SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
          70      80      90     100     110     120

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1269

g791.pep	130	140	150	160	170	180
	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
g791.pep	190	200	210	220	230	240
	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPGKAPSAYNPIVNPERRAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPGKAPSAYNPIVNPERRAKLRQKYILNNMLE					
	190	200	210	220	230	240
g791.pep	250	260	270	280	290	300
	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEYKYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEYKYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
g791.pep	310	320	330	340	350	360
	RTDHQKAATEALRKALRNFDRGSSYRGAENYIDLKSKSEDVEETVSQYLSGLYTVDKMVPA					
m791	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLKSKSEDVEETVSQYLSGLYTVDKMVPA					
	310	320	330	340	350	360
g791.pep	370	380	390	400	410	420
	VVLDTVKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
m791	VVLDTVKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
g791.pep	430	440	450	460	470	480
	AVVQEPLQGGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPLQGGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
g791.pep	490	500	510	520	530	540
	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
g791.pep	550	560	570	580	590	600
	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
g791.pep	610	620	630	640	650	660
	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAALGRDIAKGTG					
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAALGRDIAKGTG					
	610	620	630	640	650	660
g791.pep	670	680	690	700	710	720
	TTNDNKDAWFVGFNPVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGQKG					
m791	TTNDNKDAWFVGFNPVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKGQKG					
	670	680	690	700	710	720
g791.pep	730	740	750	760	770	780
	MKMPEGVSSNGEYMKERMVTDPLGLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVSSNGEYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
g791.pep	790	800				
	RQDVQETPVLPSNTDSKQQQLDSLEX					
m791	RQDMQETPVLPSNTGSKQQQLDSLEX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACCTGCCG CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGGAAATCAT
201 CGGTATGTAT GGGGAGCAGC GGGCGGAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTATT AGCAGTGAAG AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAATTCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTG
601 ACTTTGGGCG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGCGTGTGA ATGAGGAATC GCATTACGAG CGGTTTGTTC GGGAAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTCGATC CGCGGCAGCA GCTACCGCGG TGCGGAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGCGCGCG CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGAGC GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGAATG AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTGCGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GGGCGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTTCGC ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTGCGC GCGCCAAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACCG ATATTGCCGG TAAACCGGTT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAAACCGATC CGGGCTTGAC GCTGACAAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGCG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGCGACGGC AGGCGGCGGA TGACGAAATC CGCCAAGATA
2351 TGCAGGAAAC GCCGCTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTCT TGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```
1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEORREFTRI GDFPEVLRNA VIAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMWPA VVLDVTKKKK VVIQLPGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDARTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPKGG
501 PNGSVWTPKN SDGRYSYIIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPVDTTA VYIGFDPKPS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKGG MKMPEGVVSS NGEYMKERM VTDPLGLTLDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*
```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

a791.pep	MVNYYSAMIKKILTTCTFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY
m791	MVNYYSAMIKKILTTCTFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAVGNVVS
	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAVGNVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPGKAPSAYNPIVNERAKLRQKYILNNMLE
	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPGKAPSAYNPIVNERAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFVYTTV
	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	RADHQKVATEALRKALRNFDGSSYRGAENYIDLKSEDVEETVSQYLSGLYTVDRKMVPA
	RADHQKVATEALRKALRNFDGSSYRGAENYIDLKSEDVEETVSQYLSGLYTVDRKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	AVVQEPQLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	AVVQEPQLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	KGMTASTVVNDAPISLPKGPNPNSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
	KGMTASTVVNDAPISLPKGPNPNSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	GVGYAQQYIIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	GVGYAQQYIIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	DRDGRRLRAQMQLVAGQNAQDAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	DRDGRRLRAQMQLVAGQNAQDAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRVGGTIAVPVWVDYMRFALKGKQKGG
	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRVGGTIAVPVWVDYMRFALKGKQKGG
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	MKMPEGVVSSNGEYYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV
	MKMPEGVVSSNGEYYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1 ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTTC
251 Cgggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGAAGAGGCG GGCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATT TAACTCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA GCTGCGTCCC GtatTttTA TAAAAACCG GcgcagGACC
551 TGACCAAAAC GCAGggcgGc aaactgacgg tactcgtccc cgccccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggtt cggcaaatTA ccccaagcg aaacggactg
701 attgttcag atattgaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1 MFRIVKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQAQ KLTVLVPAPF
201 YYSHPKSKR LRNKTNIIVL RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1 ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGCGCAGG CGGCTTCGAT TGGGCGGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTTG AACTGTATT TAACTCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA GCGCGTCCC GGTATTTTA TCAATACCC GCGCCAAGC
551 TGACCAAAAC GCAGCGGCA AACTGACGG CCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAA CCGATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1 MFRIIKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRNY IRKGEEAAT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAQ KLTARVPAPL
201 YYADHPKSKR LRNKTNIIVL RMGSALPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRNRNSGEVKAGGSTISQQLAK					

[illegible]

```
a792.seq
1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCGTATTGTG ACGGCAACAT CATACCTACG CGCGCCGTCG
101 CGCCCCATCG GACTGCGCTT ATGTGCGATG GGTAGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTGCGCAT GGATTACGCG TGGATGCCCT ACAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CGGGCAGCGG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATAGGCGCG
301 AACCAGAAC ACGGCAAAAT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAAG
401 GCGAAGAAGC GCGGATTACC GCAGATTGGA AAGCCGTTAC CGACAAGAGC
451 AGGATTTTTG AACTGTATTT AAACCTCAAT GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA CGCCGCTCCC GGTATTTTTA TCAAAATACC CGCCGCAAGC
551 TGACCAAAAC GACGGCGGCA GCAATTGACG TCGCGGCTCC GCGCCGCGTC
601 TACTAGCCCG ACCATCCGAA AAGCAAACGG CTCGCAACA AAACCAATAT
651 CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA
```

a792.pep

1	MFRIIKWLIA	LPVGIFIFFN	AYVYGNIIITY	RAVAPHRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WMFYKRISTN	LKKALIASED	ARFAGHGGFD	WGGIQNAIRR
101	NRNSGKVKAG	GSTISQQLAK	NLFNLNRSY	IRKGEEAAIT	AMMEAVTDKD
151	RIFELYLNSI	EWHYGVFGEA	AASRYFFQIP	AAKLTKQQAQ	KLTRVPAPL
201	YYADHPKSKR	LRNKNTIVLR	RMSGAEPLFS	DTD*	

	10	20	30	40	50	60
a792.pep	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR				
m792	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
a792.pep	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK				
m792	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK				
	70	80	90	100	110	120
	130	140	150	160	170	180
a792.pep	NLFLNRSRYYIRKGEEAAITAMMEAVT	DKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP				
m792	NLFLNRSRYYIRKGEEAAITAMMEAVT	DKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP				
	130	140	150	160	170	180
	190	200	210	220	230	
a792.pep	AAKLTQQAAKLTARVPAPLYADHPKSKRLRNKTN	IVLRRMGSAELPESD	TDX			
m792	AAKLTQQAAKLTARVPAPLYADHPKSKRLRNKTN	IVLRRMGSAELPESD	TDX			
	190	200	210	220	230	

g793.seq

1274

```

1  ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTTGTTTGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAAAGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTGTC CGTGCCATAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAG AATTAACG
501 CCATTACCCG ATGGGCAACC TGTTCACACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTCGAAC TTTCGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTG CCGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCAGCA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGCGAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAA CCGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGCGCG CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1201 ACTGCAAGTT TGTGAGAAA TTGGCGCAGG TGCGGCGCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATG GAGCCTGCTG CAATTGGCGC
1301 GCGCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCGCC GCAAGGCAAA CGCATATTCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGGC GGGTGCCTG GACGGTTTCG ATGTCGGCGC TAAACCCGGC
1501 ACGGCGCGCA AGTTCTGCAA CGGCGTTTAT GCCGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CGGCCAAAAA CCCCCTGTGT ATTGTGGCGG
1601 TAACCATCCA CGAACCAGCT GCCCAGCGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCGCCCTT TCAAAAAAAT TATGGCGCGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCGCACC AAGCCACTGA CCGCGCAGC CGTCAAAACA CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

```

g793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSAAQ LERLSELVDV PVDVLRNKLK QKGSFNIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFHAVIG FTDIDGKGQE GLELSLEDSL
201 YGEDGAEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDFNRPQ RADSEQRNRH
301 AVTMDIEPGS AIKPFVIAKA LDAGRTDLNE RLNTQPKYIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSARFGAEEM YDFYHELIG VMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGyGLQLSL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVGAKTG
501 TARKEVNGRY ADNKHVATFI GFAPARNPRV IVAVTIDEPT AHGYVGGVVA
551 GPPFKKIMGG SLNILGISPT KPLTAAAVKT PS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

```

m793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCCGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAAAC TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGC CCGACGGAGT CCCTGTTGTC CGTGCCATAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAA GCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAG AATTAACG
501 CCATTACCCG ATGGGCAACC TGTTCGACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTCGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTG CCGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCCGC CGGCGAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTG GCAATCAAA CCGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1275

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1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGCGGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCACCG
1451 GTACGGCGGG TCGGTGGGAC GGTTCGATG TCGCGCGGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCCGT TTTGCCCCCG CAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGCGGCGGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```

1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMIAVLFA GLIARGLYLQ
51  TVTYNLFKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHY PMGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEEVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRP RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELGIGV RMHSGFPGET
401 AGLLRNRRW RPIEQATMSF GYGLQLSLLQ LARAYTALH DGVLLPVSE
451 KQAVAPQGR IFEKSTAREV RNLMSVTPEP GGTGTAGAVD GFDVGAKTGT
501 ARKPFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

	10	20	30	40	50	60
g793.pep	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAMAVLFACLIARGLYLQTVTYNLFKEQ					
m793	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMIAVLFAGLIARGLYLQTVTYNLFKEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
g793.pep	GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
	130	140	150	160	170	180
g793.pep	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
	190	200	210	220	230	240
g793.pep	FTDIDGKGQEGLELSLEDSLYGEDGAEEVLRDRQGNIVDSLSPRNKAPQNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEDGAEEVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
	250	260	270	280	290	300
g793.pep	QRIQTLAYEELNKAVEYHQA KAGTVVVL DARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQA KAGTVVVL DARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
	310	320	330	340	350	360
g793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIM					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRD-THVYPSLDVRGIM					
	310	320	330	340	350	
	370	380	390	400	410	420
g793.pep	QKSSNVGTSKLSARFGAEMYDFYHELGIGV RMHSGFPGETAGLLRNRRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEMYDFYHELGIGV RMHSGFPGETAGLLRNRRWRPIEQATMS					
	360	370	380	390	400	410

1276

```

      430      440      450      460      470      480
g793.pep  FGYGLQLSLLQLARAYTALTHDGVLLPLSFEKQAVAPQGGKRIKKESTAREVRNLMVSVTE
          |||
m793      FGYGLQLSLLQLARAYTALTHDGVLLPLSFEKQAVAPQGGKRIKKESTAREVRNLMVSVTE
      420      430      440      450      460      470

      490      500      510      520      530      540
g793.pep  PGGTGTAGAVDGFVDVGAKTGTARKFVNTRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          |||
m793      PGGTGTAGAVDGFVDVGAKTGTARKFVNTRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
      480      490      500      510      520      530

      550      560      570      580
g793.pep  AHGYYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX
          |||
m793      AHGYYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX
      540      550      560      570      580

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAG CCGATGACCA GTAAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGTATGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCATAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGATG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGG AAACCTTTGA TTTGAAAAG AATTAAACG
501 CCATTACCCG ATGGCAACC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTGTTGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTGG CCGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CCGTCGAATA CCATCAGGCA AAAGCCGGA CCGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAACCGA TTTGAACGAA CGGCTGAATA
1001 CCGAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATCAGTTGGG CATCGGTGTG CGTATGCACT CGGCCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCCGT CAGCTTTGAA
1351 AAACAGCGCG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGGCGGG TGCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCCGT TTTGCCCCCG CAAAATATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGCATTTC
1701 CCGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYD MGNLFAHVIG FTDIDGRGQE GLESLSDSL
201 HGEDGAIEVVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNRRRW RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSTF
451 KQAVAPQKKR IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGARTGT
501 ARKFVNTRYA DNKHIAITFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

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a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMIAIVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMIAIVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
	PVDVLRNKLQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLQKGSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLESLSDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLESLSDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAKAGTVVVDLARTGEILALANTPAYDPNRPGRADSEQRRNR					
m793	QRIQTLAYEELNKAVEYHQAKAGTVVVDLARTGEILALANTPAYDPNRPGRADSEQRRNR					
	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQKRIKKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQKRIKKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	550	560	570	580		
	HGYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX					
m793	HGYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCTGCAAAAC AAGCCGGTCC GCCGCCCGG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTG CGCAAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTTCCCG CCTTCAAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTAAAGC AACGGTACGG
401 TAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCAC
451 CCCGTTTTC ATCAGGAAAA CCGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGCATC CGCAATATCA CGGGCGCCT GATGCTCGAC CACAGCCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTTCGCCG
601 TTTATGACGC CCCCAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTTCGC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTCCGTCAA AAAACTGATG CGCGCATCTT TTTCGGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCGTCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGT GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG CCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGGCGGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

g794.pep

```

1 VRFNHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNF
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAEKTFGS NYRWATEFKS NGTVNDGLTD GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVGSF DHFEADSGSP
201 FMTFPNPFTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLLRK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVAKNIISGG
501 DGWLDALKMC KERRA*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

m794.seq

```

1 GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAAC AAGCCGGCCC GCGGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCGCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GCGCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCTCCGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTGCGGACG AATTACCGCT GGGCGACCGA GTTTAAAGC AACGCTACGG
401 TAAACGACCG CACGCTTGAC GGAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTC AATCAGGAAA CCTGCTTGAT GCTCAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CCGCAGCCCC GACGATTTTC AAGCCGACAG CGGTTTCGCCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCGTGC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGT GAAAACGGTT CGGGCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG CCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

m794.pep

```

1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSQVFP

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1279

101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
 151 PVFNQENLLD AQKQLREOGI LNTGHLMLD HSLWGEVGSF DFEADSGSP
 201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
 251 AACPSIKKLM RASFSNTLKL LRGNIPECL GKPVGVRMFA LDELIRQSFT
 301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILT DMNKRSDNLIA
 351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLVLENGSGLSRKE
 401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
 451 TGTLLNNVRL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
 501 DGWLDKLMC KERRA*

g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRENHFIMVTIIIVIS	PANKPVRRPGVPTYP	ALPYNCFYVTDSPMN	FPKTAASLLLLL		
m794	VRLNHFIMIAIIIVIS	PANKPARRHSVPTYP	ALPYNCFYVTDSPMN	FPKTAASLLLLL		
	10	20	30	40	50	60
g794.pep	ASLAHAALDTGRIPQNE	IAVYVQELDSGKVIID	HRAGIPVNPASTMKL	VTAFAAFKTFGS		
m794	ASLAHAALDTGRIPQNE	IAVYVQELDSGKVIID	HRSDVPVNPASTMKL	VTAFAAFKTFGS		
	70	80	90	100	110	120
g794.pep	NYRWATEFKSNGTVND	GTLDGNLYWAGSGDP	VFNQENLLAVQRQ	LRDKGIRNITGR	MLD	
m794	NYRWATEFKSNGTVND	GTLDGNLYWAGSGDP	VFNQENLLDAQK	QLREOGILNITG	HMLD	
	130	140	150	160	170	180
g794.pep	HSLWGEVGSFDPHFEAD	SGSPFMTPPNPTMLS	SAGMVMVRAERNAAG	STDILTDPPLPHIFA		
m794	HSLWGEVGSFDPHFEAD	SGSPFMTPPNPTMLS	SAGMVMVRAERNAAG	STDILTDPPLPHIFA		
	190	200	210	220	230	240
g794.pep	QNNLKITASQAACPSV	KKLMRASFSGNTLKL	RGNIPECLGKPVGR	MFALDELIRQSFT		
m794	QNNLKITASQAACPSI	KKLMRASFSNTLKL	RGNIPECLGKPVGR	MFALDELIRQSFT		
	250	260	270	280	290	300
g794.pep	NRWLLGGGRISDGIGI	ADTPEGAQTLAVAH	SKPMKEILTMNKRSD	NLIARSVFLKLGSD		
m794	NHWLLGGGRISDGIGI	ADTPEGAQTLAVAH	AKPMKEILTMNKRSD	NLIARSVFLKLGSD		
	310	320	330	340	350	360
g794.pep	GKLPVSEQAASAVRREL	AVSGIDVADLVLENG	SGLSRKERV	TARMAQMLETAYF	SPFA	
m794	GKLPVSEQAASAVRREL	AVSGIDVADLVLENG	SGLSRKERV	TARMAQMLETAYF	SPFA	
	370	380	390	400	410	420
g794.pep	QDFIDTLPIAGTDGTL	RNRFKQSGGLRLK	TGTLLNNVRLAGY	WLGDKPM	AVVVIINSGR	
m794	QDFIDTLPIAGTDGTL	RNRFKQSGGLRLK	TGTLLNNVRLAGY	WLGDKPM	AVVVIINSGR	
	430	440	450	460	470	480
g794.pep	AVSLLPDLDNFVANNI	ISGGDGWLDKLMCK	KERRAX			
m794	AVSLLPDLDNFVANNI	ISGGDGWLDKLMCK	KERRAX			
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

a794.seq

1 GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTT
 51 CCCTGCAAAAC AAGCCGGCCC GCCGCCACAG CGTCCCACT TATCCGGCTT
 101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
 151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
 201 GCTCGATACA GGTCCGATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
 251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGCTC

1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTTC AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGACAGTAC CGACATCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAAAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCGG GATGTTTCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGCGCGCG AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAACT CGGCGGCGAC GGCAAACTGC CGCGCGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CAGGCTCTGC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCACAAATG TTGGAAACGG CTTATTTTCA
1251 CCCGTTTGCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG CGCGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGTTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

```
a794.pep
1  VRLNHFMIA I I I I YVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51  KTAASL L L L L ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTL DGNLYWAGSGD
151 PVFNQENLLA VQRLREQGI RNITGHLMLD HSLWGEVGS PDDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILT DMNKRSDNLI
351 RSVFLKGGD GKLPVSEQA ASAVRRELAV SGIDVADLV ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLLRK
451 TGTLLNVRL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDARLMC KERRA*
```

a794/m794 98.6% identity in 515 aa overlap

```
10 20 30 40 50 60
a794.pep VRLNHFMIA I I I I YVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP KTAASL L L L L
|||||
m794 VRLNHFMIA I I I I YVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP KTAASL L L L L
10 20 30 40 50 60

70 80 90 100 110 120
a794.pep ASLAHALDTGRIPQNEIAV YVQELDSGKV IIDHRSDVPV NPASTMKLVT AFAAFKTFGS
|||||
m794 ASLAHALDTGRIPQNEIAV YVQELDSGKV IIDHRSDVPV NPASTMKLVT AFAAFKTFGS
70 80 90 100 110 120

130 140 150 160 170 180
a794.pep NYRWATEFKS NGTVNDGTL DGNLYWAGSGD PVFNQENLLA VQRLREQGIRNITGHLMLD
|||||
m794 NYRWATEFKS NGTVNDGTL DGNLYWAGSGD PVFNQENLLA VQRLREQGIRNITGHLMLD
130 140 150 160 170 180

190 200 210 220 230 240
a794.pep HSLWGEVGS PDDFEADSGSP FMTPPNPTMLSAGMVMVRAE RNAADSTDILTDPPLPHIFA
|||||
m794 HSLWGEVGS PDDFEADSGSP FMTPPNPTMLSAGMVMVRAE RNAAGSTDILTDPPLPHIFA
190 200 210 220 230 240

250 260 270 280 290 300
a794.pep QNNLKITASQAACPSIKKLM RASFSDNTLKLRGNIPESCLGKPVGVRMFALDELIRQSFT
|||||
m794 QNNLKITASQAACPSIKKLM RASFSDNTLKLRGNIPESCLGKPVGVRMFALDELIRQSFT
250 260 270 280 290 300

310 320 330 340 350 360
a794.pep NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILT DMNKRSDNLI ARSVFLKGGD
```



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|||||
m794 NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
      310      320      330      340      350      360
      370      380      390      400      410      420
a794.pep GKLPAYSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
|||||
m794 GKLPAYSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
      370      380      390      400      410      420
      430      440      450      460      470      480
a794.pep QDFIDTLPIAGTDGTLRNRFKQSGGLRLKLTGT LNNVRALAGYWLGDKPMV VVIINSGR
|||||
m794 QDFIDTLPIAGTDGTLRNRFKQSGGLRLKLTGT LNNVRALAGYWLGDKPMV VVIINSGR
      430      440      450      460      470      480
      490      500      510
a794.pep AVSLLPDLNDFVANNIISGGDGWLDAKLMCKERRAX
|||||
m794 AVSLLPDLNDFVANNIISGGDGWLDAKLMCKERRAX
      490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

g900.seq

```

1  ATGccgTCTG AAATGCCGTC TGAACCGTGG CAGGCGGAGG TTCGACCGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATTCGC GCGCTTCTTT GCGCGCcttg cctGCAAAAT
151 CTCTTCGATT TCGGAAGGAT TAGAGGTCAA TCGGTTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCCGCTCG
251 CCCCAGCCA AGCCGTCGCG AAGCATTTCG GTAAATCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTGTGCTT TCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaag
551 cggccggcAa tgtcgcgcgc cATTTCgacg tgttgGATTT GGTCGCGCCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
701 CCGTTTTCCG CATTGGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCCGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCCTC GGGGTCGAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tggGTGGATT GGTAATCAT
901 CTCTGCTCG TGGCATTGTA TGATGCCGTG GTAATCGCG AGGAAGAGGA
951 AGGATTCGGT ATCGGGGTTT TCGCGCGCGC GGACGGCGGG GCGGATGGCG
1001 CCGACGTAGT TGCCAGATG CGGGGTGCCG GTGGTGGTTA CGCCGGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAAaA. gatgcgCCGA TTATACCGGA TTTGCCACAT ACATCCAGCC
1151 GacaACagaC TTTCCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng>

g900.pep

```

1  MPSEMPSETW QAEVRTALGL FQRADADRIA YFIQQFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAFQFCQ FGVDfRRRKf FRLAPsQAVG KHLRkFRFR
101 RRGEgFIDFK QRAfVGLfRL ARLfHVGNDF VDRfLGfFVv FPKRngIAVG
151 FGHfAfvQfD QHfDfVfVfDfH fGqGEEfLET VGEAAGNVAR hPDvLDLVAP
201 DGDFVGVEHQ NVGSHQNRIT EQTHfHTEIG VFLPVfRIGL NGGFVGVGAV
251 HQTlGGDAGQ NPVQLHHfGN VALAVEGGAL GVESAGKPSG GNGlGGLVNH
301 LLLVAFDDAV VIGEEEGfFG IGVLRADGG ADGADVVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMPsEREK DAPIIpdLPH TSSRQTFPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

m900.seq

```

1  ATGCCGTCTG AAACGCGGCA GCGGAGGTT CCGACGGCAT CGGGTTcATT
51  TCAACGGGCG GATGcCGACC GCATCgG.TA CTTTGTCCAA TAATTcGCGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTG

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1282

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151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CCGCGTTGAT TTTGCGCGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATCCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TGGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGCGCATG
551 TCGCGCGCCA TTTGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCCTGCCC GTTTTCTGCA
701 TTGCGCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
751 GGCAGTGATG CAGGTGAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGTG GTGCGTCCG GGTGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTGGGTAT
951 CGAGGTTTTG CGCGCGCGG ACGGCGGGG GATGCGGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGT GGTGGTTACG CCGGTGAGAA CTCGTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCGGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

m900.pep

```

1 MPSETRQAEV RTASGSFQRA DADRIXFYVQ *FACFFTRFR RACLQNLFDL
51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPR NGVAVGFGHF
151 ASVQTDQEFV VFIDFHFGQG BEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTAIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNLRLV
301 AFDDTVVIGE EEEFGIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

m900/g900

	10	20	30	40	50
m900.pep	MPSETRQAEVRTASGSFQRADADRIXFYVQXFACFFTRFR RACLQNLFDLRRVGGQ				
g900	MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ				
	10	20	30	40	50
	60	70	80	90	100
m900.pep	LVVAFARFGEFGVD FRRQKFFGFT PRQAVGKHFRKFHRFRRRGE GFVDFKQWAFVGLFRL				
g900	CVVAFACQFCQFGVD FRRRKPFRLAPSQAVGKHLRKFRRFRRRGE GFIDFKQRAFVGLFRL				
	70	80	90	100	110
	120	130	140	150	160
m900.pep	ARLFHIGDDEVDRLGFFVVFPRKNGVAVGFGHFASVQTDQEFDFVDFHFGQGEEFPEA				
g900	ARLFHVGNDVDRLGFFVVFPRKNGIAGVFGHFASVQTDQEFDFVDFHFGQGEEFLET				
	130	140	150	160	170
	180	190	200	210	220
m900.pep	VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICL				
g900	VGEAAGNVARHFDVLDLVAPDGHFVGVEHQNVGSHQNRITEQTHFHTIGVFLPVFRIGL				
	190	200	210	220	230
	240				


```

      240      250      260      270      280      290
m900.pep HGGFVGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH
          :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g900      NGGFVGVGAVHQTLGGDAGQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH
          250      260      270      280      290      300

      300      310      320      330      340      350
m900.pep LRLVAFDDTVVIGEEEGFGIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL
          | ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g900      LLLVAFDDAVVIGEEEGFGIGVLRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL
          310      320      330      340      350      360

      360      370      380
m900.pep AASMPSEREKDVPIIPDLPTSSRQQTFFPYX
          :|:|||||:|||||:|||||:|||||:|||||
g900      TAAMP SEREKDAPIIPDLPTSSRQQTFFPYX
          370      380      390

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a900.seq (partial)
1 GAGGTCGCGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51 CACGTACTTT GCCCAATAAT TCGCGTGCTT CTTTACGCGC TTTTTCGCGC
101 CCTGCTGCA AAATCTCTTC GATTTCGCAA GGTGCGCGG TCAGCTCGTT
151 GTAGCGTTCG CGCGGTTCCG CGAGTTCGCG GTTGATTTC CGCGCCAAAA
201 GTTTTTTTTC CTCGCCCAA GCCAAGCCGT CGGCAAGCAT TTTCGTAAAT
251 TCTGCCGTTT CAGACGCCGT GGAGAAAGCT TTGTAGATTT CAAACAGAGG
301 GCTTTCGTGC GGTCTTCTTC GTCGCCGCG CTCTTTCATA TTGGTGATGA
351 TTTTGTTGAC CGATTTTGG GTTTTTTTGT CGTTTTCCCA AAGCGGAATG
401 GTGTGTGCCG AGGATTTTGA CATTTTGCCT CGGTCCAAC CAACCAAGAG
451 TTCGACGTTT TCGTCGATTT TCACCTCGGG CAGTGTGAAG AGTTCGCCGA
501 AGCGGTGGTT GAAGCGGCCG CCAATATCGC GTGCCATTTC AACGTTGTGG
551 ATTTGGTCGC GACCGACTGG AACTTCATGG GCATTGAACA TGAGAAATGTC
601 GGCAGTCATC AGGATAGGGT AGCTGTACAA ACCATTTC ACGCCGAAAT
651 CGGGTCTTC CTGCCCGTTT TCCGCATTTG CGTGACCGG CGCTTTGTAG
701 GCGTGGGCGC GGTTCATCAA ACCCTTGGCG GTTGACGAGG TCAGAATTCA
751 GTTCAATTCC ATCACTTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801 GCTCGGGGTC GAGTCCGCG AGCAAGCCAAG TGGCGGCAAC GGCTTGGGTG
851 GATTGGTGA TCACTCCGG CTCGTGGCAT TTGATGCATC CGTGGTAATC
901 GGCAGGAAG AGGAAGGATT CGGTATCAGG GTTTTGCGCC GCGCGGACGG
951 CGGGCGGGAT AGCACCGACG TAGTTGCCCA GATGCGGGAT GCCGGTGGTG
1001 GTTACCGCGG TCAGAACTCG TTTTGTGCTC ATAAAAATGT CCTTGC GGCA
1051 TCAATGCCGT CTGAAAGGGA AAAAGATGCC CCGATTATAC CCGATTGGCC
1101 ACCTACATCC AGCCGACAA AGACTTTTCC ATATTTAA

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```

a900.pap (partial)
  1 EVRTALGLFQ RADTDRITYF AQ*FACFFTR FLRACLQNLF DLRRVGGQLV
51 VAFARFGEFG VDFRRQKFFC RFLSQAVGKH FRFRCFRRRR GESFVDFQOR
101 VAFGLRLRLR LFHIGDDFVD RLGFFVVFVP KRNGVAVGFG HFASVQTNQE
151 FDFVDFDFHG QCEEFEPAVV EAAGNIACHF NVLDLVATDW NFMGIEHNE
201 GSHEDRVAVQ THFHAEIGVF LPVFRICLHG GFVGGAHVQ TLGGDAGQNP
251 VQFHFFGNVA LVTEGGALGV ESAGKPSGNG GLGLLVNHLR LVAFDDTVVI
301 GEEEGFGIR LRADGAGD STDVVAQMRD AGGGYAGQNS FFAHKNVLAA
351 SMPSEREKDA PIIPDLPPTS SRQTFPY*

```

```

      10       20       30       40       50       60
m900.pep    MPSETROAEVRTASGSFORADADRIXFYVQXFACFFTRFRACLQNLFDLRRVGGQLVVA
             ||||| |·|||||:||:||||:||||| ||||| ||||| ||||| ||||| |||||
a900         EVRTALGLFQRADTDRIITYFAQXFACFFTRFLRACLQNLFDLRRVGGQLVVA
              10       20       30       40       50
            70       80       90      100      110      120

```


The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

m901.pep

1 MPDFSMSNLA VAFSITLAAG LFTVLXSGLV MFSKTPNPRV LSFGLAFAGG
51 AMVYVSLTEI PSKSEAEFAE IYDKDHAFAA ATMAFLAGMG GIALIDRIYP

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELPAA KRYSDGHETV
 251 YGLTGMMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq
 1 ATGCCCGATT TTTGATGTC CAATTGGGCC GTTGCCCTTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTCCA
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
 251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACCCGCATG AAACCTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
 401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTGCCAC ATTGGAAAT
 451 CCAGCAGTCG GGATGCCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
 501 GGAGGGCATT TCCATCGCCG CGCGGTTTA TTTTGCCACC CGCAGCCGTA
 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGCCCA GCCGTTGGGG
 601 GCGGCTTGG GCTATTTGGT TTGCGAGCG TTTTGTGCG CTGCCGTGTT
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTG TTGGCGTTGG
 701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACGTT
 751 TACGGCTGA CAATGGGCAT GCGGTGATT GCCGTAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep
 1 MPDFMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
 101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLP FLSPAVFGSV FGVIAGVMVF LALDELPAA KRYSDGHETV
 251 YGLTGMMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFMSNLA	VAFSITLAAG	LFTVLXSLV	MFSKTPNPRV	LSFGLAFAGG	AMVYVSLTEI
a901	10	20	30	40	50	60
	MPDFMSNLA	VAFSITLAAG	LFTVLGSLV	MFSKTPNPRV	LSFGLAFAGG	AMVYVSLTEI
m901.pep	70	80	90	100	110	120
	FSKSSEAF AEIYDKDHAF	AAATMAFLAGM	GIALIDRLVP	NPHE TLDAQD	PSFQESKRRH	
a901	70	80	90	100	110	120
	FSKSSEAF AEIYDKDHAF	AAATMAFLAGM	GIALIDRLVP	NPHE TLDAQD	PSFQESKRRH	
m901.pep	130	140	150	160	170	180
	IARVGMMAF	AITAHNFPEGL	ATFFATLEN	PAVGMPLALA	IAIHNIPEGI	SIAAPVYFAT
a901	130	140	150	160	170	180
	IARVGMMAF	AITAHNFPEGL	ATFFATLEN	PAVGMPLALA	IAIHNIPEGI	SIAAPVYFAT
m901.pep	190	200	210	220	230	240
	RSRKTWAC	LLSGLAEPLG	AALGYLVLP	FLSPAVFGSV	FGVIAGVMVF	LALDELPAA
a901	190	200	210	220	230	240
	RSRKTWAC	LLSGLAEPLG	AALGYLVLP	FLSPAVFGSV	FGVIAGVMVF	LALDELPAA
m901.pep	250	260	270			
	KRYSDGHETV	YGLTGMMAVI	AVSLVLFHF			
a901	250	260	270			
	KRYSDGHETV	YGLTGMMAVI	AVSLVLFHF			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCGG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTC
151 ACGCCGCGCC TGTTCCGCGT CCGGCATTTT GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCGATG
251 GCGCGGATGT GGTTCAAAAT GGCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGCGGCG TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTGGT CTCGGcgatg agttCGTAAC
501 gcGCTCGCC TTTGTACATT TGCGTGcgcg CGcgcccggtg aacggcaagGg
551 gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgGg gcagggttttg
601 atcgctcgte tgccaacceca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgG CTCGTCTGc
701 ATCagcGCGC TACCGGCTTG GACGTGCGAC ACTTTCTtgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcGg
801 catCCGCCAT CtgttcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCTT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQON GGSAPCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAIIF GDFGDGGQVL
201 IVVVPTQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDLRLPE SDVVTTRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTG GGGCGGTAGG
51  CGCACGCCCC ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTCGCGCGC CGCACTGTCC AAGCGGTTGA TTTACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTGCGCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTCCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTTTGTTTG
401 AGGACGCGTT GGGCTTTTGG CGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTC AGACGGCATT TGGTTTCGGC GATGAGTTCG TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCGTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCCGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTGGACATT GCAGACTTTT TAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTGATAAA ATAGCCCGG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902.pep

```

1  LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQCQTQRR
101 QNTVFGIMFQ IAEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT CLFAVGHF				
g902	MPSEPERRHGNTALPFPPIAARPTVGFSKGPKITGKCVLRRRIVQAVDFTPRLFAVGHF				
	10	20	30	40	50
	60				
m902.pep	70	80	90	100	110
	VDVPAYVFACDAHTGGVAVKRVY GADVQNSG GAFQCQTQRR QNTVFGIMFQ IAEPRPA				
g902	ADVPAVFACDAHTDGLTIKRVHGADVQNGGSAFCQTQRRXNAVFGIMLQIAEKPRPA				
	70	80	90	100	110
	120				
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASV				
g902	LRAAPYHDAVGGGLFEDGGGFLRRSDVAVDPGRDVQTAFGLGDEFVTRLAFVHLRARAPV				
	130	140	150	160	170
	180				
m902.pep	180	190	200	210	220
	DGKGGDAAI FGDGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGL				
g902	NGKGGNAAI FGDGDDGQVLIVVPTQTGFEGNGYARRLDHRLQNGGNQRLVLHQRATGL				
	190	200	210	220	230
	240				
m902.pep	240	250	260	270	280
	DIADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSIS				
g902	DVAHFLGGAHIDVDDL RPESDVVTRRI RHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
	250	260	270	280	290
	300				
m902.pep	300	310	320	330	340
	ERRVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLY				
g902	ERRIAGQHFAHRPTCAKRPTEAEGFVGNARHRRKCDGVVDKITADVHNGPAFQKSAPLY				
	310	320	330	340	350
	360				
m902.pep	IFX				
g902	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51 CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTCAAG ATAACCTGCA

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```
101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCAACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAACACCGG TGTTCCGGCT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTC CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTCGCTG CCGGTGCGTC CGTGGACGGC AAGGCGGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGTACCGG CTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATCTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAATCTC
951 GGCAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```
1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLRRTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCTQGRR
101 *NTVFGVMFQ IAEPRSALR AAPIYHNAVCG GLFEDGLGFL RRGNAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGNAAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *
```

m902/a902 94.7% identity in 360 aa overlap

m902.pep	10	20	30	40	50	60
	LHFQRIIKCS	EGIWAVGARPT	TVGFFGKSFK	ITCKHVLRRTV	QAVDFTTCL	FAVGHFVD
a902	LHFQRIIKCS	EGIWAVGARPT	TVGFFGKSFK	ITCKHVLRRTV	QAVDFTTCL	FAVGHFVD
	10	20	30	40	50	60
m902.pep	70	80	90	100	110	120
	VPAYVFACDA	HTGGVAVKRV	YGADVQNSG	GAFCTQGR	RQNTVFGIM	FQIAEPRPALR
a902	VPAYVFACDA	HTGGVAVKRV	HGSDVVQNS	GCTQGRRX	NTVFGVMFQ	IAEPRSALR
	70	80	90	100	110	120
m902.pep	130	140	150	160	170	180
	AAPYHNAVGG	GLFEDGLR	RSNAVDPDR	VDVQTAFG	FGEFVTRFA	FVHLRTRASVDG
a902	AAPYHNAVCG	GLFEDGLR	RGNAVDPDR	VQTAFGFN	QVVSRAFA	VHLRARASVDG
	130	140	150	160	170	180
m902.pep	190	200	210	220	230	240
	KGGDAIFGD	FGDDGQV	LMVVVPTQ	TGFEGNGY	ACRTDDGF	QNGGNQRLV
a902	KGNAAIFGD	FGDDGQV	LMVVVPTQ	TGFEGNGY	ARRFDHRL	QNGGNQRLV
	190	200	210	220	230	240
m902.pep	250	260	270	280	290	300
	ADFFSGTAHV	DVDKLRPK	ADVTRGIR	HLLRIASG	NLHGNNAA	FIGKIAAV
a902	ADFFSGTAHV	DVDKLRPK	ADVTRGIR	HLLRIASG	NLHGNNAA	FIGKIAAV
	250	260	270	280	290	300
m902.pep	310	320	330	340	350	360
	RVAGQHFHR	PTCAKISAK	SAERFVGN	ARHRRKCD	GVVDKIAA	DVHNGSAF
a902	RVAGQHFHR	PTCAKISAK	SAERFVGN	ARHRRKCD	GVVDKIAA	DVHNGSAF
	310	320	330	340	350	360

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```

a902      |||||
          RVAGQHF AHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

m902.pep    X
            |
a902        X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcg gatgaggCAA GCCCCTGCTT
51  TCCTATTTCT GAGGTGGaAT TGGTGGGTGA aGaaacggct aAATTCCGgt
101 tTGCCTcaaa ccaTGCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg ggcacatTAA TCAAAtcatG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TctgcgtccC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgCAG GACGTATTGC
351 AGCATTCCAA AACAAATTTC CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgtttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTA CTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCCTCGG TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCCG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGACAAC GGCCTAA AAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATTT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACC CGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACCGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGTTATATCG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GCGGCAACC TGCATTACGA TATATTTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatattt CAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51  LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL LNLRLDEQL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMPYVNYGRS IGGTPDEENF DHRKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQA VSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWRE TKS YIDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVIRGFDE MSLPAERGWY WRNDLSWQFK
451 PGHQLYL GAD VGHVSGQSAK WLSGQTLA GT AIGIRGQIKL GGNLHYDI FT
501 GRALKKPEYF QTKKWTGFPQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTTAACTG ATGCAAATGT
51  CCGTTTCGAG CAACCATTGG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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1290

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151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CaaCCACAGA ATATGGATTC GGAATCTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCAATC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAGAAC TGGCTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCAGT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTTCATATG ACGCGGTTTG GCGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAT CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCCGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAACAAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACCTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AYTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATT C AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCGCT ACACCGTTCG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCCG ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTTACA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NKFPLYRNR
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNVDYNGKQ
301 YQSSLAAERM LWRNRLHKT VGMKLWTRQT KYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGDI LPGTSRMKII
401 TASLDAAPF XLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYL ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL PAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKT V RKFSFLPSVL
          |:::| |:::| |:::| |:::| |:::|
g903      MATQVGGANSDEASPCFPISEVELVGEETAKFRFALNHA
          10      20      30

          70      80      90      100     110     120
m903.pep  MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI QPQNMDSGIL KLRVSAGEIG
          : : | : | : : : : : | : | : | : : | : : | : :
g903      LCQTHFVSGK L HAGDINQIMSLAQNAL IGRGYTTTRI LAAPQDLNSGK LQTLMPGYLR
          40      50      60      70      80      90

```


[illegible]

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAAC TG	ATGCCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	AAC TGGGATG	TGTTTAGGTT	CCAATAATT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGCTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTG	GGGAATTCTG	AAATTACGGG	TAGTCACAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	ATGGCCAGTAT	TAGTGCATTG	AATAACAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCGCGATGT	AGAGCAGGGC	TTGGAAAAAC	TGCGTCGTTT
501	GCCGAGTGTT	AAACACAGATA	TTCCAGATTAT	ACCGTCCGAA	GAGGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTTCAGT

1292

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601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCGTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAA CCGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAACCGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATT CAGCTCAATG GAACAAAACG CCTTGGGTTG
1301 CCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTGTAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```

1  MQRQQHIDAE LLTDANVRFE OPLEKNNYVL SEDETPCTRV NYISLDDKTA
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL OKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NKFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAER LWRNRFHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPGTSRMKII
401 TAGLDAAPF MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE LLTDANVRFE OPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL					
a903	MQRQQHIDAE LLTDANVRFE OPLEKNNYVL SEDETPCTRV NYISLDDKTAR KFSLPSVL					
	10	20	30	40	50	60
m903.pep	70	80	90	100	110	120
	MKETAFKTM CLGSNNLSRL OKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG					
a903	MKETAFKTM CLGSNNLSRL OKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG					
	70	80	90	100	110	120
m903.pep	130	140	150	160	170	180
	DIRYEEKRDG KSAEGSISAF NKFPLYRNK ILNLRDVEQ GLENLRLPSV KTDIQIIPSE					
a903	DIRYEEKRDG KSAEGSISAF NKFPLYRNK ILNLRDVEQ GLENLRLPSV KTDIQIIPSE					
	130	140	150	160	170	180
m903.pep	190	200	210	220	230	240
	EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL					
a903	EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL					
	190	200	210	220	230	240
m903.pep	250	260	270	280	290	300
	AHKTDLT DATGTETESGSR SYSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ					
a903	VHKTDLTDATGTETESGSR SYSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ					

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	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKTSVGMLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKTSVGMLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRGTMQRQSMPEENGDDIPGTSRMKIITASLDAAAPFMLGKQQFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYQNTLTWYFHPNHQFFYL					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYQNTLTWYFHPNHQFFYL					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCCGCGTC GGGGCCGCTg gaGACGATGG
51  CGACCGGCGC GCCGAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTTCCACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATAACCGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCGACC GCAGCGGCGC GCGCGGCCG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACCAAT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TCGCGCCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTCTGTTCA CACGCGgggac acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTACAG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CCGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTGGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCGGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRRFAV GAGGDDGDRR AADFFNPFQI CFGIGRCVV AFHADSRFAP

```



```

51 AGHGFVNRFA GFHRIARTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNIIOH LRTYARACRS RAGETVGRGN EGSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRSG
251 VMQVLELDV IGKDGIOFFT QFFRMQQTIG ANGAACHFVF VGRADAAAGR
301 ADFAAGNARC AGLVERDVVR QDQAGRGRDF QTAFDVPHAC RVQLVDFAQQ
351 GFGGNDNART DEAIQSFVQD TARNQAGNSF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITRY*

```

m904.seq

1	ATGATGCAGC	ACAATCGTTT	CTTCTCGGTC	GGGCGCGTG	GAGACGATGG
51	CGACCGGCGC	GCCGAGACT	TCTTCAATCC	GTTTCAATA	TGCTTTGGCG
101	TTTTCGGGCA	ATGCGCGTA	GTCCTTCAAG	CGAAAGTGG	ATTCGCGCCA
151	GCCGGGCGAT	GTTTCGTAAA	TCGGCTTGCA	GGTTTCCACC	GCATCGGAAC
201	CGCAAGCGAG	GATGTCGGTT	TGCGCGCGT	CGGGCAATTC	ATAGCCGACG
251	CAGATATTGA	TGTTTTCAAC	GTCCTCAGT	ACATCGAGTT	TAGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGGATGGA	CGGTTTTCAGG	GCGGGCGCAT
351	CAAACCGACC	GCAGCGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTAC	GCCTACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGC	TGGTATAGGC	TTTGCAGATG	CCCAAAACAT
501	AATCCAGCAT	TGAGGACCT	ACGCGCGCGC	CTGCGGAAGC	TGCGCCCGCC
551	AGACAGTTGG	ACGAGGTAAC	GAAAGGATAA	TGCGCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCGC	TTTTTGTTTT
651	TCTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGGCGC	AATGCGCGGC
701	GCGACTTTTT	CGATAACCCG	CATCAGCTCT	TCCGCTTTAA	CCGGCTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACATTGTA	ATAGGCAAGG	ACGGATCTCA
801	GTTTTTCACG	CAGTTTtYCA	GGATGACGCA	AATCGGCGCG	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCCG	GGCCGCTCGT
901	GCGGATTTTG	CCTTTGCCCG	GCG.ATcTTC	GCGGGCTTGG	TCGAGCGCGA
951	TGTGGTAAGG	CAGGATCAGC	GGGCAGGTCG	GCGCGATTTT	CAGACGGCCT
1001	TCGACGTTTT	TCACGCCTGC	CGCGTTTCAAC	TCGTCGATTT	CGCCCAACAG
1051	GGCTTTCGGG	GAGACGACAA	GCCCGCAACC	GATGAAGCAG	TCCAAACCTT
1101	CATGCAGGAT	GCCGCTCGGA	ATCAGGCGCA	AAATGGTTTT	TTTGGCGCGG
1151	ACAACCAAGG	TATGGCCCGC	ATTGTGGCCG	CCTTGAAGC	GCACCaCGCC
1201	GCCGCTTTCT	TCCGCCAGCC	AGTCAACGAT	TTTACCTTTA	CCCTCGTCGC
1251	CCCACGTGTC	GCCGATTAsT	ACAACATTTT	TAGCCATAGC	CATATAACCT
1301	ATCGATATTA	A			

m904 . pep

1	MMQHNRRFSV	GAGGDDGDRR	AADFFNPFQI	CFGVFGQCAV	VLHAESGFAP
51	AGHGFVNRLA	GFHRIGTARQ	DVGFAAVGQF	IADADIDGFN	AVHYIEFSNT
101	HTGNAVLDLG	AFQGGGIKPA	AAACASGYRT	EFVSAFCQTY	AYFVEQFGRE
151	RARTDARGIG	FDDAQNTIQH	LRTYARACRS	CARQTVGRGN	EGISAVVDVQ
201	QRTLRAFQKQ	PFAVFVFLVQ	HAGHVGNHRR	NARRDFFDNR	HHVFRFNRLG
251	IVQMLQLDIV	IGKDGIQFFT	QFXRMQQIGG	ANGAACHFVF	VGRADAAAGR
301	ADFAFAAXIF	AGLVERDVVR	QDQRAQRDRF	QTAFDVFMAC	RVQLVDFAQQ
351	GFGGDDNART	DEAVQTFMQD	AARNQAQNGF	FAADNQGMAR	IVAALAEHHA
401	AGFRQPVND	FTFTLVAPLC	ADXYNIESH	HITVRY*	

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

m904/g904

	10	20	30	40	50	60
m904.pep	MMQHNR	RFSV	GAGDDG	DRRAAD	FFNP	FQICPGVFGQCAVVLHAESGFAPAGHG
	10	20	30	40	50	60
g904	MMQHNR	RF	AVGAGGDDG	DRRAAD	FFNP	FQICPGIGRQCVVAFHADSRFAPAGHG
	10	20	30	40	50	60
	70	80	90	100	110	120

1295

m904 . pep	GFHRI GTARQDVGF AAVGQFIADADIDGFNAVHYIEFSNTH TGNV DLDGAFQGGGIKPA
g904	GFHRI RTARQDVGF AAAWQFVADADIDGFNAVHYIEFGNAHTGNV DLDGAFQGGGIKPA
	70 80 90 100 110 120
m904 . pep	130 140 150 160 170 180
	AAACASGYRTEFVS AFCTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAARAAGYRTEFVSALRQTCA YFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904 . pep	190 200 210 220 230 240
	CARQTVGRGNEGISAVVDVQORTLRAF KQOFFAVFVFLVQHAGHVG NHRNRARRDFFDNR
g904	RAGETVGRGNEGVS AVVDVQORTLRAF KQOFFAVFVFPVQHAGHVG NHRNRARRDFFDNR
	190 200 210 220 230 240
m904 . pep	250 260 270 280 290 300
	HHVFRFNRLGIVQMLQLDIVIGKDG IQFFTQFXRMQQIGGANGAACHFV FVGRADAAAGR
g904	HHVFRFNRS GVMQVLELDVVIGKDG IQFFTQFPMQQIGGANGAACHFV FVGRADAAAGR
	250 260 270 280 290 300
m904 . pep	310 320 330 340 350 360
	ADFAFAARIFAGLVERDVVRQDORAGRRDFQTAFDV FHACRVQLVDF AQQGFGGDDNART
g904	ADFAFAARCFAGLVERDVVRQDORAGRRDFQTAFDV FHACRVQLVDF AQQGFGGGNDNART
	310 320 330 340 350 360
m904 . pep	370 380 390 400 410 420
	DEAVQTFMQDAARNQAONGFFAADNQGMARIVAAL EAHHAAGFFRQPVNDFTFTLVAPLC
g904	DEAIQSFVQDTARNQAONGFFAADQGMARIVAAL EAHDAAGFFRQPVNDFTFTLVAPLC
	370 380 390 400 410 420
m904 . pep	430
	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTCGCTCCA
151	ACCGGGCATG	GTTTCGTAAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	GCCGTCCTAT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACCAGCC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGGCCT	ACGCCCGCGC	CTGCCGAAGC	CGCGCCGGCG
551	AGGCAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCCG	TTTTTGT TTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGGCGT	AATGCGCGGC
701	GCGACTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTACAG	CAGTTTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCGT
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

1296

```
951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGAAGC GCACCAGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

a904.pep

```
1 MMQHNRF FAV GAGGDDGDRR TADFFNPFI CFGIGR*CVV AFHAESGFAP
51 TGHGFVNRLA GFYRIRARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVLDLD AFQGGGKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQQ FFAVFVFTVQ HAGHVGNNRR NARRDFFDNR HHVFRFHLRG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQAGRRDF QTAFDVFHAC RVQLVDFQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMTR IVAALEAHHA
401 SGFFRQPVND FTTLVAPLC ADYNNIFSHS HITXRY*
```

m904/a904 91.3% identity in 436 aa overlap

m904.pep	10	20	30	40	50	60
	MMQHNRF	SVGAGGDDGDRRAADFFNPFI	CFGVFGQCAVVLHAESGFAPAGHGFVNRLA			
a904	10	20	30	40	50	60
	MMQHNRF	FAVGAGGDDGDRRTADFFNPFI	CFGIGRXCVAFAHAESGFAPTGHGFVNRLA			
m904.pep	70	80	90	100	110	120
	GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNTH	TGNAVLDLDAFQGGGKPA				
a904	70	80	90	100	110	120
	GFYRIRARQDVGFAAVGQFVADADIDGFNAVHYIEFGNTH	TGNAVLDLDAFQGGGKPA				
m904.pep	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIQHLRTYARACRS					
a904	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTCSDFEQFGRERARTDARGIGFDDAQNIQHLRAYARACRS					
m904.pep	190	200	210	220	230	240
	CARQTVGRGNEGISAVVDVQORTLRAFQQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR					
a904	190	200	210	220	230	240
	RAGEAVGRSNEGVS AVVDVQORTLRAFQQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR					
m904.pep	250	260	270	280	290	300
	HHVFRFNLGIVQMLQLDIVIGKDGIOFFTQFXRMQIGGANGAACHFVFVGRADAAAGR					
a904	250	260	270	280	290	300
	HHVFRFHLGIVQMLQLDVVISKDGIOFFTQFFRMQIGGANGAACHFVFVGRADAAAGR					
m904.pep	310	320	330	340	350	360
	ADFAFAAXIFAGLVERDVVRQDQAGRRDFQTAFDVFHACRVQLVDFQQGFGGDDNART					
a904	310	320	330	340	350	360
	ADFAFAARCFSGLVERDVIRQDQAGRRDFQTAFDVFHACRVQLVDFQQGFGGDDNART					
m904.pep	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFFTTLVAPLC					
a904	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFFTTLVAPLC					

1297

```

m904.pep      ADXYNIFSHSHITYRYX
              || ||||| |||| |||
a904          ADYYNIFSHSHITXRYX
              430

```

g906.seq not found yet

g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51  GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACTTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAACAAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFSG FKPNPWDAAS FWELKNYANP YPGSASAALD
51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTgcaAC GCCGCCGCCT
51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGCCA AGATTCTGCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51  GTTGTGTGCC GCCGGTGCCT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGCCA AGGTTCTGCC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTkTGG AAAAActACA TCGGCAAAACC GGCGCACAAc
451 CTGTTGACA TCCGCACCAA CTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLSPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAlSGVGA RGLMQVMPXW KNYIGKPAHN

```


1298

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGLSGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPPRL					
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
m907	VFDNPKEGERWLSAMSARLARFVPEEBERRRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
g907.pep	RARIIS					
m907	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

1	ATGAAAAAAC	CGACCGATAC	CCTACCCGTC	AATCTGCAAC	GCCGCCGCGCT
51	ATTGTGTGCT	GCCGGCGCGC	TGTTGCTCAG	CCCGCTGGCA	CAAGCCGCGC
101	CGCAACGTGA	AGAAACGCTT	GCCGACGATG	TGGCTTCCGT	GATGAGGAGC
151	TCTGTCGGCA	GCATAAATCC	GCCGAGGCTG	GTGTTGACA	ATCCGAAAGA
201	GGGCGAGCGT	TGGCTGTCCG	CGATGTCTGC	TCGGTTGGCA	AGGTTCTGTC
251	CCGATGAGGA	GGAGCGGCGC	AGGCTGCTGG	TCAATATCCA	GTACGAAAGC
301	AGCCGGGCGC	GTTTGGATAC	GCAGATTGTG	TTGGGGCTGA	TTGAGGTGGA
351	AAGCGCGTTC	CGCCAGTATG	CAATCAGCGG	TGTCGGCGCG	CGCGGCCTGA
401	TGCAGGTTAT	GCCGTTTGG	AAAACTACA	TCGGCAAACC	GGCGCACAAC
451	CTGTTCGACA	TCCGCACCAA	CCTGCGTTAC	GGCTGTACCA	TCCTGCGCCA
501	TTACCGGAAT	CTTGAAAAAG	GCAACATCGT	CCGCGCACTC	GCCCGTTTGA
551	ACGGTAGCCT	CGGCAGCAAT	AAATATCCGA	ACGCCGTTTT	GGGCGCGTGG
601	CGCAACCGCT	GGCAGTGGCG	TTGA		

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

1	MKKPTDTLPV	NLQRRRLCA	AGALLSPLA	QAGAQREETL	ADDVASVMRS
51	SVGSINPPRL	VFDNPKEGER	WLSAMSARLA	RFVPDEEERR	RLLVNIQYES
101	SRAGLDTQIV	LGLIEVESAF	RQYAISGVGA	RGLMQVMPFW	KNYIGKPAHN
151	LFDIRTNLRY	GCTILRHYRN	LEKGNIVRAL	ARFNGLSGSN	KYPNAVLGAW
201	RNRWQWR*				

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPPRL					
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQREETLADDVASVMRSSVGSINPPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEERRRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
a907	VFDNPKEGERWLSAMSARLARFVPEEERRRRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

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	70	80	90	100	110	120
m907.pep	130	140	150	160	170	180
	ROYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
a907	ROYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180
m907.pep	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

g908.seq

```

1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTGCG GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

g908.pep

```

1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNQTAT LFPIIREQVK PDSIVYTDY RSYDVLDVSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

m908.seq

```

1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGA AATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTGCG GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATATAC GGATTGTTAT CgTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

m908.pep

```

1  MRKSRLSQYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNQTAT LFPIIREQVK PDSIVYTDY RSYDVLDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

g908/m908

	10	20	30	40	50	60
g908.pep	MXKSRLSRYKQNKLI GLFV AGVTARTAAELVGIN KNTAAY DFHRLRLLIYQNGPHLEMF					

1300

```

      |||||:||||| |||:||||| |||||:||||| |||||:|||||
m908  MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMF
      10      20      30      40      50      60

      70      80      90      100     110     120
g908.pep GEVEADESYFGGQKRGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLPPIIREQVK
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m908  GEVEADESYFGGQKRGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLPPIIREQVK
      70      80      90      100     110     120

      130     140     150     160
g908.pep PDSIVYTD CYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m908  PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

```

a908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAATAAAC TCATTGAGCT
51  ATTTGTCCGA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGA AATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

```

a908.pep
1  MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNNTAAY YFHLRLLLIY
51  QNSPHLEMF GEVEADESYF GGQKRGKRG GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LPPIIREQVK PDSIVYTD CYRSYDVLDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

m908/a908 98.2% identity in 166 aa overlap

```

      10      20      30      40      50      60
m908.pep MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMF
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a908  MRKSRLSQYKQXKLIELFVAGVTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMF
      10      20      30      40      50      60

      70      80      90      100     110     120
m908.pep GEVEADESYFGGQKRGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLPPIIREQVK
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a908  GEVEADESYFGGQKRGKRGGAAGKVAVFGLLKRNGKVYTVTVPNTQTATLPPIIREQVK
      70      80      90      100     110     120

      130     140     150     160
m908.pep PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a908  PDSIVYTD CYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

```

g909.seq (partial)
1  atgcgtaaaa ccgtacttat cCTgaccatc tccgcgcgcc tttgtcggg
51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
101 caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```


1301

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
 201 caacccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
 251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
 301 acgggggagg ggaagcgatc ggcgagg..

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
 51 KKVDCDEYGG ERRAVLNqK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
 101 TGEgKRSAR..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTGTCTGGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACC
 201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AACCAAAGTT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

1 MRKTFLEFLTA AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQT GNADEEHRQ HWQKPKFQNR *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	KKVDCDEYGG
	10	20	30	40	50	60

	70	80	90
m909.pep	ERHAVLPNQT	GNADEEHRQ	HWQKPKFQNRX
	:		:: :: : :
g909	ERRAVLNQK	RGKPTRRAA	TLGKPSFRAR
	70	80	90

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTGTCTGGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACC
 201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AGCCCAAATT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

1 MRKTFILILMT AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
 51 KNMNYNQYRP ERHAVLPNQT GNADEEHRQ HWQKPKFQNR *

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
a909	MRKTFILILMT	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQ	TGNNADEEHRQHWQKPKFQNRX	
a909	ERHAVLPNQ	TGNNADEEHRQHWQKPKFQNRX	
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCACACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATG GGTAAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLSAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

g910/m910

	10	20	30	40	50	60
g910.pep	MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW					
m910	MKKLLLAADVSLSAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDHW					
	10	20	30	40	50	60
	70	80	90			
g910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
m910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATG GGCACACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTTG TCTTACCCCG
251 ACCTGAAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

a910.pep


```

      10      20      30      40      50      60
m910.pep  MKKLLLAAVVSLSAAGFAGDSAEERQIYGDPHFEQNRRTKAVKMLEQRGYQVYDVDADDHW
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a910      MKKLLLVAVVSLSAATAFAGDSAEERQIYGDPHYEQNRRTKAVKMLEQRGYQVHDVDADDHW
          10      20      30      40      50      60

      70      80      90
m910.pep  GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a910      GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          70      80      90

```

q911.seq

1	ATGAAAAAGA	ACATATTGGA	ATTTTGGGTC	GGACTGTTCC	TCTTGATCGG
51	CGCGGCGGCG	GTTGCTTTTC	TCGCTTTCGG	CGTGGCGGGC	GGCGCGGGGT
101	TCGGCGGTTT	GGACAAAACT	TACGCCGTTT	ATGCCGATTT	CGGCGACATC
151	GGCGGTTTGA	AGGTCAATGC	CCCCGTCAA	TCCGAGGGCG	TATTGGTCGG
201	GCGCGTCGGC	GCTATCGGGC	TTGACCCGAA	ATCCTATCAG	GCGAGGGTGC
251	GCCTTGATTT	GGACGGCAAG	TATCAGTTCA	GCAGTGACGT	TTCGCGCAA
301	ATCCTGACTT	CGGGACTTTT	GGCGGAACAG	TACATCGGGC	TGCAGCAGGG
351	CGGCGATACG	GA AAACTTTG	TCGCGCGCGA	CACCATCTCC	GTAACCTAGTT
401	CTGCAATGGT	TCTGAAAAAC	CTGATCGGTA	AATTATGAC	CAGCTTCGCC
451	GAGAAAAACG	CTGAGGGCGG	CAATGCGGAA	AAAGCCGcaq	aAtaa

g911.pep

```

1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFDDI
51  GGLKVNAPVK SAGVLVGRVQ AIGLDPKSYQ ARVRLDLGDK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNAEGGNAE KAAE*

```

m911.seq

1	ATGAAGAAGA	ACATATTGGA	ATTTTGGGTC	GGACTGTTGG	TCTTGATTGG
51	CGCGGCGCGG	GTTGCTTTTC	TCGCTTTCCG	CGTGGCCGGC	GGTGC GCGGT
101	TCGGCGGTTC	GGACAAAACT	TACGCCGTTT	ATGCCGATTT	CGGCGACATC
151	GGCGGTTTGA	AGGTCAATGC	CCCGTCAAA	TCCGAGGCG	TATTGGTCGG
201	GCGCGTCGGC	GCTATCGGAC	TTGACCCGAA	ATCCTATCAG	GCGAGGGTGC
251	GCCTCGATTT	GGACGGCAAG	TATCAGTTCA	GCAGCGACGT	TCCGCGCCAA
301	ATCCTGACTT	CGGGACTTTT	GGCGAGCAG	TACATCGGGC	TGCAGCAGGG
351	CGGCGACACG	GAAAACTTTC	CTCGCGCGCA	CACCATCTCC	GTAACCAATT
401	CTGCAATGGT	TCTGAAAAAC	CTTATCGGCA	AATTTCATGAC	GAGTTTGTCC
451	GAGAAAAATG	CCGACGGCGG	CAATGCGGAA	AAAGCCGCGC	AATAA

m911.pcp

```

1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSQA
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF_911.ng) from *N. gonorrhoeae*:

g911/m911

10 20 30 40 50 60

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNABGGNAEKAEX
          |||||||||||||||||||||||||||||||||||||||||||||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1  ATGAAAAAGA ACATATTGGA ATTTGGGTC GGACTGTTTC TCCTGATTGG
51  CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTT GCACAAACT TACGCCGTTT ATGCCGATT CCGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGACGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTG GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCTGACTT CGGACTTTT GGGCGAGCAG TACATCGGCG TGCAGCAGGG
351 CCGCGACACG GAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGAAAC CTTATCGGCA AATTCATGAC GAGTTTGGCC
451 GAGAAAATG CCGACGGCG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

          10      20      30      40      50      60
m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          |||||||||||||||||||||||||||||||||||||||||||||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTgAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTgGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```


g912.pap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

m912.seq

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

m912.pep

1 MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQATQVLS ILKNGDANTA
51 RQKABAYAIP YFDFQRTMAL AVGNPWRITAS DAQKQALAKE FQTLRLRTYS
101 GTMLKLKLAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKRYTYNVAI EGASLVTVYR NQFGEIIKAK GVDGLIAELK AKNGGK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

q912/m912

	10	20	30	40	50	60
g912.pep	VKKSS	FISALGIGILSIGMA	FASPADAVGQIR	QATQVLTILKSGDAASARPKAEAYAVP		
	:	:	:	:	:	:
m912	MKKSSLISALGIGILSIGMA	FAPAADAVSQIR	QATQVLSILKNGDANTARQKAEAYAI			
	10	20	30	40	50	60
	70	80	90	100	110	120
g912.pep	YFDFQ	RM TALAVGNPWR	TASDAQKQALAKEFQ	TLLIRTYSGTMLKPK	NATNVN	KDNP
m912	YFDFQ	RM TALAVGNPWR	TASDAQKQALAKEFQ	TLLIRTYSGTMLK	LKNANVN	KDNP
	70	80	90	100	110	120
	130	140	150	160	170	180
g912.pep	KGKKEI	IVRAEVGIPGQK	PVNMDFTTYQSGG	KYRTYNVAIEG	TSLVTVYRNQ	FGEIIKAK
	:	:				
m912	KGKKEI	IVRAEVGVPGQK	PVNMDFTTYQSGG	KYRTYNVAIEG	ASLVTVYRNQ	FGEIIKAK
	130	140	150	160	170	180
	190					
g912.pep	GIDGLIAELKAKNGGKX					

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m912
 190
 GVDGLIAELKAKNGGKX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

a912.seq
 1 ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
 51 CGGCATGGCA TTGCGCGCCC CTGCGGACGC GGTAACCAA ATCCGTCAAA
 101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
 151 CGCCAAAAAG CCGAAGCCTA TGCATTCCG TATTTCGATT TCCAACGTAT
 201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
 251 AACAAAGCGTT GGCCAAAGAA TTCAAACCC TGCTGATCCG CACCTATTCC
 301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
 351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
 401 TACCCGGGCA AAAACCGGTC AACATGGACT TCACCACCTA CCAAAGCGGC
 451 GGTAAATACC GTACTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
 501 CGTGTACCGC AACCAATTCC GCGAAATTAT CAAAGCGAAA GCGGTGGACG
 551 GACTGATTGC CGAGTTGAAG GCTAAAACG GCAGCAAGTA A

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

a912.pep
 1 MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQATQVLS ILKSGDANTA
 51 RQKAEAYAIP YFDFQRTAL AVGNPWRTAS DAQKQALAKE FQTLIRTYQS
 101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
 151 GKYRTYNVAI EGASLVTYR NQFGEIIRAK GVDGLIAELK AKNGSK*

m912/a912 98.0% identity in 196 aa overlap

m912.pep	10	20	30	40	50	60
	MKKSSLISALGIGILSIGMAFAAPADAVSQIRQATQVLSILKNGDANTARQKAEAYAIP					
a912	MKKSSFISALGIGILSIGMAFAAPADAVNQIRQATQVLSILKSGDANTARQKAEAYAIP					
	10	20	30	40	50	60
m912.pep	70	80	90	100	110	120
	YFDFQRTALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN					
a912	YFDFQRTALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN					
	70	80	90	100	110	120
m912.pep	130	140	150	160	170	180
	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEIIRAK					
a912	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEIIRAK					
	130	140	150	160	170	180
m912.pep	190					
	GVDGLIAELKAKNGGKX					
a912	GVDGLIAELKAKNGSKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

g913.seq
 1 atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCGCG
 51 CCTGCAATT GCAGAAACCC GCCCGCCGA CCTTATGAA GGCTACAACC
 101 GCGCGGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTGCCCCCT
 151 GCGCGCGCG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCGGCGT
 201 GTCCAATTTT TTAACAACC TGCAGGACGT GGTCAAGTTT GGCAGCAATA
 251 TCTTGCGTTT GGacatCAAA cgcgcAAGcg aAGACCTcgT CCGcgtcggc
 301 atCAATACCA CCTTCGGTTT GgGcgGGCTC ATTGATATTG CCGGcgGgGg
 351 cggcggtccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
 401 GctgGAAAAa cagcaATTAT TTCGTgttgC CCGtcttagg cccgtccacc

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```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcgttttc catacccctg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggc ctcctcgatt tgaccgacag TCtggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTT ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

```

g913.pep
1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVTP KPVRAVSNNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGWNKSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWTG AAAAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAEE
251 PAVHEDSVSE TQAEAAAGEAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

```

m913.seq
1 ATGAAAAAAA CCGCCTATGC CTCCTCCTG CTGATCGGGT TCGCTTCCGC
51 CCTGTCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTGCCCCCT
151 GCGCGCGCGG GCTACGCAA AGTTGCGCCG AAACCCGTCG GCGCCGCGCT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCAGCTTC GGCAGCAATA
251 TCTTGCGCTT GGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGCGCGCGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTGTC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGgTACGGAA GATAACATCG
701 ACATCGACGA ATTGCTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

```

m913.pep
1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVAP KPVRAVSNNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWNKSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWTG AVSAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

```

g913/m913
          10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVTP
          |||||:|||||
m913      MKKTAYAFLLLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVAP
          10      20      30      40      50      60

          70      80      90     100     110     120
g913.pep  KPVRAVSNNFFNNLRDVVSFSGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||||
m913      KPVRAVSNNFFNNLRDVVSFSGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP
          70      80      90     100     110     120

```


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	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPVHEDSVSETQAEAAAGEAETQPGTQPX					
m913	VESAETGAAETAQEDSVSETQAEAAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

a913.seq

1	ATGAAAAAA	CCGCCTATGC	CTTCCTCCTG	CTGATCGGGT	TCGCTTCCGC
51	CCCTGCATTT	GCCGAAACCC	GCCCCGCCGA	CCCTTATGAA	GGCTACAACC
101	GCGCCGTTTT	CAAATCAAC	GACCAAGCCG	ACCGCTACAT	TTTCGCCCTT
151	GCCGCGCGCG	GCTACCGCAA	AGTTGCGCCG	AAACCCGTCC	GCGCCGGCGT
201	GTCCAATTTT	TTTAACAACC	TGTGCGACGT	GGTCAGCTTC	GGCAGCAATA
251	TCTTGCGCTT	AGACATCAAA	CGCGCAAGCG	AAGACCTTGT	CCGCGTCGGT
301	ATCAACACCA	CTTTCGGTTT	GGGCGGGCTT	ATCGACATCG	CCGGCGCGGG
351	CGGCATTCCC	GACAATAAAA	ACACCTTGGG	CGACACGTTT	GCTTCGTGGG
401	GATGGAAAAA	CAGCAATTAT	TTCGTGTTGC	CCGTCTTAGG	GCCGTCCACC
451	GTCCGCGACG	CGCTCGGCAC	GGGTATTACC	TCCGTTTATT	CGCCCAAGAA
501	TATCGTCTTC	CGCACCCCTG	TCGGACGCTG	GGGCACGACT	GCCGTATCCG
551	CCGTCAGTAC	GCGCGAAGGC	CTGCTCGATT	TGACCGACAG	TCTGGACGAA
601	GCCGCCATCG	ACAAATACAG	CTACACGCGC	GACCTCTATA	TGAAAGTCCG
651	TGCGCGGCAG	ACCGGTGCAA	CACCTGCCGA	AGGTACGGAA	GATAACATCG
701	ACATCGACGA	ATTGGTCGAA	AGTGCCGAAA	CCGGCGCGGC	GGAAACTGCC
751	GTTCAAGAAG	ATTCCGTATC	CGAAACACAG	GCAGAAGCAG	CAGGGGAAGC
801	CGAAACGCAA	CCTGGAACAC	AACCTGGAAC	ACAACCTTAA	

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

a913.pep

1	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP
51	AARGYRKVAP	KPVRAGVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG
101	INTTFGLGGL	IDIAGAGGIP	DNKNTLGDTF	ASWGWKNSNY	FVLPVLPST
151	VRDALGTGIT	SVYSPKNIVE	RTPVGRWGTT	AVSAVSTREG	LLDLTDSLDE
201	AAIDKYSYTR	DLYMKVRRAR	TGATPAEGTE	DNIDIDELVE	SAETGAAETA
251	VQEDSVSETQ	AEAAAGEAETQ	PGTQPGTQP*		

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLLLIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLLLIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVRAGVSNFFNNLCDVVSFSGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGIP					
a913	KPVRAGVSNFFNNLCDVVSFSGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTCGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCG
451 taggctTCGA CGATTTTTTG CACCAGAGGA TGCCGACAA CGTCTCGCC
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCAATTGT TCGGGCGTg tgTtttGcgC TTCGTGAGG ATGATGTATG
701 CGCCGTTGag cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPADF RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCKRFD*CI GWIDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTCGACGAT TTTTGCACC AAAGGATGCC GGACAACGTC
501 TCGCCGGTAA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTGTATGT TTTTGGGCAG GTCGATTTGG
601 CTGGTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGGTCAG
651 GAACATTTTC ATTTGTTTCG GCGTGGTGT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAAGCTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPADF RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCKRFDXCI GWIDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```


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151 DSXASTIFCT KGCRTTSSPV KWKYSPSTL CSFSRASFPN DLMFLGRSIW
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng)
 from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAPADRI SDLEARLAQLEHRVAVLES GGN TVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPAPADRI GDLEARLAQLEHRVAVLES GGN TVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
g914.pep	70	80	90	100	110	119
	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCRKFDXCIGWTDKETD					
	70	80	90	100	110	120
g914.pep	120	130	140	150	160	170
	-ELGFRLCFSLPDFPCIGFQTALCQSCSADSXASTIFCTRGCRRTTSSPVKWKYSPATP					
m914	TELGFRICFSLPDFPCIGFQTALCQSCSADSXASTIFCTKGCRRTTSSPVKWKYSPSTL					
	130	140	150	160	170	180
g914.pep	180	190	200	210	220	230
	CSFSRASFPNDLMFLGRSIWLVSFVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPNDLMFLGRSIWLVSFVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
g914.pep	240	LPRIX				
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TTCCGTTCAA ATCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTGCA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTT TGCCGATTTCG
451 TAGGCTTCGA CGATTTTTTG CACCAAAGGA TGCCGGACAA CGTCTTCGCC
501 GGTAAAGGTG TGGAAATACA GCCCTTCCAC GCCGTGCAGT TTCTCACGCG
551 CATCTTTTAA TCCCGATTG ATGTTTTTGG GCAGGTCGAT TTGGCTGGTG
601 TCGCCGTA* TGACGGCTT* CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCAATTGT TCGGGCGTGG TGTTTTGGCG TTCGTGAGG ATGATGTATG
701 CGCCGTTGAG CGTCTGCCG CGCATATAG
  
```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 ICRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFPNDL MFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVFCASSR MMYAPLSVLP RI*
  
```


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m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPADFADRGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPADFADRGDLEARLAQLEHRVAVLESGSNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGFRICFSLPDFPCIGFQTALECSQSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTL					
a914	TELGFRICFSLPDFPCIGFQTALECSQSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMLFGRSIWLVSPVMTAFAPKPMRVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMLFGRSIWLVSPVMTAFAPKPMRVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcgggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga ttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

```

1  MKKTLLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAPYVIDS GFIGMGAEAD ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC.tg
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCcCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG

```


1312

451 GTTGTGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

m915.pep

1 MKKTLAIVA VSALSXCRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

m915/g915

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEAGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g915	MKKTLAIVAVFALSACRQAEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
g915	DQPVWFSTVQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g915	GFIGGGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

a915.seq

1 ATGAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCTTT ACCCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCAGA TTTTCTTGAA CGGCAAAACC GATCAGCCCG TTGGTTCTC
 201 CACCATCAAG CAGATGTTG GCTATACCAA GCTGCCCGAA GAGCCTAAG
 251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATA AGGCGGTAAG
 451 GTTGTGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

a915.pep

1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGGAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSXCRQAEAGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLAIVAVSALSACRQAEAGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
a915	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					

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	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgacgc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCCG
251 GTTACGACAT TGTGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCCT GAAATGATGA GGCTGATGGA CGGGTTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCCGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAaaaaATC CGCGTGATGA TGCCGAAAGA GGGCGTGGG ATTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCTCTGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTG ATGGAGGACG
1001 AATTAAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNLKI YNWSEYVDPE
51  TVADFEKKNG IKVTDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDQWDLV FNPEYTFKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEBAGGKEKI RVMPKKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACCTGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGTTCGAT CCCGCCCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCCGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

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1314

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751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTTGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTTATCA TGGTGCCTAT CCAGCCGCGC GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

```

1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51 TVADFEKKNG IKVTYDVYDS DETLESKVLK GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDLDIAKRR AEEAGGKEKI RVMPKKEGVI IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAENQNVLKIYNWSEYVDPETVADFEKKNG					
g917	:					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	:					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	:					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLSAAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
g917						
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFPGGDLNIAKRRAEAGGKEKIRVMPKKEGVGIWVDSFVIPKDAKNVANAHK					
g917						
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNFSFIMVPIQPA					
g917	: : :					
	310	320	330	340	350	360

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m917.pep ALKFMVRQWQDVKAGKX
 |||||
 g917 ALKFMVRQWQDVKAGKX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
 1 ATGACCAAAC ATCTGCCCTT GCGCGTCTTG ACTGCTTTGC TGCTTGCAGC
 51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGCGC CCGGCGGAAA
 101 ACCGAAACGT ATTGAAAATT TACAACGGT CGGAATACGT CGATCCGGAA
 151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
 201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCTG
 251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAAG
 301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
 351 CCTCAACCCC GAAATGATGA GGCTGATGGA CCGGGTCGAT CCCGGCCACG
 401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
 451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGTGCCGG ACAACCACTG
 501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
 551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACATAT
 601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
 651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG
 701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
 751 GCGCGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CCGGCGGCAA
 801 GGAAAAAATC CGCGTGATGA TGCCCAAGA GGGCGTGGG ATTTGGGTGG
 851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
 901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
 1051 AGCTTTATCA TGGTGCCTAT CCAGCCGCGC GCATTGAAGT TTATGGTGCG
 1101 CCAGTGCGAG GATGTGAAGG CCGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
 1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
 51 TVADFEKNG IKVTYDVYDS DETLESKVL T GKSQYDIVAP SNAFVGRQIK
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
 151 ERVKALGTD KLPDQWDLV FDPEYTSKLK QCGISYLD SA AEIYPMVLNY
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
 251 GGDNLIAKRR AEEAGGKEKI RVMPKKEVG IWVDSFVI PK DAKNVANA HK
 301 YINDFLDPEV SAKNGNEVTY APSSKPAREL MEDEFKNDNT IFPTEDLKN
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKALGTDKLPDQWDLVFDPEYTSKLK					
a917	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKALGTDKLPDQWDLVFDPEYTSKLK					
	130	140	150	160	170	180
m917.pep	QCGISYLD SA AEIYPMVLNYLGNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
a917	QCGISYLD SA AEIYPMVLNYLGNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	QCGISYLD SA AEIYPMVLNYLGNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
a917	QCGISYLD SA AEIYPMVLNYLGNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					

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a917      QCGISYLDAAEIYPMVLNLYGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           |||||
a917      RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVITYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           |||||
a917      YINDFLDPEVSAKNGNFVITYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWDVKAGKX
           |||||
a917      ALKFMVRQWDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC  ACCTGCTCCG  CTCCGCCCTG  TACGGcatCG  CCGCCgccAT
51  CctcgCGGCC  TGCCAAAgca  gGAGCATCCA  AACCTTTCGG  CAACCCGACA
101 CATCCGTCAT  CAACGGCCCC  GACCGGCCGG  CCGGCATCCC  CGACCCCGCC
151 GGAACGACGG  TTGCCGGCGG  CGGGGCCGTC  TATACCGTTG  TGCCGCACCT
201 GTCCATGCCC  CACTGGGCGG  CGCaggATTT  TGCCAAAAGC  CTGCAATCCT
251 TCCGCCTCGG  CTGCGCCAAT  TTGAAAAACC  GCCAAGGCTG  GCAGGATGTG
301 TGCGCCCAAG  CCTTTCAAAC  CCCCCTGCAT  TCCTTTCAGG  CAAAGcGgTT
351 TTTTGAACGC  TATTTACGCG  cgtGGCaggT  tgcaggcaAC  GGAAGcCTTG
401 Caggtagggt  TACCGGCTAT  TACGAACCGG  TGCTGAAGGG  CGACGGCAGG
451 CGGACGGAAC  GGGCCCGCTT  CCCGATTAC  GGTATTCCCG  ACGATTTTAT
501 CTCCGTCGCC  CTGCTGCCCG  GTTGGCGGG  CGGAAAAAAC  CTTGTCCGCA
551 TCAGGCAGac  ggGAAAAAAC  AGCGGCACGA  TCGACAATGC  CGCGGCACG
601 CATACGCGCG  ACCTCTCCCG  ATTCCCCATC  ACCGCGCGCA  CAACGGcaat
651 caaaGGCAGG  TTTGAaggAA  GCCGCTTCCT  CCCTTACCAC  ACGCGCAACC
701 AAAtcaacGG  CGGCgcgcTT  GACGGCAaag  cccCCATCCT  CggttacgcC
751 GAagaccCcG  tcgaacttTT  TTTATGCAC  AtccaaggCT  CGGGCCGCTT
801 GAAAAACCCG  tccggcaaat  acatCCGAt  cggatagcgc  gacAAAAACG
851 AACatccgTa  tgtttccatc  ggACGctata  TGGCGGACAA  AGGCTACCTC
901 AAGctcgggc  agACCTCGAT  GCAGGgcata  aaagcCTATA  TGCGGCAAAA
951 TCCGCAACGC  CTCGCCGAAG  TTTTGGGTCA  AAACCCAGC  TATATCTTTT
1001 TCCGCAGGCT  TGCCGGAAGC  GGCAATGAGG  GCCCGTCGG  CGCACTGGGC
1051 ACGCCACTGA  TGGGGGAATA  CGCCGGCGCA  ATCGACCGGC  ACTACATTAC
1101 CTTGGGCGCG  CCCTTATTTG  TCGCCACCGC  CCATCCGTT  ACCCGCAAAG
1151 CCCTCAACCG  CCTGATTATG  GCGCAGGATA  CAGGCAGCGC  GATCAAAGGC
1201 GCGGTGCGCG  TGGATTATTT  TTGGGTTTAC  GGCGACGAAG  CCGGCGAACT
1251 TGCCGCAAA  CAGAAAACCA  CGGGATACGT  CTGGCAGCTC  CTGCCAACG
1301 GCATGAAGCC  CGAATACCGC  CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

g919.pep

```

1  MKKHLRSAL  YGIAAAILAA  CQSRSIQTFP  QPDTSVINGP  DRPAGIPDPA
51  GTTVAGGGAV  YTVVPHLSP  HWAQDFAKS  LQSPRLGCAN  LKNRQGNQDV
101 CAQAFQTPVH  SFQAKRFFER  YFTPWQVAGN  GSLAGTVTGY  YEPVLKGDGR
151 RTERARFPPI  GIPDDFISVP  LPAGLRGGKN  LVRIQTGKXN  SGTIDNAGGT
201 HTADLSRFPPI  TARITAIKGR  FEGRFLPYH  TRNQINGGAL  DGKAPILGYA
251 EDPVELFFMH  IQSGRLKTP  SGKYIRIGYA  DKNEHPYVSI  GRIMADKGYL
301 KLGQTSMQGI  KAYMRQNPQR  LAEVLQNPFS  YIFFRELAGS  GNEGVPVAGL
351 TPLMGEYAGA  IDRHYITLGA  PLFVATAHPV  TRKALNRLIM  AQDTGSAIKG
401 AVRVDYFWGY  GDEAGELAGK  QKTTGYVWQL  LPNGMKPEYR  P*

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m919.seq
1  ATGAAAAAAT  ACCTATTCCG  CGCCGCCCTG  TACGGCATCG  CCGCCGCCAT
51  CCTCGCCGCC  TGCCAAAGCA  AGAGCATCCA  AACCTTTCGG  CAACCCGACA
101 CATCCGCTCAT  CAACGGCCCG  CGCCGGCCGG  TCGGCATCCC  CGACCCCGCC
151 GGAACGACGG  TCGCGCGCGG  CGCGGCCGTC  TATACCGTTC  TACCCGACCT
201 GTCCCTGCCC  CACTGGGCGG  CGCAGGATT  GCGCAAAGTC  CTGCAATCCT
251 TCCGCTCGG  CTGCGCCAAT  TTGAAAAACC  GCCAAGGCTG  GCAGGATGTG
301 TCGCCCCAAG  CCTTTCAAAC  CCCCCTCCAT  TCCTTTCAGG  CAAAACAGTT
351 TTTGAACGC  TATTTACAGC  CGTGGCAGGT  TGCAGGCAAC  GGAAGCCTTG
401 CCGGTACGGT  TACCGGCTAT  TACGAACCGG  TGCTGAAGGG  CGACGCACAGG
451 CGGACGGCAC  AAGCGCGCTT  CCGGATTTAC  GGTATTCGCG  ACGATTTTAT
501 CTCGCTCCCC  CTGCTGCGG  GTTTCGGGAG  CGGAAAAGCC  TTGTGTCGCA
551 TCAGGCAGAC  GGGAAAAAAC  AGCGGCACAA  TCGACAATAC  CGGCGGCACA
601 CATACCGCCG  ACCTCTCCG  ATTCCCATC  ACCCGCGCGA  CAACAGCAAT
651 CAAAGGCAGG  TTTGAAGGAA  CGCGCTTCCT  CCCCTACCAC  ACGCGCAACC
701 AAATCAACGG  CGGCGCGCTT  GACGGCAAG  CCCCATACT  CGGTTACGCC
751 GAAGACCTG  TCGAACTTTT  TTTATGCA  ATCCAGGCT  CCGGACGCTC
801 GAAAACCCG  TCCGGCAAAT  ACATCCGCAT  CGCGTATGCC  GACAAAAACG
851 AACATCCyTA  CGTTTCCATC  GGACGCTATA  TGGCGGATAA  GGGCTACCTC
901 AAATCGGAC  AAACCTCCAT  GCAGGGCATT  AAGTCTTATA  TCGGGCAAAA
951 TCCGCAACGC  CTCGCCGAAG  TTTTGGGTCA  AAACCCACCG  TATATCTTTT
1001 TCCGCGAGCT  TGC CGGAAGC  AGCAATGAC  GCCTGTCCG  CGCACTGGGC
1051 ACGCCGCTGA  TGGGGGAATA  TGCCGGCGCA  GTCCAGCGC  ACTACATTAC
1101 CTTGGGTGCG  CCTTATTTG  TCGCCACCGC  CCATCCGTT  ACCCGAAAG
1151 CCTCAACCG  CTTGATTATG  GCGCAGGATA  CCGGCAGCGC  GATTAAAGGC
1201 GCGGTGCGCG  TGGATTATTT  TTGGGGATAC  GGCAGACGAG  CCGCGAAGT
1251 TGCCGGCAAA  CAGAAAACCA  CGGGATATGT  CTGGCAGCTC  CTACCCAACG
GTATGAAGCC CGAATACCGc CGGTAA

```

m919.pep

```

1  MKKYLYRAAL YGIAAAILAA CQSKSIQTFF QPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAADQFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTFVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DQKAPILGYA
251 KDFVELTFMH IQSGSRRLKP SGKYIRIGYA DKNEHPYVSI GRYMADRGYL
301 ELQPQTSMQH KSYMGRNQR LAEVLGNQPS YIFFRELGS SNDGFPVGLG
351 TPLMGSYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTGYVWQL LPNGMKPEYR p+

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF
919.ng) from *N. gonorrhoeae*:
m919/q919

	10	20	30	40	50	60
m919.pep	MKKYLFR AALYGIAAAAILAACQSKSIQTFFPQDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	: : : : : :					
g919	MKKHLRLSALYGIAAAAILAACQSRSIQTFFPQDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
	: : :					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYIEPVLKGDGRRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNGSLAGTVTGYIEPVLKGDGRRRTERARFPPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDFVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
g919	DGKAPILGYAEDFVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTSMQGIKSYMQRNPQRLAEVLGQNPYSYIFFRELAGSSNDGPVVGALGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRNPQRLAEVLGQNPYSYIFFRELAGSGNEGPVVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

a919.seq

```

1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGCGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGCGCGCGG CGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCTGCCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCGTTCCAG CAAAACAGTT
351 TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTATTTCG TCGCCACCGC CCATCCGGTT ACCCGCAAAG

```


1319

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
 1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT
 1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCCAACG
 1301 GTATGAAGCC CGAATACCGC CCGTAA

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
    51 GTTVGGGGAV YTVVPHLSLP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
   101 CAQAFQTPVH SVQAKOFFER YTFWQVAGN GSLAGTVTGY YEPVLKGDDR
   151 RTAQAARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
   201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
   251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
   301 KLGQTSMQGI KAYMQNPQR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
   351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
   401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep MKKYLFRALYGI AAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
      10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKOFFER
          |||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKOFFER
      70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep YTFWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQAARFPIYGIPDDFISVPLPAGLRSGKA
          |||||
a919      YTFWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQAARFPIYGIPDDFISVPLPAGLRSGKA
      130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKN SGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
          |||||
a919      LVRIRQTGKN SGTIDNTGGTHTADLSQFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          |||||
a919      DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
      250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
          |||||
a919      KLGQTSMQGIKAYMQNPORLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
      310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          |||||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      370     380     390     400     410     420

      430     440
m919.pep QKTTGYVWQLLPNGMKPEYRPX
          |||||
a919      QKTTGYVWQLLPNGMKPEYRPX
      430     440

```


Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCGAATAT CAGCCTACTT TCCCGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTGCGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCT GGAAATCGTC
301 CCGCTGGACA ATCccgcccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgTtCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT cGacaccac cgacggcgaa ggcgaaagtgg acatcatCCC
501 CTTCGgccaa GGCTTtttga aAgcGAGTGT CGAATAcaaa gccgAttctc
551 CCGATcaaAG CCTGTGccga AAACAggcgA ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTAa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAEY OPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGGG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCGGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTGAAACAC AAAACCGACT TCCCGGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAI I
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```



```

g920.pep      10      20      30
               PMQLVTEKGKENMIQRGTINYQYRSNRPVK
               |||||
m920      GGEYLKADLGYGEFFPELEPIAKDRLHIFSKPMQLVTEKGKENMIQRGTINYQYRSNRPVK
               40      50      60      70      80      90

               40      50      60      70      80      90
g920.pep      DGSYLVTA EYQPTFRSKNKAGWKQAGIKEMP DASYCEQTRMFGKNIVNVGHESADTAIIT
               |||||
m920      DGSYLVIA EYQPTFWSKXKAGWKQAGIKEMP DASYCEQTRMFGKNIVNVGHESADTAIIT
               100     110     120     130     140     150

               100     110     120     130     140     150
g920.pep      KPVGQNLEIVPLDNPADIHVGXRFKVRVLF RGEPLPNATVTATFDGFDTS DRSKTHKTEA
               |||||
m920      KPVGQNLEIVPLDNPANIHVGERFKVRVLF RGEPLPNATVTATFDGFDTS DRSKTHXKEA
               160     170     180     190     200     210

               160     170     180     190     200
g920.pep      QAFSDTTDGEGEVDIIPLRQGFWKASVEYKADFPDQSLCRKQANYTTLTFQIAHSHHX
               |||||
m920      QAFSDSTDDKGEVDIIXLRQGFWKANVEHKTDFPDQSVCKQANYSTLTFQIGHSHHX
               220     230     240     250     260

```

```

a920.seq
1  TGAAGAGAAA CATTGACACT GCTCGCGGTT TCCGCCCTAT TTGCCGCATC
51  CGCCCACGCC CACCGCGTCT GGGTCGAAC CGCCACACG CACGGCGCGG
101 AATACCTTAA AGCCGACTTG GGCATCGCG AATTTCCTCA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAG CAACCGATGC AGCTGGTTAT
201 CGAAAAAGGC AAGGAAACA TGATTCAACG CGGCACATAC AACTACCATG
251 ACCGAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAACAAA ATGCTGAGC CAAGCTATTG CGAACAAAC CGAATGTTC
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAATCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGCGCAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGAGCCGA GCAAAACGCA CAAAACGAA GCATAGGCTT TCCTCGCAGC
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGGCG CAAGGCTTCT
701 GGAAGCCCAA TGTCGAACAC AAAGCCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GCCATTGCA
801 CCATTAA

```

a920.pep

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDRHLHFS	KPMQLVTEKG	KENMIQRYCT	NYQYRSNRFP	KDGSYLVAIE
101	YQPTFSKKNK	AGWKQAGIKQ	KPDASYCEQT	RPMFGKNIVNV	GHSADTAII
151	TKPVGQNLEI	VPLDNPANIH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFDT
201	SDRSKTHKTE	AQAFSDSTND	KGEVDIIPLR	QGFWKANVEH	KADFPDQSVC
251	QKQANYSYTL	FOIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATSAAHHRVWVETAHTHGGEYLLKADLGYGEFFELEPIAKDRLHIFS					
a920	XKKTLLTLLAVSALFAASAHAHRVWVETAHTHGGEYLLKADLGYGEFFELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMIQRTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKKAGWKQAGIKE					
a920	KPMQLVTEKGKENMIQRTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLIVPLDNPANIHVGERFKVRVL					
a920	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTATFDGFDTSDRSKTHXKEAQAFSDSTDDKGEVDIIXLRQGFWKANVEH					
a920	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQSVQCQKQANYSTLTFOIGHSHHX					
a920	KADFPDQSVQCQKQANYSTLTFOIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCggtt TcCGCACTAT TTGCCACATc
51  cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgcccACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGccAAAG ACCgCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCCTG AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCGGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAAGAA ATGCTGACG CAAGCTATTG CGAACAAACC CGTATGTTCT
401 GTAAAAACAT TGTCAACGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTGCGC CAAGGCTTTT
701 GGAAGCGGAG TGTGGAATAC AAAGCCGATT TCCCCGATCA AAGCCTGTGC
751 CAAAACAGG CGAACTACAC AACTTTAACC TTCCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV SALFATSAP HRVWVETAHT HGGEYLLKADL GYGEFFELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRTY NYQYRSNRPV KDGSYLVTAE
101 YOPTFRSKNK AGWKQAGIKE MPDASYCEQ TRMFGKNIVN GHESADTAII
151 TKPVGQNLVI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDTTDG KGEVDIIPLR QGFWRASVEY KADFPDQSLC
251 KQQANYTTLT FOIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACACGCC CACCGCGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```


1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVNVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGONLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFDQSVK
251 QKQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATSAHAHRVNVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAHPRVNVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE					
	70	80	90	100	110	120
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGONLEIVPLDNPANIHVGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGONLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDTDDKGEVDIIPLRQGFWKASVEY					
	190	200	210	220	230	240
m920-1.pep	KTDFFDQSVKQKQANYSTLTFQIGHSHHX					
g920-1	KADFFDQSLCQKQANYTTLTFQIGHSHHX					
	250	260	269			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAGAGAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51 CGCCACACGCC CACCGCGTCT GGGTCGAAAC CGCCACACAG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCGA
801 CCATTAA

```


This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

a920.pep
 1 *KKTLTLLAV SALFAASANA HRVWVETAHT HGGEYLKADL GYGEPPELEP
 51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLIVIAE
 101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
 151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
 201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSVK
 251 QKQANYSTLT FQIGHSHH*

m920-1/a920 98.9% identity in 267 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATS	SAHAHRVWVETAHTHG	GEYLKADLGYGEFPELEPI	AKDRLHIFS		
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQR	GTNYQYRSNRPVKDGS	YLIVIAEYQPTFWSKN	KAGWKQAGIKE		
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKN	IVNVGHESADTAII	TKPVGQNLEIVPLDNP	ANIHVGERFKVRVL		
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFD	GFDTSDRSKTHKTEA	QAFSDSTDDKGEVDI	IPLRQGFWKANVEH		
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFPDQSVCKQKQAN	YSTLTFFQIGHSHHX				
a920	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX				
	250	260				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

g921.seq
 1 ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
 51 Ccagtctatt tatGtgccca cattgacgga aatccccgTg aatcccatca
 101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCTTCG
 151 CATTGGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTGCA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GCGGTAGAC AGCCAGCGCG GCGAAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

g921.pep
 1 MKKYLIPLSI AAVLSGCQSI YVPTLTETIPV NPINTVKTEA PAKGFRLAPS
 51 HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
 101 YEIYLRSAVD SQRGENTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
 151 FLMEVMMQMP LK*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

m921.seq
 1 ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
 51 CCACTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
 101 ATACCGTCAA AACGGAAGCA CTGCAAAAG GTTTCCGCCT TGCCTCTTCG
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA

251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTT GGCATAGAC AGCCAGCGGG GCGCAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCCTTGGCG GGCTGGCAGC
401 AGCGTTGGAA AAATATGGAT GTCAAAACCA ACAACCCGC AATTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

1 MKKYLPLSL AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRGLASS
51 HWTDVAKISD EATRLGYQVG IGMKTKVQAA QYLNNFRKRL VGRNAVDDSM
101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 FLMEVMKMQP LK*

m921/g921

1	ATGAAAAAA	ACCTTATCCC	TCTTTCCATT	GTGGCAGTTC	TTTCCGGCTG
51	CCAGTCTATT	TATGTGCCCA	CATTGACGGA	AATCCCCGTG	AATCCTATCA
101	ATACCGGTCAA	AACGGAAGAA	CCTGCAAAG	GTTTCCGCT	TGCTCTTCG
151	CATTGGACGG	ATGTGTCCAA	AATGACGAT	GAAGCGACG	GCTTGGGCTA
201	TCAGGTGGGT	ATCGGTAAAA	TGACCAAGT	TACGGCGCG	CAATATCTGA
251	ACAACTTCAG	AAAACGCCTG	GTCCGACGCA	ATGCCGTGCA	TGACAGTATG
301	TATGAAATCT	ACCTCGGCTT	GGCGATAGAC	AGCCAGCGGG	GCGCAATCAA
351	TACGGAACAC	TCCAAGCTGT	ATATCCAGAA	TGCTTGC	GCGTGGCAGC
401	AGCGTTGGAA	AAATATGGAT	GTCAAACCA	ACAACCCCG	ATTTACCAAC
451	TTTTTGATGG	AAGTGATGAA	GATGCAGCCC	TGAAATGA	

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLESS
51 HWTDVAKISD EATRLGYQVG IGMKTKVQAA QYLNNFRKRL VGRNAVDDSM
101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 FLMEVMKMOP LK*

10 20 30 40 50 60
 m921.pep MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLLASSHWTDVAKISD
 |||||:|||||
 a921 MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLLASSHWTDVAKISD
 10 20 30 40 50 60

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	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMMQMPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMMQMPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAC CGGTATCCGA CAGCGGTTT GCCGCCAATG CAAATGTCCG
201  CCGTTTGTG GACGATGAAG TCGGGAAGG GGATTTTTC CAGGCGGAAT
251  GGCAGGATTT TTTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATT
301  ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGgttcc gCacggGAAa
351  ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401  gcgcggttat cgatgatgtg gcgCAAAaT acggcgtGCC TGCCGAGCTT
451  ATCGTGGCGA TTATCGGGAT TGAACGAAT TACGGCAAAA ATACGGGCAG
501  TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551  GCGCCGGGTT TTTCCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601  GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651  GGGTATGCCG CAATTTATGC CTTCCAGCTA CCGGAAATGG GCGGTGGATT
701  ATGacgggga cggacatCGG GATATatggg GCAACGTcgg tgatgtcgcg
751  gcatcggTTG CCAATTatag gaagCAGCAC GGTGCGCGCA Cgggcggtaa
801  AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CaggcAATCA
851  TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATTT GAaggCGTAc
901  ggcacatccc ccggggaaac GCTCGCAGAT GATGAAAAGy cgGTTTGTGTT
951  CAAACTGGAA ACCGCACCCG GCGTGTGTTGA ATATTATTG GCGTTGAACA
1001  ATTTTATAC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAACGgcg
1051  gtcaggGACA TTGCCAATTC GCTCGCGCGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KRESRPAPDA
51  AAVPVSDSGF AANANVRRFV DDEVGKGDFS QAEWQDFFDK AAYKADIVKI
101  MHRPSTSRPW YVFTGNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151  IVAIIGIETN YGKNTGSFRV ADALATLGFY YPRRAGFFQK ELVELLKLAK
201  EGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251  ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGETAL TRTVADLKAY
301  GIIPGETLAD DEKAVLPKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMVYTA
351  VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACCC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAT TTGACGCGC AGCCGTACCG GTATCCGACA GCGGTTTGC
201  CGCCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251  ATTTTTCCTG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301  GCGGACATCG TCAAGATTAT GCACCGCCCC TCACATCGC GTCCGTGGTA
351  TGTGTTCCGC ACGGGAATTT CCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401  GGTGTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451  GCGTGCGCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501  CGGCAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551  GCTTTGATTA CCCCCCGCGC GCCGGGTTTT TCCAAAAGA ATTGGTCGAG

```


m922.ppt

1	MKKRKILPLA	ICLAALSACT	AMEARPPRAN	EAQAPRAVEM	KKESRPAFDA
51	AAVFDAAAVP	VSDSGFAANA	NVRRFVDDVE	GKGFDSRAEW	QDFFDKAAVK
101	ADIVKIMHRP	STSRPWYVFR	TGNSGKAKFR	GARRFYAENR	ALIDDDVAQKY
151	GVPAELIVAV	IGIETNYGKN	TGSFPRVADAL	ATLGFDYPRR	AGFFQKELVE
201	LLKLAKEEGG	DVFAFKGSYA	GAMGMPQFMP	SSYRKWAVDY	DGDGHRDIWG
251	NVGDVAASVA	NYMKQHGWRV	GGKMLVSATL	APGADVQAI	GKKTALTRTV
301	ADLKAYGIIP	GEELADDEKA	VLFKLETAPG	VFEYYLGLNN	FYTVWQYNHS
351	RMVYTVARDI	ANSLGSGPGI.*			

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/q922

```

10          20          30          40          50          60
m922.pep   MKRKRILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAFDAAAVFDAAAVP
           |:|||||
g922        MEKRRKILPLAICLAALSACTAMEARTPRANEQAQAPRADEMKKESRPAFDAA-----AVP
           10          20          30          40          50

70          80          90          100         110         120
m922.pep   VSDSGFAANANVRRFVDDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR
           |||:|||||
g922        VSDSGFAANANVRRFVDDEVGKGDFSQAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR
           60          70          80          90          100         110

130         140         150         160         170         180
m922.pep   TGN SGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL
           |||:|||||
g922        TGN SGRAKFPHGARRFYAENRAVIDDVAQKYGVPAELIVAIIGIETNYGKNTGSFRVADAL
           120        130        140        150        160        170

190         200         210         220         230         240
m922.pep   ATLGFDPYRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
           |||
g922        ATLGFDPYRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
           180        190        200        210        220        230

250         260         270         280         290         300
m922.pep   DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV
           |||
g922        DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV
           240        250        260        270        280        290

310         320         330         340         350         360
m922.pep   ADLKAYGIIPEGELADDEKAVLFKLETAPGVFEYYLGLNFPYTVWQYNHSRMVYTVAVRDI
           |||
g922        ADLKAYGIIPEGETLADDEKAVLFKLETAPGVFEYYLGLNFPYTVWQYNHSRMVYTVAVRDI

```


1328

300 310 320 330 340 350

370

m922.pep ANSLGGPGLX
|||||

g922 ANSLGGPGLX
360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

a922.seq

1 ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CCGCTTTGTC
51 TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGCC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAAATT CCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GGCCTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTTGATTA CCCCCGCGC GCGGGTTT TCCAAAAGA ATTGGTCGAG
601 CTTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTTC CCTTTAAAGC
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCCGACG GCGGGGAAAA TACTGGTGTG TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GCGGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCC GCGGAAGAGC TTGCCGATGA
951 TGAAAAGGCG GTTTTGTTC AACTGGAAAC CGCACCCGGC GTGTTTGAAT
1001 ATTATTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCCG TTGGCGGCCC
1101 GGGATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

a922.pep

1 MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KKEsrPAFDA
51 AAVFDAAVP VSDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPAELIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHWRT GKKILVSATL APGADVQAI I GEKTA LTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

m922/a922 98.9% identity in 369 aa overlap

10 20 30 40 50 60

m922.pep MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKEsrPAFDAAAVFDAAVP
||:|||||

a922 MKNRKILPLAICLAALSACTAMEARPPRANEAQAPRADEMKKEsrPAFDAAAVFDAAVP
10 20 30 40 50 60

70 80 90 100 110 120

m922.pep VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR
|||||

a922 VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR
70 80 90 100 110 120

130 140 150 160 170 180

m922.pep TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL
|||||

a922 TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL
130 140 150 160 170 180

190 200 210 220 230 240

1329

```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKALTRTV
          ||||||||||||||||||||:||||||||||||||||||||||||||||||||||
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRTGGKILVSATLAPGADVQAIIGEKALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          ||||||||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTCTGTGC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACCT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTTGGACG GGCGCATACT TGGGTAGTAG GATGTTTCAGG CATAAAACGG
251 CGAAAACGCG TTTTGTGTGT CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTT GTTCCGCCCG AACTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRRIPEHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFVV LFRLTVSGNV
101 LATCILIDYF VPPELFFVLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTGTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACCT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GGCGCGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAACGCG TTTTGTGTGT CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCCTCG CCTTGCCGTA CTATTTGTAC TGTCTGCGGC TTCGTGCGCT
401 TGTCTTGATT TTGTTAATC CACTATAT. T ATTTGTCCC GCCTGAATT
451 TTCGTAAAC TCGGCGAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GQRRIPEHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFVV LFRLTVSGNV
101 LATLILISG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPEPF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

```

      10      20      30      40      50      60
g923.pep  MKRQAFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m923      MKRQAFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRIPEHRL
          10      20      30      40      50      60

      70      80      90      100
g923.pep  LLPALFGGWTGAYLGSRMFRHKHTAKKRFVVLFRLLTVSGNVLATCILID-----
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m923      LLPALLGGWVGAYFGSMTFKHKHTAKKRFVVLFRLLTVSGNVLATLILYSGNLNLNQYGVAS
          70      80      90      100      110      120

                                110      120
g923.pep  -----YFVPPPELFFVKLGQHLX
          ||||| ||||| ||||| |||||
m923      PCRTICTVCGFVALSXFLLIHYIYFVPPPEFFVKLGQNTX
          130      140      150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

```

1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTCACCTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTTGTTCGG
201 CGGTTGGGCG GGCGCATACT TGGGCAGCAG GATATTCAGG CATAAAACGG
251 CGAAAAGCG TTTTGTGTGT CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTTGTA CTGTCTGCGG CTTCGTCGCC
451 TTGTCCTGAT TTTTGTTAAT CCACTAT.AT TATTTGTGCC CGCCTGAATT
501 TTTCGTAAAA CTCGGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

```

1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRAVR
51  GKRRRIPEHRL LLPALFGGWA GAYLGSRIFR HKTAKKRFVV LFRLTVSGNV
101 LATLILYSG LNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA
151 LS*FLLIHYX YFVPPPEFFVK LGQNT*

```

m923/a923 84.6% identity in 175 aa overlap

```

      10      20      30      40      50      60
m923.pep  MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRIPEHRL
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a923      MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL
          10      20      30      40      50      60

      70      80      90      100      110      120
m923.pep  LLPALLGGWVGAYFGSMTFKHKHTAKKRFVVLFRLLTVSGNVLATLILYSGNLNLNQYGVAS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a923      LLPALFGGWAGAYLGSRIFRHKHTAKKRFVVLFRLLTVSGNVLATLILYSGNLNLNQYGVAS
          70      80      90      100      110      120

                                130      140      150      159
m923.pep  PC-----RTICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a923      PXAQRERFSKVLKHQVNRFR TICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX
          130      140      150      160      170

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1  ATGAAACAAA TGCTTTTGGC cgtcggcggtg ggcgcggtgt TGGCGGGCTG
51  CCGCAaggat gccggcggtt acgaggggTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKCCGQT QAYLDARNAL PSNQTYYQORQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CCGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
.....

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKNINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAMKDKIIAHQKCCGQT				
	60	70	80	90	100
					110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CCGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNFYLN
51  KINVFTGKEE SLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAAGAGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTAATTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTTGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNFYFL
51  NKIHVVTGKE ESLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMKDKI IAHQKKGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNFYFLNKIHVVTGKE					
	: : : : :					
g925-1	MKQMLLAVGVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKK-KGNFYFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKGQT					
	: : : : :					
g925-1	ESLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX					
	: : : : :					
g925-1	AQAYLDARNALPSNQTYQQRQAAIEQLKRRFEAEFDELEKEIKCNK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51  AAAAGACGGC GCGCTTTTGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTCAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51  KTDAAAMKDKI IAHQKKGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
		: : :		
m925-1		AGGYEGYWREKSDKKEGMIAVKKEKGNFYFLNKIHVVTGKEESLLSEKDGALSINTGIGE		
	30	40	50	60
	40	50	60	70
		80	90	

a925-1.pep IPIKLSDDGKELYVERRQYVKTDAAAMKDKIIIAHKQKCGQTAQAYLDARNALPSNQTYQQH
|||||
m925-1 IPIKLSDDGKELYVERRQYVKTDAAAMKDKIIIAHKQKCGQTAQAYRDARNALPSNQTYQQH
90 100 110 120 130 140

100 110 120
a925-1.pep QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||:|:|:
m925-1 LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLIX
150 160 170

q926.seq (partial)

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

g926.pep (partial)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

m926.seq

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

m926.pep

g926/m926 91.6% identity in 155 aa overlap

	10	20	30	40	50	60
g926.pep	MKHTVSASVILLLTAC	QLPQN	NENLWQ	PSEHIS	SFAAEGRLAV	KAEGKGSYANFDWTYQ
m926	MKHTVSASVILLLTAC	QLPQN	NENLWQ	PSEHIS	SFAAEGRLAV	KAEGKGSYANFDWTYQ
	10	20	30	40	50	60
	70	80	90	100	110	120
g926.pep	PPVETININTPLGSTL	QQLCQ	DRD	GALAVD	GKGNVYQ	AEGTEDLSRQLVGF
m926	PPVETININTPLGSTL	QQLCQ	DRD	GALAVD	GKGNVYQ	AEESAELSRLVGF
	70	80	90	100	110	120
	130	140	150	160		
g926.pep	WAEGRRVAGAPYRIR	SDGILEQ	YGWTIG	ONCROWG	ASPNV	ATR

1334

||:||||| |||||:|:| :|
 m926 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
 130 140 150 160 170 180

a926.seq

1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
 51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
 101 GCAGTTTCAC GCGGAAGGG CGTTGGCAG TGAAAGCGGA AGGGAAAGGT
 151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
 201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
 251 ACGGCGCATT GGCAGTGGAC GCGAAAGGAA ATGTCTATCA GCGGAAAGT
 301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACCTGC CAATCCAATA
 351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CTTACCGCA
 401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
 451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
 501 GAACATCAGG CTGGTTTTC ACGAGATTGG TATGCCGTCT GAAACCGAAA
 551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep

1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEKGK
 51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNYQAES
 101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
 151 ADSSGQVRTL QLNNNGNLNIR LVFTEIGMPS ETETQECCAA RIQ*

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAEGRRLAVKAEKGKSYANFDWTYQ					
a926	MKHTVSASVILLTACAQLPQNNENLWQPSEHTRSFTAEGRLAVKAEKGKSYANFDWTYQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
	:					
a926	ETETQECCAAARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq

1 atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
 51 CAGCCCGca GCcgatTcaa accaTCCGTC CGGACaAAAT GCCCCGGCCA
 101 ATACCGAATC cgacGgaaAA AACAttaccC TGctcaatgc cTcgtacgat
 151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaaCATA
 201 CCAATCCGAA CACCCGGCA CATCCGTCAG CATCCAACAA TCCACGGCG
 251 GCTTCAGCA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
 351 GGTAAGAAAA GGCTGGCAAC AAGCCCTCCC CGATCAGGCC GCACCCTACA

1335

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
 501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA
 551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAAGCTCGT CGCATCCATC
 601 CTCAAAAACA CACCCGTTT TGAAAACGGC GGACGGC.C CGCCGCCACC
 651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
 701 agCcaactac gtCAGCAAAA AACTGA

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VTRYFYKEYD HLFVGTYQSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
 101 VTMNQSSDID LLEKXGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
 151 DWNDLAKDGV NIVIAKTSN GRYAFLGAYG YGLKANNGNE QEAQKLVASI
 201 LKNTPVFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

1 ATGAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
 51 CAGCCCCGCA GCCGATCAA ACCATCCGTC CGACAAAAT GCCCGGCCA
 101 ATACCGAAT CGACGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
 151 GTGGCAGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
 251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
 401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCA ACAGATCCGC
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
 501 CAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
 551 GTCTGAAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
 601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GCKCgCCACC
 651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGTAAAA
 701 CGAAGCCAAC TACGTCAGC AAAAActGA

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
 101 VTMNQSSDID LLEKKGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
 151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
 201 SILKNTPVFE NGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
	: :					
m927	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
g927.pep	HLFVGTYQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK					
	:					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
	130	140	150	160	170	
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNRYAFLGA					
	130	140	150	160	170	180

1336

```

      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTVPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTS
          |||||::|||
m927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          |||
m927      AKNX
          240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTCCTT  GTCCGAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAAA  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTGA AAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAA ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTVPFE  NGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          |||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWDLAKDGVNIVIANPKTSNGNGRYAFLGA
          |||||
a927      GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWDLAKDGVNIVIANPKTSNGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
          |||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

```


m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTGGAAGAA AAACgctggG CATCGGTTAC AGTCTCGCTC
 401 TTTCGGAAct GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
 451 GGCGGCATTA TACATCgaT TATGCagteg attgCcgga GttacggctC
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
 551 tcaattaTCA TTCcaatCCC atttcgctcg ctAtggctat taCTGcaact
 601 gCCCCcaacc CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
 651 ttcccgctCT Tcttgggggg cgTGGGcgtg ggcaatGGCT Gttcccgcg
 701 ttatcgctt TTtctgTTATG CCTTGATTT TATATTTTT GTATCCGCCT
 751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTGCCAAAG ACCGCTGAG
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
 951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAA
 1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
 1051 TTTTAAATA AActcggact gattaaatGG TTCTCCGAG TGTGGCGGA
 1101 AagtgtcggC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
 1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
 1201 ATTACCGCTA TGTTCCGCGC ATTTCTCGCT GCTGCCGTTT CACTGAATGC
 1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
 1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG
 1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCAITTTG TGGAAAGTTC
 1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep
 1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
 151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMAITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
 401 TTTCGGAAct GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC


```

451 GCGCGCATTACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCCGA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTGTCGCG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATT TATATTTwyT STATCCGCCT
751 GAAATTAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCCG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTC CCGCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTTGGCGGA
1101 AAGTGTCCGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GCGCGCATCC AACATTATGA
1301 TGACCCCTAC TCATTATGCG ACCGGTACTT CGCTGTGAT TTTCCGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGTTG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK QAWTLLAMF VGVIAAIIGK
51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLA MYA HYMFASHTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTIMGEWWK AGFIMSUVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
g929.pep	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLMRIGYLFIAV					
	70	80	90	100	110	120
g929.pep	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
g929.pep	LALVNYHNSPISAMAITATAPNPLIVNLIAENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSPISAMFITATAPNPLIVNLIAENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

1339

	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNAVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
m929	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKLGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPIVFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPIVFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

a929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGTGC GGCATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGTTAC AGTCTCGCTC
401 TTTCCGAAct GCTGCTGGCT CCCGTACCC CTTCCAATAC CGCGCGCGGC
451 GGC GGCACTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTGCTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGCTCT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTTTT GTATCCGCCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTATATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGA CTGTTGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGCGCGGA
1101 AAGTGTGCGC GGTGTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTTCG
1351 GGTACACCA CAATGGGAGA ATGGTGAAG GCGGTTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```


1340

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

a929.pep
 1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
 51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
 151 GGIIHPIMQS IAGSYGSNPA KGTGKMGKY LALVNYHNSP ISSAMFITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
 401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

m929/a929 99.6% identity in 487 aa overlap

m929.pep	10	20	30	40	50	60
	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPAWTLLAMFVGIVIAAIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPAWTLLAMFIGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
m929.pep	70	80	90	100	110	120
	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
a929	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
m929.pep	130	140	150	160	170	180
	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTGKMGKY					
a929	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTGKMGKY					
	130	140	150	160	170	180
m929.pep	190	200	210	220	230	240
	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
a929	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240
m929.pep	250	260	270	280	290	300
	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
a929	PLILYFLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
m929.pep	310	320	330	340	350	360
	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAF LNKLGLIKW					
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAF LNKLGLIKW					
	310	320	330	340	350	360
m929.pep	370	380	390	400	410	420
	FSGVLAESVGG LGVSGTAAGVILVLAYMYAHYMFAS TTAHITAMFGAFFAAVSLNAPAM					
a929	FSGVLAESVGG LGVSGTAAGVILVLAYMYAHYMFAS TTAHITAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
m929.pep	430	440	450	460	470	480
	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					

a929 WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

```
m930.seq
1  ATGAAACTTC CTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGT TTGCCATTAA GAAAGGGTGT TGGGAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG aAGCTTCAAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

```
m930.pep
1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNP AEIRM QODIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWVLEGEHHA
101 RPQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

```
g930-1.seq (partial)
1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTG GAATAGTGGC AAGCTTCAAT TAACCTGTAT GCCGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
201 ACGTATTGCA GCATTCCAAA ACAAAATTC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTGGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCC
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GGCGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGA CTGAGTG ATATGTTCTA
501 TGTAATTTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAAATTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCGGC TTCAACCGCC TGTGTATATG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAACTGTGG ACGAGGGAAA CAAAAGTTA
801 CATTGATGAT GCCGAACCTGA CTGTACAACG GCGTAAACCC ACAGGTTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TCGCGCGGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GGCAGCAACG TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATCGGG CCAAACCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG CCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGTTATTC GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

```
g930-1.pep (partial)
1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNKYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYSVLKLV TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLYKHKGTGM KDALRAPEEA FEGGTSRMKI WTASADVNTF FOIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGO IKLGGNLHYD
```


451 IFTGRALKKP EYFQTKKVV T GFQVGYSE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```

1  ATGAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAC GAAGTGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGTA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG ACAAATTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGGA ACAAGGACTG GAAATCTCA AACGCTCTCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAAAC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTCTT
851 ATGTAAATTA TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAAGTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCCCTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCGG CTCAACCCG CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA ACAAAAAGTT
1151 ACATTGATGA TGCCGAAC TGCGTACAAC GCGGTAAAC TGCGGGTTGG
1201 TTGGCAGAAC TTCCACAA AGAATATATC GGTCGCAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAACCGC GCACCGCAT GAAAGATGCT CTGCCGCGCC
1301 CTGAAGAAAG CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTCAAATC GGTAAACAGC TATTGCGCTA
1401 TGACACATCC GTTATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAATCTGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTAGGACA ATCCGCCAAA TGGTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GCGGGCAACC TGCATTACGA
1701 TATATTTACC GGCCGCGCAT TGAAAAGCC CGAATTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQIMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAFAF NKFPTRSNDL
201 LNLRLDLEQL ENLKRLLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHRRKGGSN NYAVHYSAPF GKWTWAFNHN GYRYHQAVSG LSEVYDYNKG
351 SYNTDFGFNR LLYRDAKRRT YLGVLWMRE TKSIIIDAEI TVQRRKTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWY WRNLSWQFK PGHQLYLQAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*

```

m930-1/g930-1 95.4% identity in 478 aa overlap

```

          90      100      110      120      130      140
m930-1.pep  AINEVVLEGEHHARFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI
g930-1.pep  |||||:|||||
          10      20      30
          150      160      170      180      190      200
m930-1.pep  LAAPQDLNSGKLQTLTIPSYLRSIRIDRSNDDQTHAGRIAFAFQNKFPTRSDLLNLRDLE
g930-1.pep  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
          40      50      60      70      80      90
          210      220      230      240      250      260
m930-1.pep  QGLENLKRLLPTAEADLQIVPVEGEPNQSDVVVQWRQRLPYRVSVGMDSNGSEATGKYQG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```


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```

g930-1.pep  QGLENLKCLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150
m930-1.pep  270      280      290      300      310      320
              NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  160      170      180      190      200      210
              NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
m930-1.pep  330      340      350      360      370      380
              NHNGYRYHQAVSGLSEVYDYGKSYNTDFGFNRLLYRDAKRKTYLGVKLWMRETKSYIDD
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  220      230      240      250      260      270
              NHNGYRYHQAVSGLSEVYDYGKSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDD
m930-1.pep  390      400      410      420      430      440
              AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALARPEEAFGEGTSRMKI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  280      290      300      310      320      330
              AELTVQRRKTTGWLAELSHKGYIGRSTADFKLKYKHGTGMKDALARPEEAFGEGTSRMKI
m930-1.pep  450      460      470      480      490      500
              WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLSAER
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  340      350      360      370      380      390
              WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAER
m930-1.pep  510      520      530      540      550      560
              GWYWRNDSLWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  400      410      420      430      440      450
              GWYWRNDSLWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
m930-1.pep  570      580      590
              IFTGRALKKPEFFQSRKWASGFQVGYTF
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  460      470
              IFTGRALKKPEYFQTKKWVTGFQVGYSEFX

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAACCC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCAAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCC TTTCCCAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```


The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

```
m931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTGCG GTTGTGTGTC
551 GGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```
m931.pep..
1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHVRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMV RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMETDMGNIRLVLDSEKASKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLDSEKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNLKNVTGVTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNLKNVTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNVVPVQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

```
a931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
```


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451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLDESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLDESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVFVQPVKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVFVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFVG FKNPFWDAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTGC CACTCACCGC

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```

51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTGAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCCCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GCGCGGTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTGTG TAGGGGCATT GTTATGTTGC CGTTTGATT TCAGACGGCA
651 TTTTGTTC AAGCGTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1 MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQOOL AQQADDTVYQ
51 LTPFAVKDTI PAQAQANGNN QPVTGKRRR AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPQCA HQQGFHAQF
151 PCKTTGGAGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQAF
201 LYLGLALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1 ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51 ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCG TGCCGAAGCA CAGGCAAACG GCAACAACgG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCCTGGTC GCGCGGGCGG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAAATCAC ACGGGCAGGC AACCAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGCAGCCT ACCATCAGTC CGCAGCCCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGGC
401 CAKGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCCG
451 CCCCCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCCG CGCGCCAATG
501 CCGTCTGAAG AGCTTTTACA CGGCATTThT GCATTTGTTA GGGACATTGT
551 TATGTTGCCG TTGATTTC AGACGGCATT TTGTTTCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1 ..RLEQQQKQIE ALQOOLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51 TGXRRRAVYL RPIDRKLAAA KPGRRGGRRV YRQAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQOG FEHAQPPCKT TGGAXAALPP DNAPXROLPP
151 PRYARFRQEA VNPARGCRLK SPQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

			10	20	30	
m934 .pep			RLEQQQKQIEALQOOLAQQAADDTVYQLTPEAVKDTI			
g934	MKKIIASALIATFALTACQDDTQARLERQQKQIEALQOOLAQQAADDTVYQLTPEAVKDTI					
	10	20	30	40	50	60
	40	50	60	70	80	90
m934 .pep	PAEAQANGNNGQPVTVGXRRRAVYLRPIDRKLAAAKPGRRGGRRVYRQAGKQIHTGRQPR					
g934	PAQAQANGNNGQPVTVGKRRRAVYLRPIDRKLAAAKPDWRGGRRVYRQAGKQIHTGGQPR					
	70	80	90	100	110	120
	100	110	120	130	140	150

m934.pep
QSSRRPARACSLPSVRTPQCAHQGFEHAQPCKTTGGAXAALPPDNAPXRQLPPRYARF
| | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g934
QPRRPSRACCLPSVRTPQCAHQGFEHAQPCKTTGGAGAALPPDNAPARQLPPSRYARF
 130 140 150 160 170 180

 160 170 180 190 200
m934.pep
RQEAVNPAPQCRLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX
| : | | | | | | | | : | | | | : | | | | : | | | | | | | | | | | |
g934
RQKAVNPAPQCRLKGFQTAFLYLLGALLCCRLIFRRHFVSKRLMSGWQFX
 190 200 210 220 230

a934.seq

1	ATGAAAAAAA	TCATCGCCTC	CGCGCTTATC	GCAACATTCTG	CACTCGCGCG
51	CTGCCAAGAC	GACGCGCAGG	CGCGGCTCGA	ACAGCAGCAG	AAACAGATTG
101	AAGCCCTGCA	ACAGCAGCTC	GCACAGCAGG	CAGACGATAC	GGTTTACCAA
151	CTGACTCCCG	AAGCAGTCAA	AGACACCATT	CCTGCCGAAG	CACAGGCAAA
201	CGGCAACAAC	GGGCAACCTG	TTACCGG.TA	AAGACGGGCA	GCAGTATATT
251	TACGACCAAT	CGCAGGAAG	CTGTGCTGCT	CAAAAGCTTG	TCGGCGCGGG
301	GGCAGGCGCG	TTTATCGGCA	ACGCGCTGGC	AAACAAATTCT	ACACGGGCAG
351	GCAACCAAGA	CAGTCCCCTG	GCCCGGCGCG	CGCGTGCCCG	CTACCATCAG
401	TCCGCACATC	CCAATGCGCG	CACCAAGCAG	GATTGTAACA	CGCGCAGCCT
451	CGGTGCAAAA	CAACAGGCGG	CGCAGGCGCA	GCGTTACCGC	CCGACAACGC
501	GCCCCGCCGC	CAATTACCGC	CGCCCCGCCA	TGCGCGGTTT	CGGCAGAAGG
551	CGGTAATATC	GGCGTGCCAA	TGCCGCTCTA	AGGGCTTTCA	GACGGCATTT
601	TTGTATTTGT	TAGGGACATT	GTTATGTTGC	CGTTTGATTT	TTAGACGGCA
651	TTTTGTTTCC	AAGAGTTTGA	TGTCGGGATG	GCAATTCTGA	

a934.pep

1	<u>MKKIIASALI</u>	<u>ATFALAACQD</u>	DAQARLEQQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAEAQANGNN	QGPVTX*RRR	AVYLRFIDRK	LAAAKPGRRG
101	GRRVYRQRAG	KQIHTGRQPR	QSRFPARACR	LPSVRTSQCA	HQOGFEHAQP
151	PKCTGGGAGA	ALPPDNAPAR	QLPPRHARF	RQKAVNPACQ	CRLKGFQTAF
201	LYLLGTLLCC	RLFRHHFVS	KSLMSGWQF*		

```

m934.pep      10      20      30
                RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
a934          10      20      30      40      50      60
                MKKIIASALIIATFALAACQDDAARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI

m934.pep      40      50      60      70      80      90
                PAEAQANGNNGQPVGTGXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
a934          70      80      90      100     110     120
                PAEAQANGNNGQPVTTXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR

m934.pep      100     110     120     130     140     150
                QSRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
a934          130     140     150     160     170     180
                QSRRPARACRLPSVRTSQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF

m934.pep      160     170     180     190     200
                RQEAVNPARQCRLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX
a934          190     200     210     220     230
                RQKAVNPACQCRLKGFQTAFLYLLGLTLLCCRLIFRRHFVSKSLMSGWQFX

```

g935.seq not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCG TATTGCCGCG AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC AAAAAAATC
801 AGCTTATGAC GACGGGTTCC GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTGC
901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTGC CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GCGCGGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGGCTG
1251 GCGCGAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTTTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTGC
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

a935.pep

```

1 MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVDNDAPRV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNPVYA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
a935	MLYFRYGLVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
	10	20	30	40	50	60
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVINGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
m935.pep	LTPHADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTGTTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGGC CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAACG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCGGCG TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGAAAAAAT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GCGGAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CCGCACGAGC TATTATTCA GTAAAAAATC
801 AGCTTATGAT GACGGGTTTC GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCT
901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CCGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCCAAA CCGGGATGG CAATTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCAGCGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGGTTG
1251 GGCAGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CCGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCT
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFFLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVERYREL HGENAADERI LLDLAAAEFD
151 DFLKLSAERH FAZAAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFRAYLWQ QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNRRLLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNPVYA KRRNSEVFFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTGTTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGGC CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAACG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCGGCG TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```


1350

	310	320	330	340	350	360
m935.pep	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935						
	310	320	330	340	350	360
	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAE					
a935						
	370	380	390	400	410	420
	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAE					
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVASAYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935						
	430	440	450	460	470	480
	WRQLGGLNSRVASAYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	490	500				
m935.pep	GRTESNVPYAKRRNSEVFVSADWRFX					
a935						
	490	500				
	GRTESNVPYAKRRNSEVFVSADWRFX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGCGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAATC CGTCATCGAC CGcgcgAACA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCTT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAATAACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCGGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCTT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```


1351

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/g936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	: : : : : :					
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHLHLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	: : : : : :					
g936	ARSYLQNNQTKGYTPQISVVGYNRHLHLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CCGTCCTCAG
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGC	GCGGCGGTCTG
101	GCGCGAAATC	CGCCGTCGAC	CGCCGAACCA	CCGGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCACC	GCCCGCTCCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTCGGCTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAAACAG
301	TTCGTCGGTC	AGATTGCACG	TTCCGAACAG	GCCGCCGAAG	GCGTGTACAA
351	CTACATTACC	GTCGCCTCCC	TGCCGCGCAC	TGCCGCGGAC	ATCGCCGCGG
401	ACACTTGGAA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACCTACGT
501	TATGGGCATC	CTCACCCCGG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCGT	CGGCGTACAA	AAAGTCATCA	CCCTTACCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936.pep

1	MKPKPHTVRT	LTAAVLSLAL	GGCVSAVVGG	AAVGAKSVD	RRTTGAQTDD
51	NVMALRIETT	ARSYLQNNQ	TKGYTPQISV	VGYNRHLHLL	GQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	QR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	: : : : : :					
a936	MKPKPHTVRTLTAAVLSLALGGCFSAVVGGAAVGAKSVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHLHLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	: : : : : :					
a936	ARSYLQNNQTKGYTPQISVVGYNRHLHLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936.pep	VASLPRTA					


```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAATC CGTCATCGAC CGcgaACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGCTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACCTTGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCGGTCGAC CGCGGAACCA CCGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGCTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACCTTGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATCA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1  MKPKPHTVRT LIAAIFSLAL SGQSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

Seq ID 4

m936-1/g936-1 95.5% identity in 202 aa overlap

```

          10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSVIDRRTTGAQTDDNVMALRIETT
          10      20      30      40      50      60

          70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      ARSYLRQNNQTKGYTPQISVVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT
          70      80      90      100     110     120

          130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```


1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGCGGTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTGC
101 GCGCGAATC CGCCGTCGAC CGCCGAACCA CCGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCA AATCTCCGT TCGGCTACA
251 ACCGCCACCT GCTGTGCTC GGACAAGTCG CCACCGAAG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCAAG GCGGTACAA
351 CTACATTACC GTCCCTCCC TGCCGCGCAC TGCCGCGGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGCGGTACAA AAAGTCATCA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVSAVVGG AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TRGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAASAVDRRTTGAQTDDNVMALRIETT
              ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
a936-1      MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGVGAASAVDRRTTGAQTDDNVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTRGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT
              |||||
a936-1      ARSYLRQNNQTRGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTAgT ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51  CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAaactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACCTGCCT CACCGGTTTA CATTcagACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGAAGTaccg GCAataccgA CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACCTGacg GCAACGGCAA

```



```

351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
401 TCCTtaAAGa cgGCAAAAAT CCCGCACTCA TCGCTTTCCT CGAAAGCACG
451 GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCGGGAAAAT CGTGGCTCAT
501 CGGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCTT TCCCTCACCG
551 CCGCCTACCG CATCAACGGC AGCAAAACCC TTTCAGACGA CGTCAAATAC
601 AAAGCAGGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
651 CGACAGAATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCG
701 ACCGCATAGA CGGCAAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
751 CATTTTCGCG CAGGTTTCGG TTTCACCAA ACCGCGGCTT TAAACGCATC
801 CGCACGTTTC AACGTTTCAG GGCAAAGCAG TTCCGAACTG AAATTGGGCG
851 TACAGCATAC ATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:

g937.pep

```

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETSL TYLNSNSRA
51 ALASPVIYQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIY
101 SGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
151 VYEKSRNKAS SGKSWLIGAT TYKAIDPIVL SLTAAYRING SKTSLDDVKY
201 KAGNYWMLNP NISFAANDRI SLTGGIQWL KQPDRIKDGK ESARNTSTYA
251 HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVOHTF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

```

1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTTG CCGCACCAGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAgAAAaCGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCGACGCT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCAACATCT CATTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pep..

```

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENN
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTND DMLVGTGLR YGLTGNTDIY
101 SGSYLWHEER RKLGNKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRPDRTDGK RESSNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

	10	20	30	40	50	59
g937.pep	MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETS	TYLNSNSRAALASPVIYQ				
	:: :: :: : : ::					
m937	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETS	TYLNSENNRAELAAPVYIQ				
	10	20	30	40	50	60
g937.pep	60	70	80	90	100	110
	TGSASFIPVPT	EIQENGSTND	MLAGTLGLRY	GLTGNTDIY	YSGSYLWHEER	KLDGNGKTR

[illegible]

a937.seq

1	ATGAAGCGCA	TCTTTTGGCC	CGCCTTGCCC	GCCATCCTGC	CTTTATCCGC
51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGCA
101	AATGGAAACT	GGAAACTTCC	CTTACCTACC	TGAACGCGCA	AAACAACCGC
151	CGCGAACTTG	CCGCACCGGT	TTACATCCAA	ACCGCGCGAA	CCTCGTTTAT
201	CCCCATTCCG	ACCGAAATCC	AAGAAAACGG	CAGCAATACC	GATATGCTCG
251	TTGGCAGCCT	CGGTTTGCGC	TACGGACTGA	CCGGGAATAC	CGACATTTAC
301	GGCAGCGGCA	GCTATCTGTG	GCACGAGAA	CGCAAACCTG	ACGGCAACGG
351	CAAAACCCGA	ACAAACGGGA	TGTCCGAGT	ATCCCTCGGC	ATCAGCCACA
401	CCTTCCTTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	TCTTGAAGAC
451	ACGGTTTACG	AAAAATCGCG	CAACAAAGCC	TCGTGCGGAA	AATCCTGGCT
501	CATCGGCGCC	ACCACCTACA	AAGCCATCGA	CCCCGTCGTC	CTCTCATTGA
551	CCGCTGCCTA	CCGATTCAAC	GGCAGCAAAA	CCCTTTCAAG	CAACACCAAA
601	TACAAGCAG	GCAATTACTG	GATGCTGAAT	CCCAATATAT	CCTTCGCGCG
651	CAACGACAGA	ATCAGCCTCA	CGGGCGGCAT	CCCATGGCTG	CGTACGACGC
701	CCGACCGTCT	GGACGGCAAA	AAAGAATCCG	CAAGAAACAC	ATCCACCTAT
751	GCCCATTTCG	GCGCAGGTTT	CGGTTTCACC	AAAACCACGG	CTTTAAACGC
801	ATCCGCACGT	TTCAACGTTT	CAGGGCAAAG	CAGTTCGGAA	CTGAAATTTG
851	CGGTACACGA	TACGTTTTAA			

a937.pep

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSENNRR
51	AELAAPVYIQ	TGATSFIPIP	TEIQENGST	DMLVGTGLGR	YGLTGNTDIY
101	GSQSYLWHEE	RKLDGNGKTR	NKRMSDVSIG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIDPVV	LSLTAAYRIN	GSKTLSNSTK
201	YKAGNYWMLN	PNISFAANDR	ISLTGGIQWL	KQFPDRLDGK	KESARNTSTY
251	AHFGAGGFGT	KTALNASAR	FNVSQSSE	LKFGVQHTF*	

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
a937	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m937.pep	TGATSFIPIPTEIQENGSTNDMLVGTGLGLRYGLTGNTDIYGGSGSYLWHEERKLDGNSKTR					
a937	TGATSFIPIPTEIQENGSTNDMLVGTGLGLRYGLTGNTDIYGGSGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACITTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACITTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTACAGCATC AGGCATATAT
501 TGTGTAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTGAA AGCGGTGCGC
601 AACTTTATCC AAGTTTGCG TTA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTHGSAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPKNPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVEQ MNAYKSGQRK NTIMEDIANR MSEEDLKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLLAFVLAAGAVSASP KADVEKGKQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					
a939	MKRLTLLAFVLAAGAVSASP KADVEKGKQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					

1357

```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNAP
              |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVNLSDQDILNVSAFYAKQQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGCG GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAKHKT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCASKSAEGSCGASKSAEG
              10      20      30      40      50      60
              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |:|||||
g950          SCGAAASKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```


This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

a950.pep

```

1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKS AHG SCGASKSAEG
51  SCGAAGSKAG EGRCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

```

a950.pep      10      20      30      40      50      60
               MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHGSCGASKSAEGSCGAAGSKAG
               |||||||
m950          10      20      30      40      50      60
               MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHGSCGASKSAEGSCGAAGSKAG
               |||||||

a950.pep      70      80      90     100
               EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
               |||||||
m950          70      80      90     100
               EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
               |||||||
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

g951.seq

```

1  ATGATTATGT TACCCGCCCG TTCTACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGCTGTTT ACGCTGTTGG CCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAAAC CACAAATCC
301 CCCGAAGTCG CCGAACGCGC CTGGGAAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG CCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG CCGGGGTGGC TCGGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CCGGTGGGAA GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCG CCGTCCGGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTCGG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAATA TTGCCCCCA CTTTAATGAC GTTGCGTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCGG TCTGGCAGGA AATGGAAATT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGAA CGTGTGTTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTTGA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCG GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACCTTC GCGGCGGGA
1351 AGCAGCGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTACGA
1401 ACAGTTCGGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAATC AACCCGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAGGCGGAC GCGGAAAGCG CGTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCATT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGACG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTCCCGA GCCTTCCCGA AAACCCCGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

g951.pep

```

1  MIMLPARFTI LSVLAALLA GQAYAAGAAD VELPKEVGKV LRKHRRYSEE
```



```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHLDGLG EVLAQSDDDVQ KRRIFLLLVQ AAVQQGGVAQ KASKAVRRRA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTET LPPTLMTLRL
251 TARKYPEILD GFEEQTDTON LSAVWQEMEI MNLVSLRKPQ DAYARLNVLL
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRDRYA KVRQWLKKVS APEYLFDKGV LAAAAAAELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGMIAADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYLGKD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

m951.seq

```

1 ATGATTATGT TACCTAACCG TTCAAAATG TTAAGTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACACCCGAA GGAAAGTCGA AAGGTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCCGCGG TGGGCGAGCG
201 GGTTAATCAG ATATTACGT TGCTGGGAGG GGAACCCGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCGG TGTCGCTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGCGGG GGTGGCTGCG GAACGTGCTG
451 AGTGAAGAGG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGCGACGAA GGACAGAACC GCAGGCTGTT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGGCGTTGA AATATGAACA TCTGCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGACGCG AAAAGGAAA GGCATCGGA GCTTTCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCACCTTT AATGACGTTG
751 CGCTGACTG CACGCAATA TCCCGAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGCTG GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CTTGCACAGG CTGGATGATG CCTATGCGCG TTGAAACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTGAG CAGCGATATT
951 GCGGCGAAAC CGAAAAGAAG GTGCTTCCGT TATCGACGCG TACGCCGAAA
1001 AGGCATACGG CAGGGGGACG GAGGAACAGC GGAGCAGGGC GCGGCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAAG TCAGGCAAGT
1101 GCTGAAATAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CCGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGCGCGC TTTGCGGCAG
1201 ATCGGCAGG TGCGGAAACT TCCCGAACAG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTGG TCCAAAATAC AGATGCTCGC CCGTGCAGAG CTGCCCGATA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCTTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTGAGTTGT
1401 TTACGATCGG CTGGCAAGC GGAATAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGCGATAC CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGCGGTA TTACCTGAAA GCGACGCGG AAAGCGCGCT GCCGTATCTG
1651 CGGTATTGCT TTGAAACGA CCCCAGGCC GAAGTTGCCG CCCATTGGG
1701 CGAAGTGTG TGGGCATTGG CCGAACCGGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCCGAAAAC CTCGGAAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

m951.pep

```

1 MIMLPNRFKM LTVLTATLIA GQVSAAGGGA GDMKQPEVG KVFRKQORYS
51 EEEIKNERAR LAAGGERVNO IFTLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSEVAERAL EMASVNAFE QAEMIYQKWR QIEPIGKAQ KRAGWLRNVL
151 RERGNHLDG LEEVLAQADE GQNRVFLLL AQAAVQDGL AQKASKAVRR
201 AALKYEHLP EAAADVVSFV QGREKEKAI ALQRLAKLDT EILPPTLMTL
251 RLRTARKYPEI LDGFEEQTDI QNL SAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLENPNADL YIQAILAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRDR YAKVRQWLKK VSAPEYLFDK GVLA AAAAVE LDGGRALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LKPKREALRG LDKIIEKPPA
451 GSNTLQAEAL LVQSVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNLGY
501 SLLTDSKRLD EGFALLQTAY QINPDDTAVN DSIWAYYLGK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

1360

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGAGDMKQPKVEVGKVFRRKQRYSEEEIKNERAR					
g951	10	20	30	40	50	
	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKVEVGKVLRRHRYSEEEIKNERAR					
m951.pep	70	80	90	100	110	120
	LAAVGERVNIQIFTLGGETALQKGAGTALATYMLMLERTKSPVAERALEMAVSLNAFE					
g951	60	70	80	90	100	110
	LAAVGERVNRVFTLLGGETALQKGAGTALATYMLMLERTKSPVAERALEMAVSLNAFE					
m951.pep	130	140	150	160	170	180
	QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLGLEEVLAQADEGQNRVFLLL					
g951	120	130	140	150	160	170
	QAEMIYQKWRQIEPIPGEAQKRAGWLRNVLRERGNQHLGLEEVLAQSDDDVQKRRI FLLL					
m951.pep	190	200	210	220	230	240
	AQAAVQQDGLAQKASKAVRRAALKYEHLPAAVADVFSVQGREKEKAIGALQRLAKLDT					
g951	180	190	200	210	220	230
	VQAAVQQGGVAQKASKAVRRAALKYEHLPAAVADVFGVQGREKEKAIEALQRLAKLDT					
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	240	250	260	270	280	290
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLRKPDDAYARLNV					
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAAI LAANRKEGASVIDGYAEKAYGRGTGEQSRRAALTAAMMYADRRD					
g951	300	310	320	330	340	350
	LLERNPNANLYIQAAI LAANRKEGASVIDGYAEKAYGRGTGEQSGRAAMTAAMIYADRRD					
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQQGRYFTADNL					
g951	360	370	380	390	400	410
	YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQQGRYFTADNL					
m951.pep	430	440	450	460	470	480
	SKIQMLALS KLPDKREALRGLDKIIEKPPAGSNTLQAEALVORSVVYDRLGKRKKMISD					
g951	420	430	440	450	460	470
	SKIQMLALS KLPDKREALIGLNNIIAKLSAAGSTEPLAEALQRSIIYEQFGKRGMIA D					
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNNGYSLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	480	490	500	510	520	530
	LETALKLTPDNAQIMNNGYSLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQA AHLTGDKKIWRETL					
g951	540	550	560	570	580	590
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQA AHLRGDKKIWRETL					
m951.pep	610					
	KRHGIALPQPSRKPRK					
g951	600	610				
	KRYGIALPEPSRKPRKX					

1	ATGTTACCCG	CCCgTTTCAC	CATTTTATCT	GTGCTCGCGG	CAGCCTGCT
51	TGCCGGGGAG	GGGTATTCCG	CCGGCGCGCG	GGATGCGAAG	CCGCCGAAGG
101	AAGTCGGAA	GGTTTTCAGA	AGACGACAGC	GTTCACAGCA	GGAAGAATATC
151	AAAAACGAAC	GCGCACGGCT	TGCGGCAGTG	GGCCAGCGGG	TTAATCAGAT
201	ATTTACGTTG	CTGGGAGGGG	AAACCGCCTT	GC AAAAGGGG	CAGCGCGGAA
251	CGGCTCTGCG	AACCTATATG	CTGATGTTGG	AACGCACAAA	ATCCCCCGAA
301	GTCGCCGAAC	GCGCCTTGGA	AATGGCCGTG	TCGCTGAACG	CGTTTGACACA
351	GGCGGAAATG	ATTTATCAGA	AATGGCGGCA	GATTGAGCCT	ATACCGGGTA
401	AGGCGCAAAA	ACGGCGGGGG	TGGCTGCGGA	ACGTGCTGAG	GGGACAGGAGA
451	AATCAGCATC	TAGACGGACT	GGAAGAAGTG	CTGGCTCAGG	CGGACGAAAG
501	ACAGAACCGC	AGGGTGTTTT	TATTGTTGGC	ACAAGCCGCC	GTGCAACAGG
551	ACGGGTTGGC	GCAAAAAGCA	TCGAAAGCGG	TTCCGCGCGC	GGCGTGTAGA
601	TATGAACATC	TGCCGAAGC	GAGGTGTGCC	GATGTGGTGT	TCAGCGTACA
651	GGGACGCGAA	AAGGAAAAAG	CAATCGGAGC	TTTGACGCGT	TTGGCGAAGC
701	TCGATACGGA	AATATTGCCC	CCCACTTTAA	TGACGTTGCG	TCGACTGTGA
751	CGCAAAATCT	CCGAATACT	CAGCGCCTTT	TTCTGACGACA	CAGACACCCA
801	AAACCTTTCT	GCCGCTCTGC	AGGAATATGA	AATTATGAAT	CTGGTTTCCC
851	TGCACAGGCT	GGATAGTGCC	TATTCGCGCT	TGAACGTGCT	TTTGGAAACG
901	AATCCGAATG	CAGACCTGTA	TATTCAGGCA	GGCATATGTT	CGGCAAAACG
951	AAAGAAGGTT	GCTTCCGTTA	TCGACGGCTA	CGCCGAAAAG	GCATACGGCA
1001	GGGGGACGGG	GGAACAGCGG	GGCAGGGCGG	CAATGACGGC	GGCATATGATA
1051	TATGCCGACC	GAAGGGATTA	CACCAAGATC	AGGCAGTGGT	TGAAAAAAGT
1101	GTCCGCGCGC	GAATACCTGT	TCGACAAAAG	TGTGCTGGCG	GCTGCGGCGG
1151	CTGTCGAGTT	GGACGCGCGC	AGGGCGGCTT	TTCCGCGAGT	ACGAGGGGTG
1201	CGGAAACTTC	CCGAAAGCCA	GGGGCGGTAT	TTCGCGCAG	CCCATTTGTC
1251	CAAAATACAG	ATGTTTCGCC	TGTCGAAGCT	GCCCGACAAA	CGGGAGGCTT
1301	TGAGGGGGTT	GGACAAGATT	ATCGAAAAC	CGCCTGCGCG	GAGTAATACA
1351	GAGTTACAGG	CAGAGGCATT	GGTACAGCGG	CTAGTTGTTT	ACGATCGGCT
1401	TGCAAGCGCG	AAAAAAATGA	TTTCAGATCT	TGAAAGGGCG	TTCAGGCTTG
1451	CACCCGATAA	CGCTCAGATT	ATGAATAATC	TGGGCTACAG	CTGCTTTTCC
1501	GATTTCCAAC	GTTTGGACGA	AGGCTTCCGC	CTGCTTCAGA	CGGCATACCA
1551	AATCAACCCG	GAGCATACCG	CTGTCAACGA	CAGCATAGGC	TGGGCGTATT
1601	ACCTGAAAG	CGACGCGGAA	AGCGCGCTGC	CGATTCTCGC	GATTTCTGTT
1651	GA AAAACGAC	CCGAGCCCGA	AGTTGCCGCC	CATTTGGGCG	AAAGTTTGTG
1701	GGCATTGGGC	GAACCGCATC	AGGCGGTTGA	CGTATGGACG	CAGGCGGCAC
1751	ACCTTACGGG	AGACAGAGAA	ATATGGCGGG	AAACGCTCAA	ACGTCACCGG
1801	ATCGCATTCG	CCCAACCTTC	CCGAAAACCT	CGGAAATAA	

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

1	1	MLPARFTILS	VLAALLAGO	AYAAGAADAK	PPKEVGKVR	KQORYSEEEI
51		KNERALAAV	GERVNIQFTL	LGGETALQKG	QAGTALATYM	LMLERTKSPE
101		VAERALEAM	SINAVEQAEAM	IYQKWRIEP	IPGKAQKRG	WLRNVLRERG
151		NQHLDGLEEV	LAQADEGQNR	RVFTLLAQAA	VOQDGLAQKA	SKAVRRALRG
201		YEHLPAAVA	DVVFSVQGRE	KEKAGALQR	LAKLDEILP	PTLMTLRLLTA
251		RKYPEILDFG	FQETDQNLIS	AVWQEMEIMN	LYSLHRLDDA	YARLVNLER
301		NPNADLYTQA	AFLAANRRKG	ASVIDGYAEK	AVGRGTGEOR	GRAMTAAMI
351		YADRRDYTKV	RQWLLKKVASP	EYLPDKGVLA	AAAVELDGG	RAALRQIGRV
401		RKLPEQQRGY	FTADNLISKI	MFALSKLPDK	REALRGLDKI	IEKPPAGSNT
451		ELQAEALVQR	SVVYDRLGKR	KKMISDLERA	FRLPADNAQI	MNNLYGSLLS
501		DSKRLDEGFA	LLQTAYQINP	DDTAVNDSIG	WAYYLGDAE	SANPLYRYSF
551		ENDPEPEVAA	HGLEVWLALG	ERDQAVDVPST	QAAHLTKDGK	IWRETLKRHG
600		IALPORSKAP	RK*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep    MLPARFTILSLAALLAGQAYAA--AADAKPPKEVGKVFRRQORYSEEEIKNERAR
           |||::||::||::||::|||::||::|||::|||::|||::|||::|||::|||
m951        MIMLPNRFKMLTLTATLIAGQVSAAGGGADMKQPKEVGKVFRRQORYSEEEIKNERAR
           10      20      30      40      50      60
a951.pep    LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVLSNAF
           60      70      80      90     100     110

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1362

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|||||
m951      LAAVGERVNIQFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
          70      80      90      100     110     120

          120     130     140     150     160     170
a951.pep  QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          |||||
m951      QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          130     140     150     160     170     180

          180     190     200     210     220     230
a951.pep  AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAI GALQRLAKLDT
          |||||
m951      AQAAVQQDGLAQKASKAVRRAALKYEHLPEAAVADVVSQGREKEKAI GALQRLAKLDT
          190     200     210     220     230     240

          240     250     260     270     280     290
a951.pep  EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
          |||||
m951      EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
          250     260     270     280     290     300

          300     310     320     330     340     350
a951.pep  LLERNPNADLYIQAAILAANRREGASVIDGYAEKAYGRGTGEQGRAAMTAAMIYADRRD
          |||||
m951      LLERNPNADLYIQAAILAANRREGASVIDGYAEKAYGRGTGEQRAALTAAMMYADRRD
          310     320     330     340     350     360

          360     370     380     390     400     410
a951.pep  YTKVRQWLKKVSAPEYLFDRGVLA AAAAVELDGGRAALRQIGRVKRLPEQQGRYFTADNL
          |||||
m951      YAKVRQWLKKVSAPEYLFDRGVLA AAAAVELDGGRAALRQIGRVKRLPEQQGRYFTADNL
          370     380     390     400     410     420

          420     430     440     450     460     470
a951.pep  SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
          |||||
m951      SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
          430     440     450     460     470     480

          480     490     500     510     520     530
a951.pep  LERAFRLAPDNAQIMNNLGYSLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
          |||||
m951      LERAFRLAPDNAQIMNNLGYSLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
          490     500     510     520     530     540

          540     550     560     570     580     590
a951.pep  GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          |||||
m951      GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          550     560     570     580     590     600

          600     610
a951.pep  KRHGIALPQPSRKPRK
          |||||
m951      KRHGIALPQPSRKPRK
          610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

g952.seq (partial)

```

1  ..TTGTCATTATC GTTGAATGC TGCACCGATG TTAAACGATA ATCCTGTTGT
51  TTACGGAAAA ATCAAAATGC AGAGTTGGAA AGCGCGGCGG GATTTCATA
101 TTGTAAAGCA GGATTGGAT TTTCCCTGCG GGGCGGCTTC GGTGGCGACG
151 CTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTGGA
201 AAAACTGGGT AAGGAACAGA TCGCGCGGTC GTTTAGGAT ATGCGGCGCA
251 TTATGCCCGA TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301 CAGCTCGCGC AGTTGAAAAT CCCCGTCATC GTGTATCTGA AATACCGCAA
351 AGACGACCAT TTTTCGGTAT TCGCGGAGT GCATGGCAAT ACGGTTTTGC
401 TTGCCGACCC GTCGCCGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTTG
451 GAGGCTTGGC AAACCCGTA GGGAAATTG GCAGGCAAAA TTTTGGCGGT
501 CGTGCCGAAA AAAGCGGAG CGATTTCAA TAAATTGTTT TTCACACATC
551 ATCCCAAGCG GCAGACGGAG TTTGCAGTC GACAGGTAAA ATGGTGGCGT

```


601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)

```

1  ..LSYRLNAAPM FNDNPVYVGK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
51  LLNNFYGQKL TEEVLEKLG KEQMRASFED MRRIMPDLGF EAKGYALSFE
101 QLAQLKIPVI VYLKYRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL
151 EAWQTRGNL AGKILAVVPK KAEAISNKL FTHHPKRQTE FAVGQVKWWR
201 AY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq

```

1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTGTGTT
101 ACGGAAAAAT CAAAGTCAG AGTTGGAAG CGCGCGCGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCTGATT TGGGTTTGA GCGGAAGGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCGCAG TTGAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGGCA TGTTCATG AGCAGGGCGC AGTTTTGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGCC AGGTAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep

```

1  MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVO SWKARRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRR
101 MPDLGFCAK YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFTQH
201 PKRQTEFTVG QIRQARAE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952; 92.5% identity in 201 aa overlap

```

                                10      20      30      40
g952.pep                      LSYRLNAAPMFNDNPVYVGKIKLQSWKARRDFNIVKQDLD FSCG
|||||
m952      MMKFYVFLACVVVLSYRLNAAPMFNDNPVYVGKIKVQSWKARRDFNIVKQDLD FSCG
              10      20      30      40      50      60

              50      60      70      80      90      100
g952.pep    AASVATLLNNFYGQKLTEEEVLEKLGKEQMRASFEDMRRIMPDLGFCAKGYALSFEQLAQ
|||||
m952      AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFCAKGYALSFEQLAQ
              70      80      90      100      110      120

              110     120     130     140     150     160
g952.pep    LKIPVIVYLKYRKDDHFSVLRGVDGNTVLLADPSPGHVSMSRAQFLEAWQTRGNLAGKI
|||||
m952      LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSMRAQFLDAWQTRGNLAGKI
              130     140     150     160     170     180

              170     180     190     200
g952.pep    LAVVPKKAEAISNKLFFTHHPKRQTEFAVGQVKWWRAYX
|||||
m952      LAVIPKKAETISNKLFTQHPKRQTEFTVGQIRQARAE
              190     200     210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq

```

1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
```


1364

```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGCGCGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTC AATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1 MMKFKYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEE VLKLDKEQM RASFEDMRRRI
101 MPDLGFEEK YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

```

a952/m952    97.7% identity in 218 aa overlap

a952.pep      10      20      30      40      50      60
MMKFKYVFLACVVVLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG
|||||
m952          10      20      30      40      50      60
MMKFKYVFLACVVVLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG
|||||

a952.pep      70      80      90     100     110     120
AASVATLLNNFYGQTLTEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
|||||
m952          70      80      90     100     110     120
AASVATLLNNFYGQTLTEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
|||||

a952.pep     130     140     150     160     170     180
LKIPVIVYLK YRKDDHFSVL RGIDGNTVLLADPSLGHVMSRAQFXDAWQTREGNLAGKI
|||||
m952         130     140     150     160     170     180
LKIPVIVYLK YRKDDHFSVL RGIDGNTVLLADPSLGHVMSRAQFLDAWQTREGNLAGKI
|||||

a952.pep     190     200     210     219
LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAE
|||:|||||
m952         190     200     210
LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1 ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCCGCCACC TACAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGCTGACC
151 GGTTCGCTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTC GCAACCCCTC ACCGCCACCC
251 TGAATCCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACCCA AATTCAACTT CAACGGCAAA AAAGTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAATC AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGCGGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```


This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

g953.pep

```

1 MKKIIFAALA AAAVGTASAT YKVDEYHANV RFAIDHFNST TNVGGFYGLT
51 GSVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPDIRF
101 VSTKFNFNKG KLVSVVDGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVCQG
151 DFSTTIDRTK WGVLDLVNAG MTKNVRIDIQ IEAAKQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

m953.seq

```

1 ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG
101 CCATCGACCA TTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
151 ACCGGTTCGG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC ATTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAATTCAA CTCAACGGC AAAAAACTGG TTTCCGTTGA
351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAA CTCAAAGCCG
401 AAAAAATCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC
451 GCGGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

m953.pep

```

1 MKKIIFAALA AAAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL
51 TGSVEFDQAK RDGRIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNFNKG KLVSVVDGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCG
151 GDFSTTIDRT KWGMDLVNV GMTKSVRIDI QIEAAKQ*
```

Seq ID 5

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

	10	20	30	40	50	60
m953.pep	MKKIIFAALAAAAISTASAAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
g953	MKKIIFAALAAAAVGTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	
	70	80	90	100	110	120
m953.pep	RDGRIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKGKLVSVVDGNL					
g953	RDGRIDITIPVIANLQSGSQPFTHLKSADIFDAAQYPDIRFVSTKFNFNKGKLVSVVDGNL					
	60	70	80	90	100	110
	130	140	150	160	170	180
m953.pep	TMHGKTAPVKLKAEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDLVNVGMTKSVRIDI					
g953	TMHGKTAPVKLKAEKFNCYQSPMAETEVCGGDFSTTIDRTKWGVLDLVNAGMTKNVRIDI					
	120	130	140	150	160	170
m953.pep	QIEAAKQX					
g953	QIEAAKQX					
	180					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

a953.seq

```

1 ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
101 CTATCGACCA TTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
151 ACCGGTTCGG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAATTCAA CTCAACGGC AAAAAACTGG TTTCCGTTGA
```


1366

```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGGCGC
451 GCGCACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGS
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

a953.pep

```

1  MKKIIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAQYPPDIR
101 FVSTKFNENG KRLVSV DGNL TMHGKTAPVK LKAEKFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

```

a953.pep      10      20      30      40      50      60
               MKKIIIIAALAAAIGTASAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK
m953          10      20      30      40      50      60
               MKKIIIFAALAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK

a953.pep      70      80      90      100     110     120
               RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAQYPPDIRFVSTKFNENGKRLVSV DGNL
m953          70      80      90      100     110     120
               RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAQYPPDIRFVSTKFNENGKRLVSV DGNL

a953.pep      130     140     150     160     170     180
               TMHGKTAPVKLKAEKFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
m953          130     140     150     160     170     180
               TMHGKTAPVKLKAEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI

a953.pep      QIEAAKQX
m953          QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

m954.seq

```

1  ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
51  GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGCG GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTA CTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAAAACAGGC TCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

m954.pep

```

1  MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
51  RFRVLQQGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDL D KESYQNYRKS MQECKRTITE
151 AEANLPKK*

```


a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

g957.seq (partial)

```

1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51 TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGCTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGTCATG GACTCGCGCG ATTATGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG GGGGatgaag gcgaacagtc ttgtggtcgg
801 ctatgatgag gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaataattatt tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaac acggatggcg taacggcgga
951 tatgcaaaacc tatcatgctc aacaaacggt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

g957.pep (partial)

```

1 MFKFKPVL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51 AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPIQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PFAFVNAEYL
151 YRNDPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRKIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS VDNKKPQSV EYLLKNGNLF
301 IAQSSVTILK TDGVTADMQT YHAQQTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

m957.seq

```

1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51 TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGCTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTGC GACTCGCGCA ATTCTGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACC CAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAC
1051 TTGGAAAT TGGAAAAAGA GGTGCGCGT TATGCAGAGG CTGCGCGGAG
1101 ACGTTCGGGC GCGAGGCGG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

m957.pep

```

1 MFKFKPVL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVKPNPNAFV
51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPIQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PFAFVNAEYL
151 YRNDPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRKIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
```


1368

251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYLLKNGNLF
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAVAKLARLFRNA					
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNFAVAKLARLFRNA					
	10	20	30	40	50	60
g957.pep	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
g957.pep	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLNRDRPFVSVNVYGGTAHGENYETTGEYRVV					
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLNRDRPFVSVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180
g957.pep	WQPDGVSFVDAAGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m957	WQPDGVSFVDAAGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
g957.pep	DSRDYVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSVDNGKKPQSVEYLLKNGNLF					
m957	DSRNSVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSFEYLLKNGNLF					
	250	260	270	280	290	300
g957.pep	IAQSSTVTTLKTDGVTADMOTYHAQQTLYLDG					
m957	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330			
g957.pep	YAEAAARRSGGRRDLSHX					
m957	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTTTG	CACCTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAATCCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCCA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCCAGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC


```

951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CCGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

a957.pep

```

1 MFKKFKPVLL SFFALVFAPW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51 ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKKRQSFEYY LKNGNLFYAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50
m957	10	20	30	40	50
a957.pep	60	70	80	90	100
m957	60	70	80	90	100
a957.pep	110	120	130	140	150
m957	110	120	130	140	150
a957.pep	160	170	180	190	200
m957	160	170	180	190	200
a957.pep	210	220	230	240	250
m957	210	220	230	240	250
a957.pep	260	270	280	290	300
m957	260	270	280	290	300
a957.pep	310	320	330	340	350
m957	310	320	330	340	350
a957.pep	360	370			
m957	360	370			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

g958.seq

```

1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51 TTTCGCCACG CATTGCGCCG CCGATACCGT TCGCGCGGAA GAGGCGGACG

```



```

101 GCGGTGTGCG AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAGCT
151 TCCGATTGTA CCCTCGGTTC GACCTGCCTG TTTTGCAGTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCGAAG CCGCCGTCCA AGGCAGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTCCGC CTCCAACAGG ACGGTACGCT GATTCCGGGC
451 GAAACCTGA CTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACGT
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCACAATTC
601 AACACCTGTT CCGCCGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCCGAT CCGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCCTCG
701 TGTTCGGCGG CGTTCCTT TTTCTATACG CTGGGCGGA CTTCCTCGCTT
751 GACGGCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGGCGTT TCCCTTCCG TCCCTTATTA TTTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CCGGACGTTT
901 GACGGACAAA TCCGTTACCT CGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCAGATA AGAAAAGCGG CAGGAACAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCGAG GCGCGCGGGA GGCAGCCTGA ATGCCGCGCT TTCGGTTCAG
1201 AAATACCAAG CGCTGGCAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAATGGG ATTTAGCAA
1401 CAGCTGGGCG TACGTCCGCC CCAAACTCGG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCGGCGCG AAAGCATCCC GCAGCGTCGG GCGCGTTTGT
1501 CCCGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGCG GGAGTCGTGC AAACCATCGA GCGCGCGCTG TTCTACAAC
1601 ATATTCTCTG CAAATCTCAA AACGACCTGC CCAATTTCTG TTCGTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCGCTG CAGAGCGCTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATCTTATT TCAAGGATGA TCGCGTGATG CTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTGCGCTCC GCGCGCATAG
1901 GCGGGCGTTT CACCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CGCGCAGGC TACCGCCCCG CCCCCGAAA
2001 AGTGTGAAC GCCCGTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCGTCC GCTACAATA
2151 CGGTTTGA GCAAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGCGG TGTACGCCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCCGTC TTTTTCAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCGCG AGGCAGGATG GATGTCGCCG
2351 TTCCCGGCTA CATCCCCGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

```

g958.pep
1  LARLFLSKPL VLALGFCEFGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51  SDLTLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRM EGQS
101 KVKVRAEGSV IIERDGA VLN TDWADYDQSG DTVTVGDRFA LQQDGT LIRG
151 ETLYNLDDQ TGEAHNVRME TEQGGRRLQS VSRTAEMLGE GRYKLTETQF
201 NTCAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYL RPD YSGQD LTLWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
501 PVVNI DGTT FERNTRLFGG GVVQTI EPRL FYNIPAKSQ NDLPNFDSSE
551 SSFGYGQLFR ENLYYGNDR I NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSVGNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGVLN ARYKYGRNEK IYLDAGSYF YDKLSQDLDS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TIENTYKNAV FFSLQLKDL S SVGRNPAGRM DVAVPGYIPA HSLSAGRNKR
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

```

m958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
51  CTTCCGGCAGC CATTGCCCGC CCGCCGATGC CGTTGGCGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCGGA ACCCATACAG

```



```

151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAACCG
351 GACGACCCTC AATACCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
401 TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGCAGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCGG CGGCGTTCCT ATTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCGCCCGG
801 TTCGGACGGC GTTTCCTTTT CCGTTCCTTA TTATTTC AACCTGCCCA
851 ATCTCGATGC CACGTTCGCG CCCAGCGTGA TCGCGAAGC CGGCGCGGTC
901 TTTGACGGGG AGGTACGCTA CTTGCCGGCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC ACAAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGCGGCGG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTG GCGTAAAAAC ACCGGCAGGG
1301 CGCAAAATCG CGTGTCCGCA CAATTTACCC GATTACGCCA CGACAGCCGC
1351 CAAGACGGCA GCGCGCTGGT CGTCTATCCC GACATCAAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CGCTTCGGC AGCCAAGAG CCGACGCGT CAGCCGCACT
1501 CTGCCCATTG TCAACATCGA CAGCGGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTCCGC GGAGAAGTCC TGCAAAACCT CGAGCCGCGC CTGTCTTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATT CTGATTCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CCGGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGA GCGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCAATTGCC TCCGGCAGCA
1901 TCGGCAGCCG CTTATCCTC GACAGCAGCA TCCACTACAA CAAAACGAC
1951 AAACCGCCCG AGAACTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAAATACG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGGG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTGC
2351 CCGTTCGCCG CTATATCACC GCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGACCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1  LARLSLKLPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51  PLSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTL NTDWADYDQS GDTVTAGDRF ALQODGTLIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRQL SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VSLSPYYFN LAPNLDTFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLAGLSV
401 LKYQILANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSCF TFERNTRMFG GEVLQTLPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSGVKKP RNRSDWVAFS SGSSIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVKL NARYKYGRNE KIYLSKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAHEYKSSCG WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

	10	20	30	40	50	60
m958.pep	LARLFS	LKPLVL	ALGLCF	GTHCAA	ADAVAA	EETDNPT
g958	LARLFS	LKPLVL	ALGLCF	GTHCAA	-DTVA	EEADGR
	10	20	30	40	50	
	70	80	90	100	110	120
m958.pep	LFCSNE	SGSPER	TEAAVQ	SGSEAS	IPEDYTR	IVADRM
g958	LFCSNE	SGSPER	TEAAVQ	SGSEAS	VPEDYTR	IVADRM
	60	70	80	90	100	110
	130	140	150	160	170	180
m958.pep	NTDWAD	YDQSGD	TVTAGD	RFALQQ	DGTLIR	GETLT
g958	NTDWAD	YDQSGD	TVTVGD	RFALQQ	DGTLIR	GETLT
	120	130	140	150	160	170
	190	200	210	220	230	240
m958.pep	SVSR	TAEM	LGEG	HYKLT	ETQFNT	CSAGD
g958	SVSR	TAEM	LGEG	RYKLT	ETQFNT	CSAGD
	180	190	200	210	220	230
	250	260	270	280	290	300
m958.pep	IFYTP	WADF	PLDGN	RKSG	LLVPS	LSAGS
g958	IFYTP	WADF	PLDGN	RKSG	LLVPS	SVSAG
	240	250	260	270	280	290
	310	320	330	340	350	360
m958.pep	FDGQ	VRYLR	PDYAG	QSDLT	WLPHD	KKSGR
g958	FDGQ	IRYLR	PDYSG	QTDLT	WLPHD	KKSGR
	300	310	320	330	340	350
	370	380	390	400	410	420
m958.pep	YYRDF	YGNKE	IAGNV	NLRV	WLDY	GGRA
g958	YYRDF	YGGEE	IAGNV	NLRV	WLDY	GGRA
	360	370	380	390	400	410
	430	440	450	460	470	480
m958.pep	PRLS	VEWR	KNTG	RAQIG	VSAQ	TRFSD
g958	PRLS	ADWH	KNAG	RAQIG	VSAQ	TRFSD
	420	430	440	450	460	470
	490	500	510	520	530	540
m958.pep	ATYY	SLNR	FRGS	QEARR	VSRTL	PIVNI
g958	ATYY	SLDS	FGGK	ASRS	VGRVL	PVVNI
	480	490	500	510	520	530
	550	560	570	580	590	600
m958.pep	QNDL	PNFD	SSSE	SFGY	QGLF	RENLY
g958	QNDL	PNFD	SSSE	SFGY	QGLF	RENLY
	540	550	560	570	580	590
	610	620	630	640	650	660
m958.pep	QKFY	FKDD	AVML	DGSG	VKKP	PRNR
g958	QKFY	FKDD	AVML	DGSG	VKNP	PRSR
	600	610	620	630	640	650
	670	680	690	700	710	720
m958.pep	SYRPA	QGVN	ARYK	YGRNE	KIYLS	DGSG
g958	GYRPA	PGVN	ARYK	YGRNE	KIYLS	DGSG
	660	670	680	690	700	710

1373

```
          730      740      750      760      770      780
m958.pep   EAKKPIEVLAGA EYKSSCGW GAGVYAQR YVTGENTY KNAVFFSL QLKDLSSV GRNPADR
          |||||
g958        EAKKPIEMLAGA EYKSSCGW GAGVYAQR YVTGENTY KNAVFFSL QLKDLSSV GRNPAGR
          720      730      740      750      760      770

          790      800
m958.pep   MDVAVPGYITAH SLSAGR NKRKP
          |||||
g958        MDVAVPGYIPAH SLSAGR NKRKPX
          780      790      800
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```
a958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCCGA GCGTGTCCGA ACCCATAACAG
151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GCGGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTGCTGC AACGCAATCG
351 GACGACCTTC AATGCCGATT GGGCGGATTA CGACCACTCG GCGGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACCGTAC GCTGATTCCG
451 GGCAGAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCGCGCGG
801 TTCGGACGGC GTTTCCTCTT CCGTTCCCTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCGGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCGG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCAGC ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCCGAAATG GCAGCACCGG CACGACATTT CCGACAGCCT TCAGGCGGGT
1051 GTCGATTTC AACAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCG GAGGGCGGCG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAC ACCGGCAGGG
1301 CGCAAATCGG CGTGTCCGCC CAATTTACCC GCTTCAGCCA CGACAGCCCG
1351 CAAGACGGCA GCCGCTCGT CGTCTATCCC GACATCAAAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCCAAAC TCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGGC
1551 GATGTTCCGG GCGGAGTCC TGCAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTT CTGGAACACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCGGCC GTGCAAGGCC
1751 GTATTTTGGA CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGG
1801 CAGAAATTCT ACTTCAAAA CGACGCAATC ATGCTTGACG GCAGTGTCGG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGCAGCGC CTTTATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAATACGCG CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAATACGCG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTACAA
2151 CTACGGTTTT GAAGCCAAA AACCAGATAG GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGGTGACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTTCCCGG CTATATCCCC GCCCACTCTC TTTCCGCGG ACGCAACAAA
2401 CGGCCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```
a958.pep
1  LARLFSLEPL VLALGFCEFT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PLSLSLSTGC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEOG
101 SOVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQODGTILR
151 GETLTYNLEQ QTGEAHNVRM ETEHGRRRLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGGVP IFYTPWADFP
```



```

251 LDGNRKSGLL VPSLSAGSDG VLSVPPYYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SGEARRVSRT
501 LPIVNIDSGM TERNTRMFQ GGLVLTLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIC
601 QRFYFKNDV MLDGSVGGKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRNYGF EAKKPIEVL GAEEKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

a958.pep	10	20	30	40	50	60
m958	10	20	30	40	50	60
a958.pep	70	80	90	100	110	120
m958	70	80	90	100	110	120
a958.pep	130	140	150	160	170	180
m958	130	140	150	160	170	180
a958.pep	190	200	210	220	230	240
m958	190	200	210	220	230	240
a958.pep	250	260	270	280	290	300
m958	250	260	270	280	290	300
a958.pep	310	320	330	340	350	360
m958	310	320	330	340	350	360
a958.pep	370	380	390	400	410	420
m958	370	380	390	400	410	420
a958.pep	430	440	450	460	470	480
m958	430	440	450	460	470	480
a958.pep	490	500	510	520	530	540
m958	490	500	510	520	530	540

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	490	500	510	520	530	540
a958 . pep	550	560	570	580	590	600
	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
a958 . pep	610	620	630	640	650	660
	QKFYFKNDVAVMLDGSVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKDDAVMLDGSVGGKPRNRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
a958 . pep	670	680	690	700	710	720
	SYRPAQKGVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
m958	SYRPAQKGVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
	670	680	690	700	710	720
a958 . pep	730	740	750	760	770	780
	EAKKPIEVLAGA EYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
m958	EAKKPIEVLAGA EYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	730	740	750	760	770	780
a958 . pep	790	800				
	MDVAVPGYIPAHSLSAGRNRKRPX					
m958	MDVAVPGYITAHLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

```

g959 . seq
1  ATGAACATCA AACACCTTCT CTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

```

g959 . pep
1  MNIKHLLTA AATALLGISA PALAHDGHHG DDDHGHAHQ HGKQDKIISR
51  AQA EKA AAWAR VGGKITDIDL EHDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

```

m959 . seq
1  ATGAACATCA AACACCTTCT CTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

```

m959 . pep
1  MNIKHLLITS AATALLSISA PALAHDGHHG DDDHGHAHQ HNKQDKIISR
51  AQA EKA AALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

1376

m959/g959 95.4% identity in 108 aa overlap

m959.pep	10	20	30	40	50	60
	MN	IKHL	LLTSA	TALLS	ISAP	ALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR
g959	10	20	30	40	50	60
	MN	IKHL	LLTSA	TALLG	ISAP	ALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR

m959.pep	70	80	90	100	109
	VGGKITD	IDLEH	DNGRPH	YDVEIV	KNGQ
g959	70	80	90	100	109
	VGGKITD	IDLEH	DNGRPH	YDVEIV	KNGQ

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1  ATGAAGTTC AACGCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGCC CCCGACTCG CCCACCACGA CGGACACGCC GATGACGACC
101 ACGGACACGC CGCACACCA CACAGCAAAC AAGACAAAT CATCAGCCCG
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCGGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTCTCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

```

1  MNFKRLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQ EYKVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

a959.pep	10	20	30	40	50	60
	MN	FKRL	LLTAA	TALMG	ISAP	ALAHHDGHGDDDHGHAHQHSKQDKIISRAQAEKAALAR
m959	10	20	30	40	50	60
	MN	IKHL	LLTSA	TALLS	ISAP	ALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR

a959.pep	70	80	90	100	109
	VGGKITD	IDLEH	DNGRPH	YDVEIV	KNGQ
m959	70	80	90	100	109
	VGGKITD	IDLEH	DNGRPH	YDVEIV	KNGQ

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51  TAAGCCCCC TTGTTGAAG CTCGCGGCT CCTGCCGAGC TTCACCGACC
101 CCGTTGTGCC CAAGCTCTCT GCTCCCGCGC GCTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAAACCGA AATCGAAAAG CTGGCCAAAC AGCCCCAGTA
201 TGCCTATCTG AACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAAACAGG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGA
301 GCCGGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCCCT TGCCCTACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGGCG ATGTCGGCAA AACCTGAAG GAACGTGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGGTTGTAG CGGCGGCAAC GGCAGGCGTA TCCAACAAAC

```



```

551 TCGGTGCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTAACAGTTA ACCTGGCCAA TCGGGGCGAGT GCCGCGCTGA TCAACACCGC
651 TGTAAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAAT ATCTTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTCGGG GAGGCTTTGG TTAATAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGT ACAAAACGCA CAAAACGCGG TAGAAAAATA TCGGTTTAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCTA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTTAG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGGAAAA CAGCTGGCTC AAATTTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAATA ACCGGTGATA GGTTTTATT AGATGGCCAA
1501 CATAAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAT GAAACTGGG GCAGCAAAAG
1601 GTCGTAATTA AACTTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1  MQVNIQIPCM LYRRGSVKPP LFEAPRLIPS FTDPVVPKLS APGGYIVDIP
51  KGNLKTEIEK LAKQPEYAYL KQLQVARNVN WNQVQLAYDK WDYKQEGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAASFASL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKV LVVAAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKCDGGA IGAAVGEIVG EALVKNITDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTLFDETL
401 DWNDAKAVID IVVGTELNRA NKGEAAQKVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFGR QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGRFYLDGQ
501 HRNHLEVFDR NGNFRFVLNM DGSINQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1  ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51  CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAA GTCGTGAATA ACCTGACCAA AACCGTCAAT
301 GAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTGCTGTA AGAGACTAAG ACAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTCGCCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGGCGGTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCCTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1  MSMKHFPKRV LTTAILATEFC SGALATSSDD DVKKAATVAI VAAYNNGQEI

```


1378

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALED TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEAFNDIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV DAKVKAETA A GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPNVGR FNVTAAVGGY KSESVAIGT GFRETENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet
a961.pep not found yet

g972.seq not found yet
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTGGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GATGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTTCA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GTTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATG GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTGA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAALK TXSKSSERMS EVEYFSHFIS DKGKLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGI TRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQXQRTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICRKF NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFT HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKQYEYLS KVIHQNVVDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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1379

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251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCAGGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTGTAGT AAAATTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAGAAAA CGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCCGGGAT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATTT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATCTCG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWFSTFHE DTLKLVSGCP LFSDAEYMYV LSRKLEELG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQGRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSIPT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNRFRVRY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICRKF NMPVPERFDQ RKKTNLNLTFE
301 HKLHYAKNAV GLVNFMIEM GFDNSEIVES LKADSGFPGK LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNVDDY YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLKTXSKSSERMSEVEYFSHFISDGKGLLEIPQRRGKQDGVFVDWFSTFHE					
a972	LTNRGGAKLKTNKSSERMSEVEYFSHFISDGKGLLEIPQRRGKQDGVFVDWFSTFHE					
	10	20	30	40	50	60
m972.pep	70	80	90	100	110	120
	DTLLKVSQCPLFSDAEYMYVLSRKLEELGFGITRKCKSRGNKFYESMYRLGSDDDVDYGE					
a972	DTLLKVSQCPLFSDAEYMYVLSRKLEELGFGITRKCKSRGNKFYESMYRLGSDDDVDYGE					
	70	80	90	100	110	120
m972.pep	130	140	150	160	170	180
	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSIPTRITRIDLALDFFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSIPTRITRIDLALDFFDGEYTPDQ					
	130	140	150	160	170	180
m972.pep	190	200	210	220	230	240
	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNRFRVRYEKGRQLGDKE					
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNRFRVRYEKGRQLGDKE					
	190	200	210	220	230	240
m972.pep	250	260	270	280	290	300
	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQKKKLNLTFE					
a972	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQKKKLNLTFE					
	250	260	270	280	290	300

1380

	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972						
	310	320	330	340	350	360
	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPTYDVEKERKYQEYLSKVYHQNVVDYD					
a972						
	370	380	390	400	410	420
	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPTYDVEKERKYQEYLSKVYHQNVVDYD					
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGCTCGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCA aatcgctcgt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCAATC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCCGTACG GAatacggca gcgaagaagc cgacaccatc ggcggctTGG
701 TCATTcAGGA ATTGGGACAC CTGCCCCGTC GCGGCGAAAA AGTCCTTatc
751 ggcgGTTTGC agttcacgct CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSBEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTTCGGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCGCA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTcATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTcm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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1381

651 CTTCCGGCACG GAATACAGCA kCGAAGAAGC CGACACCATT GGCGGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
 751 GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLVTFEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

m973.pep	10	20	30	40	50	60
	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFPAELEV					
	10	20	30	40	50	60
m973.pep	70	80	90	100	110	120
	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	130	140	150	160	170	180
	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVTFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	190	200	210	220	230	240
	EIEDEFDEDD SADNIHAVSSERWRIHAATEIEDINTFFGT EYSXEEADTI GGLVIQELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAF FGT EYGS EADTI GGLVIQELGH					
	190	200	210	220	230	240
m973.pep	250	260	270			
	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq

1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
 51 ACTCGCCCGC GAACCGGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCCACGCA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGTA TTTGGAAGTG CGGACGCGA TGATTACGCG
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATACCG
 251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CTGCCGTCT
 401 TCGTCCCGCA AGGCAAATCG CTGACCGCCC TTTTAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

1382

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCAGC GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTAGGA ATTGGGACAC CTGCCCCTGC GCGGCGAAAA AGTCCTTATC
751 GGCGGTTTGC AGTTCACCGT CGCCCCGCC GACAACGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLLRLE
 51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFPGT EYSSEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSDLEV
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLEKVLDFSDLEV
m973.pep	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP
a973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFFEDIIEQIVG
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFFEDIIEQIVG
m973.pep	EIEDEFDEDDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFPGTEYSSEADTIGGLVIQELGH
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
 51 TGCCTGCGGC GGTCAAGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGCAATT TAAAAATCGA ATCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCGCGCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCAACCAAG TCGTCTCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTTCTCGT TCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCTCTGAT TATCAAAGAA CTGGAACACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601 AAAAACAACC CGGCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACGGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAAATATTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

```


1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

g981.pep
1 MKKWIAAALA CSALALSACG GQKDAAPA ANPGKVYRVA SNAEPAPFES
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVM
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK MNKVGVTG
151 HTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSV SDSAVIANV
201 KNNPAKGMDV VTLDPFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

m981.seq
1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51 TGCCTGCGGC GGTGAGGCA AAGATACGCG CGCGCTGCC GCCAACCCCG
101 ACAAGTGTA CCGCGTGGCT TCCAACGCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTA AACACGCGC ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCAGG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTCTCTCCGA AGATTGAAA AACATGAACA AAGTCGCGT GGTAAACGGC
451 TACACGGCGG ATTCTCCGT ATCCAAATC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGA TTCCGTGGT AGCGACAGCG CGGTCATCGC CAATTATGTG
601 AAAACAATC CGGCCAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC CGGAAAGCG CGAATACGAC
751 AAGATTACG CCAATATTT TGCAAAAGAA GACGACAGG CCGCAAATA
801 A

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

m981.pep
1 MKKWIAAALA CSALALSACG GQKDTAAPA ANPDKVYRVA SNAEPAPFES
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVM
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK MNKVGVTG
151 YTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSV SDSAVIANV
201 KNNPAKGMDV VTLDPFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKWIAAALACSALALSACGGQKDTAAPAANPDKVYRVASNAEPAPFESLDSKGNVEGF					
g981	MKKWIAAALACSALALSACGGQKDAAPAANPGKVYRVASNAEPAPFESLDSKGNVEGF					
	10	20	30	40	50	60
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMGVTITDDRQKSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMGVTITDDRQKSMDFSDPYFE					
	70	80	90	100	110	120
981.pep	ITQVVLVPGK KKVSSSEDLK MNKVGVTG YTGDFSVSKL LGNDNPKIAR FENVPLIIKE					
g981	ITQVVLVPGK KKVSSSEDLK MNKVGVTG YTGDFSVSKL LGNDNPKIAR FENVPLIIKE					
	130	140	150	160	170	180
981.pep	LENGGLDSV SDSAVIANV KNNPAKGMDV VTLDPFTTEH YGIAVRKGDE ATVKMLNDAL					
g981	LENGGLDSV SDSAVIANV KNNPAKGMDV VTLDPFTTEH YGIAVRKGDE ATVKMLNDAL					
	190	200	210	220	230	240
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				

1384

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
 51 TGCCTGCGGC GGTCAGGGTA AAGATGCCGC CGCGCCCGCC GCAATCCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTG AACAACGCCG ATGCGGACGT TGTGATGTCG
301 GCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCAG TCGTCTCGT TCCGAAAGGC AAAAAATAT
401 CTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACCGC
451 TACACGGGCG ATTTCTCGT ATCCAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAACGCG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAAACAATC CGACCAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAATATTTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
  1 MKKWIAAALA CSALALSACG GQKDAAPA ANPDKVYRVA SNAEFAPFES
 51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KISSSEDLK NMNKVGVTG
151 YTGDFSVSKL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIANV
201 KNNPTKGMDF VTLPDFTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

m981.pep	10	20	30	40	50	60
	MKKWIAAALACSALALSACGGQKDTAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQKDAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	70	80	90	100	110	120
	DVDLMNAMAKAGNEFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNEFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	130	140	150	160	170	180
	ITQVVLVPKGKVVSSSEDLKMNKVGVTGYTGDFSVSKLLGNDNPKIARFENVPLIIE					
a981	ITQVVLVPKGKVVSSSEDLKMNKVGVTGYTGDFSVSKLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
m981.pep	190	200	210	220	230	240
	LENGGLDSVVSASAVIANVYKNNPAKGMDFVTLPDFTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVSASAVIANVYKNNPTKGMDFVTLPDFTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	250	260				
	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1  atcgcacgcg aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacgcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgcCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAGAAGT CGCGTCCAAA ACCAAcgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAaggca TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGcgg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGTACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGT TTGCTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGT GGAACAAGTG GCGAAAGCCA GCCGCCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTTccGAAG Aagtcggcct GTCTTTGGAA AAAGcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGTga agaaaacact ACCGTCATcg
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GAGGCGTGGC AGTGATCAA GTCCGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCCGGTGGA AGACGCGCTG
1201 CACGTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGCGTA CAAATCGTAT TCGCGCCGT TGAAGTCTCG
1351 CTGCCCAA TCCTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCCTGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTAtC GCCGGTCTGA TGCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGAAT GGGCGGTATG GCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1  IASQNLRFDN RFLQKMNNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAAALVEE LKNIKPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLNELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFLDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGTVV
301 ISEEVGLSLE KATLDLGLQT KRIEIGEENT TVIDFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGVALL RARAALNLH TGNADQDAGV QIVLRAVES P
451 LRQIVANAGG EPSVVNVKL EGKGNYGYN A GSGEYGMIG MGVLDPKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGM GMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1  ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TGCGTCCAAA ACCAACCAGC
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAGCCG TCGCGGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGCACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGCGC TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGAAAAA CAAATCGCTG CTTTGACAA

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m982.seq

1	ATGGCAGCAA	AAGACGTACA	GTTCTGGCAAT	GAAGTCCGTC	AAAAAATGGT
51	AAACGGCGTG	AACATTCTGG	CAAACGCGAT	CCGCGTAACC	TTGGGCCCCA
101	AAGGTCCGAA	CTAGTCGTT	GACCCGCGAT	TCGGCGGCC	GCACATCACC
151	AAAGACGGCG	TAACCGTCGC	CAAGAAGAATC	GAACTGAAG	ACCAAGTTTGA
201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	TGCGTCCAAA	ACCAACGACG
251	TGGCAGGCGA	CGGTACGACT	ACCGCCACCG	TACTGGCGCA	ATCCATCGTT
301	GCCGAAGGTA	TGAAATATGT	TACCCGAGGT	ATGAATCCGA	CCGACGTTGAA
351	ACGCGGTATC	GATAAAGCCG	TGCGCGCTTT	GGTTGACGAA	CTGAAAAACA
401	TCGCCAAACC	TTGCGCACT	TCTAAAGAAA	TGCCCCAAGT	CGGCTCTATT
451	TCCGCCAATC	CCGACGAGCA	AGTCGGCGCG	ATTATCGCCG	AAGCGATGGA
501	AAAAGCTCGC	AAAGAAGGCG	TGATTACCGT	TGAAGACGGC	AAGTCTTTGG
551	AAACGAGCT	GGAGCTAGTT	GAAAGTATGC	AATTCGACCG	CGGCTACCTG
601	TCTCCTTACT	TCATCAACGA	TGCGGAAAAA	CAATTCGCTG	CTTTGGACAA
651	TCCGTTTGT	TTGTTGTTTCG	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCCTTTGTT	GGAAACAAGT	GCAAAAGCCA	GCCGTCCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGTACG	AGCCTTTGCG	ACTTTGGTCG	TGAACAACAT
801	CCGAGGCATC	CTGAAAACCG	TTGCCGTCAA	AGCCCTTGGC	TTCCGCGACC
851	GCCGCAAAAG	GATGTTGCAA	GACATCGCCA	TCCTGACCGG	CGGCGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCCTTTGGA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCTACG	AAATCGGTAA	AGCAATACAC	ACCATCATCG
1001	ACGGCTTTGG	CGACGCAAGC	CAAAATCGAG	CGCGGTGTCG	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACTGCAAGA
1101	GCGCGTGGCT	AAATTGCGAG	GCGCGCTGGC	AGTCATCAAA	GTCGGTGGCG
1151	CGACCGAAGT	GAAATGAAA	GAGAAAAAG	ACCCGCTGGA	AGCGCGCGT
1201	CAGCTACCCG	GCGCAGCCGT	TGAAGAAGGC	TGGTTTGACG	GCGGCGCGCT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGGCGTA	CAAACTCGTT	TGCGCGCCGT	TGAGTCTCCG
1351	CTGCGGCCAA	TCGTTGCCAA	GCGAGCGCGC	GAACCCAGCT	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAAG	GCAACTATCGG	TTACAACGCT	GGCAGCGGGG
1451	AATACGCGGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTATC	GCCCGCTTGA	TGCTGACCAC
1551	TGATTCTCATG	ATCGCTGAAA	TCCCCGAAGA	CAACCCGGCT	GTGCCCTGATA
1601	TGGGCGGCAT	GGGTGGTATG	GCGCGCATGA	TGTAA	

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

10 20 30 40 50 60
 m982.pep MAAKDVFQGNVVRQKLVNGVNILANAVRVTLPKGRNVVVDRAFGGPHITKDGVTVAKEI
 :|:::| |: ||||| | :|| |||||

1387

g982	IASQNLRFDNRFLOKMNNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
g982	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
g982	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
g982	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
g982	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
g982	DKEKLQERVAKLGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALNLTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA
g982	RARAALNLTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
g982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
m982.pep	GMMX
g982	GMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq

1	ATGGCAGCAA	AAGACGTACA	ATTCGGCAAT	GAAGTCCGCC	AAAAATGGT
51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
101	AAGGCCGCAA	CGTGGTGGT	GACCGCGCTT	TCGGCGGCCC	GCACATCACC
151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAAGTGAAG	ACAAGTTTGA
201	AAATATGGGC	GCGCAATGG	TGAAAGAAGT	CGCGTCCAAA	ACCAACGACG
251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCCGA	CCGACCTGAA
351	ACGCGGTATC	GACAAAGCCG	TCGCCGCTTT	GGTTGAAGAG	CTGAAAAACA

1388

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGGAAGAA CAAATCGCCG GCTTGACAA
651 TCCGTTTGTG TTGCTGTTTC ACAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GCGCGTGGC AGTAATCAAA TCGGTGCCG
1151 CGACCGAAGT GGAAATGAAA GAGAAAAAAG ACCCGGTGGA AGACGCGCTG
1201 CAGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGCGCA CATGATCGAA ATGGGCGTAC TCGACCCGCG CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGCGGCAT GGGTGGTATG GCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDPFV L LFDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGTV
301 ISEEVGLSLE KATDDLQQA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYGMIE MGVLDPAKVT
501 RSALQHAASI AGIMLTDCM IAEIPEDKPA MPDMGGMGM GGM*

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m982/a982 99.3% identity in 544 aa overlap

```

          10      20      30      40      50      60
m982.pep  MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          |||
a982       MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          10      20      30      40      50      60

          70      80      90      100     110     120
m982.pep  ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          |||
a982       ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          70      80      90      100     110     120

          130     140     150     160     170     180
m982.pep  DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          |||
a982       DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m982.pep  KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDPFVLLFDKKISNIRDLLPVLEQV
          |||
a982       KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDPFVLLFDKKISNIRDLLPVLEQV
          190     200     210     220     230     240

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m982.pep	250	260	270	280	290	300
	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
m982.pep	310	320	330	340	350	360
	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQOIETATSDY					
a982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQOIETATSDY					
	310	320	330	340	350	360
m982.pep	370	380	390	400	410	420
	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
m982.pep	430	440	450	460	470	480
	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA					
a982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKNGYGYNA					
	430	440	450	460	470	480
m982.pep	490	500	510	520	530	540
	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
a982	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGCGACGC
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTTC	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTGCT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGT	CGTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTGCG	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTGAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCTT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	cggagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

1351 AGgcgcggcg acgaaatcct cgcgggtcggg caagtccccg tcaatgacga
 1401 agcccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGGTCatgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986.pep

1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGMGSI
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986.seq

1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCACAAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
 101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
 151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
 201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
 251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
 301 GAATTTTTC AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
 351 AGCAGATGAC GCGCGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
 401 ACGGCTACAT CCTGACCAAT ACCCAGCTCG TTACCGGCAT GGGCAGTATC
 451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCAAAAC TCATCGGTTC
 501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
 551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
 601 GTCGCCGCCA TCGCGCGGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
 651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
 751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
 801 GTCGCGCGGA TTCATGGGCA TTTCTTTCG CATCCCGATT GACGTGCCA
 851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGACAA
 901 CTGGGCGTGA TTATTCAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
 951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
 1001 CCGCAGAACG TGCGGCGCTG CAGGCGGGCG ACATCGTCTC CAGCCTCGAC
 1051 GCGCGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
 1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GGCGAAGAAA
 1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
 1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
 1251 GGTGCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
 1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
 1351 AGGCGCGGCG ACGAAATTCT TGCCGTGCGG CAAGTCCCGG TCAATGACGA
 1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGATCATGCG CCGTGGCAAC ACGTGTTTA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986.pep..

1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVTGMGSI
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSM LLPDFAQL					
	: : : : : :					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSM LLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
	: : : : : :					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTA KLIGSDVQSDVALLKIDA					
	: : : : : :					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTA KLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	: : : : : :					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	: : : : : :					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVND EAGFRKAMD KAGKN					
g986	AGITLQHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVND EAGFRKAMD KAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1   GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCCGCCTC
51  GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCCGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACG GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCC CCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTTC AACGCCTCGT CCCGAACATG CCCGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAATCGCGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCG GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCTT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGCGCATC AACTCGCAAA TATACAGCCG
801 CAGCGCGGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAAAACCCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTCGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGCGCTG CGGCGGGGCG ACATCGTCTT CAGCCTCGAC
1051 GCGCGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCACAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTCTTC
1251 GGTCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCGG TCAATGACGA
1401 AGCCGCTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGAAC ACGCTGTTTA TCGCATTAAC CCTGCAATAA

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This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1   VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKDGYILTN THVVTGMGSI
151 VLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGO

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1393

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGHLLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
m986.pep	70	80	90	100	110	120
	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIQEEADD					
a986	VQSEGPVVNIQAAPAPRTQNGSSNAETSDPLADSDPFYEFFKRLVPMPEIQEEADD					
	70	80	90	100	110	120
m986.pep	130	140	150	160	170	180
	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTQDVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGXVSAKGRSLPNESYTPFIQTQDVA					
	190	200	210	220	230	240
m986.pep	250	260	270	280	290	300
	INPNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
m986.pep	310	320	330	340	350	360
	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
m986.pep	370	380	390	400	410	420
	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
m986.pep	430	440	450	460	470	480
	AGITLQTHTDSSGGHLLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
a986	AGITLQTHTDSSGGHLLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
m986.pep	490	500				
	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq

1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG

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51  TTCTTCATGG TTGCCCCAC TGAAGAAGC GACGGAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTT
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTT
351 ggacgacaAC AACAcgcgcg gcttggacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtcgt CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCGCGCG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCGCCTT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTCG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAAGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTCAATCGG TCATTCAACC TCGACCCCG TTCCGCGACG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCTG AGCCAACTT TGAAGACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

g987.pep

```

1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNTSKPVL LDNILQIRHT
51  PHNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAERG VRVRLLLDDN NTRGLDLLLL ALDSHPNI*V RLFPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHDPATRK TYPNEPEAKL WKRIAARKLS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

m987.seq

```

1  ATGAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGAAGAAGC GACGGAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTT
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCGCGCG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGGT TCGTTCAACC TCGACCCCGG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1  MKTRSLISLL CLLLSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VRVRLLEDN NTRGLDLLLL ALDHPNIEV RLFNPFVLRK
151 WRALGYLTD FRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAARKLS
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

```

          10      20      30      40      50      60
m987.pep  MKTRSLISLLCLLLSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY
          |||
g987      MKTRSLISLLCLLLSCSSWLPPLEERTESRHFNTSKPVLLDILQIRHTPHNGLSDIY
          10      20      30      40      50      60

          70      80      90      100     110     120
m987.pep  LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLEDN
          ||:
g987      LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLEDN
          70      80      90      100     110     120

          130     140     150     160     170     180
m987.pep  NTRGLDLLLLALDHPNIEVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI
          |||
g987      NTRGLDLLLLALDHPNIXVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI
          130     140     150     160     170     180

          190     200     210     220     230     240
m987.pep  LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG
          |||
g987      LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG
          190     200     210     220     230     240

          250     260     270     280     290     300
m987.pep  KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTLISDDPAKGLDRDR
          |||
g987      KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR
          250     260     270     280     290     300

          310     320     330     340     350     360
m987.pep  RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA

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1396

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g987      |||
          RKPP|IAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDVTVLTNSLQATDVA
          310      320      330      340      350      360

m987.pep  370      380      390      400      410      420
          AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          |||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          370      380      390      400      410      420

m987.pep  430      440      450      460      470      480
          SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTT|PAYAYRVTLDRHNRLQWHPATRK
          |||
g987      SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTT|PEYAYRVTLDKHNRLQWHPATRK
          430      440      450      460      470      480

m987.pep  490      500      509
          TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          |||
g987      TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51 TTCTTCATGG TTGCCCCAC TGGAGAAGC GACGGAAAGC CGTCATTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCGG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCGGCGCG ACTGCTGTTT
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCTGTTC AACCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCGCGCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCGAGCG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCTCTAC CAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCTGCAA AAGGACTCGA CCGGACCGC
901 CGCAAACCGC CGATTGCCG GCGGTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGTTT CACCCTATT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCTAACCA TGCCGTCCCT GCCACAAAAG ACAAAGGCTT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGC TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACTG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRSLISLL CLLCSCSSW LPPLEERTES RHNTSKPVR LDNILQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLLDDN NTRGLDDLL ALDHPNIEV RLFNPFVLRK
151 WRALGYLTD FRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP|IAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDRHNR LQWHPATRK TYPNEPEAKL WKRIAAILLS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPEERTESRHFNSTSKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLCSCSSWLPPEERTESRHFNSTSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
m987.pep	70	80	90	100	110	120
a987	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSDDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSDDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	130	140	150	160	170	180
a987	130	140	150	160	170	180
m987.pep	NTRGLDDLLALDHPNIEVRLFNPFVLRKWRALGYLTFPRNRRMHNKSFTADNRATI					
a987	NTRGLDDLLALDHPNIEVRLFNPFVLRKWRALGYLTFPRNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	190	200	210	220	230	240
a987	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	250	260	270	280	290	300
a987	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALRLRYRETVEQSPLYQKIQTGCIDWQSVTRRLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALRLRYRETVEQSPLYQKIQTGRIDWQSVQTRRLISDDPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	310	320	330	340	350	360
a987	310	320	330	340	350	360
m987.pep	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDIVTVLNTSLQATDVA					
a987	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDIVTVLNTSLQATDVA					
	310	320	330	340	350	360
m987.pep	370	380	390	400	410	420
a987	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGS SVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGS SVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
m987.pep	430	440	450	460	470	480
a987	430	440	450	460	470	480
m987.pep	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNR LQWHPATRK					
a987	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNR LQWHPATRK					
	430	440	450	460	470	480
m987.pep	490	500	509			
a987	490	500	509			
m987.pep	TYPNEPEAKLWKRIAAILLSLLPIEGLLX					
a987	TYPNEPEAKLWKRIAAILLSLLPIESLLX					
	490	500	509			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTAATCAAC CGCGaggcg
251 CagtTTGCGc gGcGgacaag ctgGATTGg TCAAATGccg Cgtcaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCGTT TTATACGAAC GCCAgatgcg tggTgTcatG CAcggcgaca
401 ccgttACCGT CCGTCCTGCG ggtatggaCC GCAGGGGccg ccgcGAagg
451 acgtttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TCGGCCGCTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAAt cgAAATTGCC GTGCGCAAGC ATCATTGCGC GCaccgaTTC
751 AGTGAagcgt gtGcCAAATC CGgaaAAAA Attcccgacc ATGTACGCAA
801 AAGCGATTG AAAGGCGCGC TCGATTGTG CGACCTTCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGACGCA ATTACGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCGCCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 CCGTGTATTT CCCGCGCCGT ATGATCCGA TGCTGCCGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGCGCG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTGCGC GCGGATTTT CTGTTGAAAA
1451 ACAAAACATAC GGCTTTGTTT CGCAACCATT TGGGCCCCAC GCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGCGCG
1551 CCGCGACAAC CCGTCGCGGA AAGACTATGC CGCGTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TTGTGCAAG TCATGATGT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAGAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGAAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTGCGTGAA ATATTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTGT CACTTTGGAC GATATccata tgcagcgtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGCGGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGTTGCGG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGAG AAAGCGGCAG GCGCGGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGCGGCGG GGAAGGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGOVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGFVAV LMPMEGDFV LYERQMRGVM HGDVTVTRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SQQVIVGKIE VYPEQNRPAV AKIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VYRNRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQQLG LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TTYMRDKVGE IFEGKISRGV
651 ANFGIFVTLN DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPAV AESGKKAKKP VPIKVKKRKG KS*

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1399

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```

m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51  CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCCG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAATTGCC GTGCGCAAGC ATCATTGGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TCGGAAAAAA ATTCCCGTCC ATGTACGCAA
351 AAGCGATTTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GTCGTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATT TCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCGCGCTGA CCTACAACCA AGTTTGAAAA
751 TGGATTTTCA ACGCATCGA CCATCCGTAC AAAGCCCAAA TCGACACCCT
801 TTACAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCGT TGTCCGCAAC GATGCCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTT CTGTTGAAAA
1001 ACAAGCATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCCTA
1251 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTCCGCGAA GTATTGCAAG GTAAAATCTC CGGCATGACC
1501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCAACAT GGGGACAGG
1651 GTTCCGTCC GGGTCGCCG TCGCGATTG GATGACGGAA AAATCGATTT
1701 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC

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1400

1801 GCCGAGAAAA AACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY AD SGMEIEIA VRKHHLP HQF
 101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQOTYTP
 451 KKSQALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
 501 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGD	TVTVPAGMDRR	REGTF	FLDIVERAQSKVVGRFYMDRGVAILEPED		
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA				
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA				
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLP HQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK				
g988		VRKHHLP HRFSEACAKSAKKIPDHVRKSDLKGRVLDCLPLVTIDGETARDFDDAVFAEK				
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRR VIPMLPENLSNGICSLNPDV				
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPMLPENLSNGICSLNPDV				
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL				
g988		ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSDGIGNPHKAQIDTLYKL				
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE				
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPDAE				

1401

	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
g988	LLQVMMMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNKRKTYTP					
	550	560	570	580	590	600
	460	470	480	490	500	509
m988.pep	KKSQWALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKIS-GMTSFGIFVTLD					
g988	NKSQWALGVHTSFCERRADDAGRDVENWLKTYIMRDKVGEIFEGKISRGVANFGIFVTLD					
	610	620	630	640	650	660
	510	520	530	540	550	569
m988.pep	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
	570	580	590	600	610	629
m988.pep	IAGGSGRGRKVKSSASAKPAGTAGKPKTAAEKKTAGGKVRGRGASAAAESRKKAKKP					
g988	IAGESGRRRKVKSASAKPAGAAGKSKTTAEKKTARCGKVRGRGVPFAVAESGKKAKKP					
	730	740	750	760	770	780
	630	640				
m988.pep	VPIKVKKRKGKXS					
g988	VPIKVKKRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988.seq
1  ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GGCGGACAAA TTGGATTTGG TCAAATGCCG TGTCAGGGCG
301 CACAAAGACC GCTTCGGTTT CGCGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCCTGT TCGTCTGCC GGCATGGACG GTAGGGGGCG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGCGG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCGGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGAGCGA ATTACCGTCT GGTCTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCGCGCGCGC GTGATTCCTA TGTGCGCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTTT AAAACCCAAA TCGACACGCT
1251 TTACAAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCGT GTCCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATTGTTC CGCAACCATT TGGGGCCAC GCCCGAAAAA
1501 CTCGCCGCT TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1402

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1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCGG TTTACGAACC GCATTGCCGAC GGACACTTTG GTCTTGCCCTA
1701 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTACACCG CGCCATCAAA GCGGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC GCCAGCGCGG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1901 TGCGCGATAA GGTCGGCGAA GTATTGGAAG GTAAAATCTC CGGCATGACC
1951 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
2101 GTTGCCGTCG GGGTCGCGCG TGCCGATTTC GATGACGGAA AAATCGATT
2151 TGTCTTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
2201 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC
2251 GCGGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
2301 TGCCGCGGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
2351 TAAAAAACG GAAAGCAAA TCATAA

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This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

```

a988.pep
1 MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVPSKIEAL
51 VRELSIKEEE YEFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVKA
101 HKDRFGFAVP LTPAKDGFV LYERQMRGIM HGDIVTVRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGFRFXMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSCMEIEIA VRKHHLPHQF
251 SEACAKAAK IPDHVRKSDL KGRVDLRDL LVTIDGETAR DFDDAVFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFRR VIPMLPENLS
351 NGICSLNPHV ERLCVCDMV ITYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LAALREQLGL LGLQLGGDN PSPKDYAALA GQFKGRPDAE LLQVMMMLRSM
551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
601 KKSQALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
651 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAEGER SGIRFNMGDR
701 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
751 AEKKTARGGK VRGRGASAAA ESRKKAKPV PIKVKKRKGK S*

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m988/a988 97.0% identity in 641 aa overlap

```

m988.pep
10 20 30
TVLDIVERAQSKVVGFRFYMDRGVAILEPED
|||||
a988
130 140 150 160 170 180
LYERQMRGIMHGDIVTVRPA GMDGRGRREGTVLDIVERAQSKVVGFRFXMDRGVAILEPED

40 50 60 70 80 90
KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSCMEIEIA
|||||
a988
190 200 210 220 230 240
KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSCMEIEIA

100 110 120 130 140 150
VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK
|||||
a988
250 260 270 280 290 300
VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK

160 170 180 190 200 210
VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFRRVIPMLPENLSNGICSLNPDV
:|||||
a988
310 320 330 340 350 360
IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFRRVIPMLPENLSNGICSLNPHV

220 230 240 250 260 270
ERLCMVCDMVITYAGNIKEYRFYPVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL
|||||
a988
ERLCVVCDMVITYAGNIKEYRFYPVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLYKL

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1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMI FDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLLGLQLGGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSQWALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSQWALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
	730	740	750	760	770	780
m988.pep	640	PIKVKRKRKGKSX				
	PIKVKRKRKGKSX					
a988	PIKVKRKRKGKSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq

1	ATGACCCCTT	TCACACTGAA	AAAAACCGTC	CTGCTGCTCG	GCACTGCCTT
51	TGCCGCCGCA	TCTGTCCACG	CATCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCCGA	AAGCACGGCA	AATGCCGCCG	ACGCGTCGAC	CATCTTCTAC
151	AATCCCGCCG	GCCTGACCAA	ACTCGACAGC	AGCCAGATT	CCGTCAACGC
201	CAACATCGTG	CTGCCAGCA	TTCATTATGA	AGCAGATTCC	GCCACCGACT
251	TTACCGGGCT	TCCCGTCCAA	GGTCTAAAA	ACGGCAAAAT	CACCAAAACC
301	ACGGTGCAC	CCCACATTTA	CGGCGCATAC	AAAGTCAACG	ACAATCTGAC
351	CGTGGGCTTG	GGCGTGTACG	TCCCCTTCGG	CTCTGCCACC	GAATACGAAA
401	AAGATTCCGT	GTGCGCCAC	AACATCAACA	AACTCGGTCT	GACCAGCATC
451	GCCGTCGAAC	CTGTCGCCGC	GTGGAACTC	AACGAACGCC	ATTCTTTCGG
501	CGCAGGCATC	ATCGCCCAAC	ATAATTCCGC	CGAACTGCCG	AAATATGCCG
551	ACTGAGGAAT	CCCAAAAAA	GCGCAAATGC	TGCAAGCAAC	ACCTTCTAAT
601	CCTACTGCCG	CTGCTCAAAT	CAAGGCCGAC	GGACACGCCG	ATGTCAAAGG
651	CAGCGATTGG	GGCGTCGGCT	ACCAACTGGC	GTGGATGTGG	GACATCAACG
701	ACCGCGCGCG	CGTGGGCGTG	AACTACCGTT	CCAAAGTTTC	ACACACGCTC
751	AAAGGCGATG	CCGAATGGGC	GGCAGACGGC	GCGGCGGCGA	AACAACAGTG
801	GAATGACAAAT	ATGCTCACAC	CGCTCGGTTA	CACGGCGAAT	GAAAAAGCCA
851	GTGTCAAAAT	CGTAACGCCT	GAGTCTTTGT	CCGTACACGG	CATGTACAAA

1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAAC TTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TCGGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
1 MTPFTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNNDLTVGL GYVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAIKAD GHADVKGSDW GVGQYQLAWMW DINDRVRGV NYRSKVSHTL
251 KGDAEWAADG AAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMK
301 VSDKADLFGD VTWTRHSRFN KAELFFEKEK NIANGKKS DR TTTIPNWRNT
351 YKVGLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCGCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCGG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCCTGTC AACGCCAACA TCGTGCTGCC CAGCATTTCAT TATGAGGCGG
251 ATTCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC
301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCGT CGAACCTGTC GCCGCGTGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACTTAA CGGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACATC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAACCGGT
851 ACACGGCGAA TGAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCGGCGA
951 CGTAAC TTGG ACGCGCCACA GCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGTTTTGAC AAATCGCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
1251 TGCCGCTTAC ACCCATATC ACATCAACGA CACGAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACACG CCGACATCAT CGGTCTGCAA TACACCTACA AATCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
1 MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNQVA EAAKIADGH ADVKGSWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEA RVKIVTPESL
301 SVHGMKVS D KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
 401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKTIVLLGLTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
m989	MTPSALKKTIVLLGLTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVVVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
m989	LTVGLGVVVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSKAEILTAKPPKPNVGAEEAAKIQADGHADVKGSDWGVGYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYRSKVSHTLKGDAEWAADGAAKQWQNDNMLTPLGYTANEKASVKIVTPES				
m989	NDRARVGVNYRSKVSHTLKGDAEWAADGAAKAMWS-TMLAANGYTANEKARVKIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMKVSDKADLFGDVTWTRHSRNFKAELFFEKEKNIANGKKS DR T TITPNWRNTYK				
m989	LSVHGMKVSDKADLFGDVTWTRHSRFDKAEVFEKEKT VVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
m989	VGFSGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	400
	420	430	440	450	460
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq
 1 ATGACCCCTT CCGCACTGAA AAAAACCCTC CTACTGCTCG GCACTGCCTT
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG
 101 TCAACGCGCA AAGCACGGCA AATGCCGCGG CCGCAGAAGC CGCCGACGCA
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
 201 GATTTCCTGC AACGCCAACA TCGTCTGCC CAGCATTCAT TATGAGGCGG
 251 ATTCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTC GAAAAGCGGC

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GCGGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCT GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTCTTTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCAGC GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```

a989.pep
1  MTPSALKKTIV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNHRHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWGFGYQ LAWMWDINDR ARVGVNYSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMKVSDKA DLFGDVTWTR HSRFDKAEIV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRNM SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAATH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKEK*

m989/a989 93.1% identity in 467 aa overlap

10 20 30 40 50 60
m989.pep MTPSALKKTIVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
|||||:|||||
a989 MTPSALKKTIVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
10 20 30 40 50 60

70 80 90 100 110 120
m989.pep TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
|||||:|||||
a989 TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
70 80 90 100 110 120

130 140 150 160 170 180
m989.pep LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDHRHSFGAGIIAQHT
|||||:|||||
a989 LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHT
130 140 150 160 170 180

190 200 210 220 230 240
m989.pep SAELRKYADWGIKSAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFGYQLAWMWDI
|||||:|||||
a989 SAELRKYADWGIKSAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFGYQLAWMWDI
190 200 210 220 230

250 260 270 280 290 299
m989.pep NDRARVGVNYSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
|||||:|||||
a989 NDRARVGVNYSKVSHTLKGDAEWAADAMAKQLWDANKLALLGYTPSEKARVKIVTPES

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	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSREDFKAELVFEKEKTIVNGKSDRTTITPNWRNTYKV					
a989	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSREDFKAELVFEKEKTIVNGKSDRTTITPNWRNTYKV					
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1   ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAG GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCCTGTTT GGTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TGCCTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGCGGCG CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGGC
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CCGCGTGATG
1201 GCGGCGAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCCGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGACCGGTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGGAAAA GGCAATAATG TCGGTTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GGGCGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCTT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTGTCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNYN SGILAVDNMP VVKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DINKLVEDS VLTSPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTGK WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLVGN GGFTDSEGT VGLLGSGWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTC CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CGGTAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AACTACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTAAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAACCCG GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCTGAAC ACGAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGTACGACG
701 TCGGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAATCTGA AAACGCTCGA
801 CGGGCGCAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTGCGT
851 TTAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCAAATACT TTGTTGCGGC
1001 TCGGTGCCGC CGACAGGGG GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAATTGT GGCTGCGCTT CATCGCGCGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGG GCTGCGGACG GCGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GGGCGGAGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGT ATGGCGGGG TGTTTATGCT GCGTGCGATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTGCAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGCGT TGTGCAAAA GCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGACGGG TCAAGTGCAA AGCGCGCGG
1601 GCATTGCGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTGCGG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGCGAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGAAGAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGCCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNYN SGILAVDNMP VVKYITDLY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DINKLVEDS VLTSPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQK
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

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1409

401 GGRAGQHASV NGKGAAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSEGTA VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWL*F

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDPKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDPKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
	10	20	30	40	50	60
m990.pep	70	80	90	100	110	120
a990	SGILAVDNMPVVKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEYIAQFGT					
	70	80	90	100	110	120
m990.pep	130	140	150	160	170	180
a990	KFSTLKQTMPLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
m990.pep	190	200	210	220	230	240
a990	MTLKDSLWEPRRHSDIHTLETSNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
	190	200	210	220	230	240
m990.pep	250	260	270	280	290	300
a990	ALTFEDKVSQSGVVLERRPENLKTLDGRKLIAAKTADSGSFQKQNYRQGLYELLKQC					
	250	260	270	280	290	300
m990.pep	310	320	330	340	350	360
a990	EGGFCLGVQRLAIPAEAVLYAQQAAYANTLFGRLAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
m990.pep	370	380	390	400	410	420
a990	RSHQNIIRGGAADGWRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSD					
	370	380	390	400	410	420
m990.pep	430	440	450	460	470	480
a990	LYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
m990.pep	490	500	510	520	530	540
a990	ALVAEGIVGKGNVRFYLPQAQFTYLGVNGGFTDSEGTAAGLLGSGQWQSRAGIRAKTR					
	490	500	510	520	530	540
m990.pep	550	560	570	580	590	600
a990	FALRNGVNLQPFPAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLF	X				
a990	YGKRTDGDKEAALSLKWLF	X				
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992.seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCC TGTGCTTTT GGGCGCGTTG GGTATACGG
101 GATATGACAG TGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GGCACGTCAG GGGACGTGGG TTTCGACGCG CCCGTTCCGC GACGGGCATC
201 GCGGAAATCC GGCCACAGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGATACCC TACGTCATC GACGGCGACG GCGCGAAACA TAAAATTCGG
301 ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GTACACGTTT
351 GCGCGACAAC CTGCGCGCGG CGGCGGAGGG TAGGAAAGTC AGTGACGTTG
401 TGTTTGAAAC CGACCGCTAT CAGCGCGAAG TGGCGCAGGT ATCCGCCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATTG
501 TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGCGATTTT GCCGACTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAAATCCG AAGCGCCGTG GCGGTACCGC CGGCGAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATTCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992.pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGVDSEAV RTAVAVLDVL
51  GTAGDVGFDA PVRRRASAKS GHSYTGTVSK VYDGTDLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLNMQVQ DGAAWHYKSY AKEQDQKADF ADYADAQIQ A ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDSVGEWL GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992.seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCC TGTGCTTTT GGGTGCCTTG GGTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GGGCGGCGAG GGGACGCGGG TTCCGACGCG CCCGCCCGCC GCCGAGCATC
201 GCGGAAATCC GGCCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCCCT TCACGTTATC GACGGCGACG GCGCGAAACA CAAATCCGG
301 ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GCACGCGTTT
351 GCGCGACAAC CTGCGCGCGG CGGCGGAAGG CAGGAAAGTC AGCGTGCGCG
401 TGTTTCGATAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATTG
501 TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGCGATTTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAAATCCG AAGCGCCGTG GCGGTACCGC CGAGCAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992.pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGVDSEAV RTAVAVLDVL
51  GAAGDAGSDA PARRRASAKS GHRYTGTVSK VYDGTDLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLNMQVQ DGAAWHYKSY AKEQDQKADF ADYADAQIQ A ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992.pep	MFRRRHRLKMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992	MFRRRHRLKMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA					
	10	20	30	40	50	60
m992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
m992.pep	LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTD LNLMOVDGA AWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFDTRYQREVAQV SAGKTD LNLMOVDGA AWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
m992.pep	ADYADAQIQ AERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DAVGEWLGIWX					
g992	ADYADAQIQ AERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DSVGEWLGIWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

a992.seq

```

1  ATGTTTCAGAC  GGCATCGGCA  TTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCT  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTCCGCTACT  CGACGTACTC
151 GGC GCGGCAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GCGGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTCCGCG
401 TGTTTCGACAC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGCGCG  CGTGGCATTG
501 TAAAGTTAT  GCTAAGAAGC  AGCAGGATAA  GCGCGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGGCCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

a992.pep

```

1  MFRRRHRLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGT VSK  VYDGD TLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFDTRY  QREVAQVSVG
151 KTD LNLMOVQ  DGA AWHYKSY  AKEQQDKADF  ADYADAQIQ  A  ERERKGLWKA
201 KNPQAPWAYR  RAGRS GGGNK  DWM DAVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/a992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRRHRLKMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992	MFRRRHRLKMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
	10	20	30	40	50	60
a992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
a992.pep	LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTD LNLMOVDGA AWHYKSYAKEQQDKADF					
m992	LRAAAEGRKVSVRVFDTRYQREVAQV SAGKTD LNLMOVDGA AWHYKSYAKEQQDKADF					
	130	140	150	160	170	180

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```

a992.pep      LRAAAEGRKVSVRVFDTDYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
|||||
m992          LRAAAEGRKVSVRVFDTDYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
              130      140      150      160      170      180

              190      200      210      220      230
a992.pep      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDDAVGEWLGIXW
|||||
m992          ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDDAVGEWLGIXW
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGGAAA
101 TTACCGGGCA GTATCTGCAC TATATTGCCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGTC TTGCCTACGA GCAATGAAA
301 CTGGCGGCGC AGGGTTTGA GCGCGTCCG CGTGCGGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401 TTTACATCGC CGATTTGATG CAGGCATGTT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCGCGC
501 GCAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGCATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVEITGQYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVD EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRLRNEHG ICRFHDLFNP EQGAAYVIVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

n993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATTCCG ATGGTGAAGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGTC TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGA GCGCGTCCG CGAGCCGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAAA GAAACCATCT CCGTGCGCGC
501 GCAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGCATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

n993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVRITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRLRNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLGSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA				
g993	LKVVLGSFQGPLDLLLYLIRKQ	NIDVLDIPMVEITGQYLHYIAQMEAYQFDLAAEYLLMA				
	10	20	30	40	50	60
	70	80	90	100	110	120
m993.pep	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
g993	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQAWLGILSRKHTRSHEVIKETISVRAQMTAILRRLNKGH					
g993	LPLEIAAETKLPVYIADLMQAWLGILSRKHTRSHEVIQETLSVRAQMTAILRRLNKGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAAYVVNFIALLELAKEGLVRIVQEDGFGEIRISLNHEGAHSDGISG					
g993	ICRFHDLFNPQGAAAYVVNFIALLELAKEGLVGIVQEDGFGEIRISLNHEGAHSDGIFG					
	190	200	210	220	230	240
	249					
m993.pep	TRGGRDVF					
g993	TRGGRDVF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATCCG	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAC	CTATCAGTTT
151	GATTGGCGG	CGGAATATCT	TTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCTG	CTGCTGCCGC	GTACCGAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCTGC	CGAGTTGGTG	CGCCGCCTGC	TGGCTTACGA	GCAGATGAAG
301	CTGCGCGCAC	AAGGTTTGA	TGCGCTTCT	CGTGCAGGCG	GGGATTTCGC
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCGAAG
401	TCTATATAC	CGACTTGACG	CAGGCGTGGC	TGAGTATTT	GTCTCGGGCA
451	AAACATACCC	GCAGCCACGA	AGTTATCAA	GAAACCATCT	CCGTGCGCGC
501	GCAATGACG	GCAATCCTGC	GCCGTTTGAA	CAACACGGG	ATATGCAGGT
551	TTACGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTC AAC
601	TTCAATCGAC	TGTTGGAGCT	TGCCAAAGAA	GGTTTGGTCG	GAATCGTACA
651	GGAGATCGGT	TTCCGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTCAGACGG	CATTCCGGC	ACACGGGGCG	GGCGCGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSSFQGPLDLLLYLIR	KQIDVLDIP	MVKITEQYLH	YIAQIETYQF
51	DLAAEYLLMA	AMLEIEIKSR	LLPRTETVED	EEADPRAELV
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT
151	KHTRSHEVIK	ETISVRAQMT	AILRRLNKHG	ICRFHDLFNP
201	FIALLELAKE	GLVGIVQEVG	FGEIRISLNH	EGAHSDGISG

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA				
m993	LKVVLGSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA				

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
m993	70	80	90	100	110	120
	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
a993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLSILSRKHTRSHEVIKETISVRAQMTAILRRLNKHG					
m993	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLGILSRKHTRSHEVIKETISVRAQMTAILRRLNKHG					
a993.pep	190	200	210	220	230	240
	ICRFHDLFNPEQGAAYVVNFIALLELAKEGLVGIVQEVGFGEIRISLNHEGAHSDGISG					
m993	190	200	210	220	230	240
	ICRFHDLFNPKQGAAYVVNFIALLELAKEGLVRIVQEDGFGEIRISLNHEGAHSDGISG					
a993.pep	249					
	TRGGRDVF					
m993	249					
	TRGGRDVF					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TTCTTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GCGGAATCCT ACCCGCGCA ACTGCAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGCGCTGCG
251 CCGCGCTGTT GGCACGCAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAAAAGT TCCCAGGAG CAGACCCGCG CCAATATCGC
351 GAAATCATC GAAACCGTGC AAAAGGAAA CATTCCCGCC GTCTCGTCG
401 GCGTGCCGCA CATCACTG GCGCGTTGT TCGGGCATT GAGCGACCAT
451 CCGCTGTATG AGGATTGTG CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGGTGGGCG GAAATTTGG GCAATAATA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTCG CCGAAAATT GAATCAATTT
601 TTGAGAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLIGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPAQLQR LTGWNIVNGG VSGDTSQAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPEE QTRANIAKII ETVQKENIPA VLVGVPHITL GALEGHLSDH
151 PLYEDLSEFY GIPFEGGAWA EILGNNLKS DOIHANGRGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TGCTTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCTT
151 GCGGAATCCT ACCCGCGCA ACTGCAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCTGCG
251 CCGCGCTGTT GGCACGCAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAAAAGT TCCCAGGAG CAGACCCGCG CCAATATCGC
351 GAAATCATC GAAACCGTGC AGAAGGAAA CATCCCGCC GTCTCGTCG
401 GCGTGCCGCA CATCACTG GGTGCGTTGT TCGGGCATT GAGCGACCAT
451 CCGCTGTATG AGGATTGTG CGAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CCGGTGGGCG GAAATTTGG GCGATAATA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTCG CCGAAGATT GAATCAATTT
601 TTGAGAAAC AGGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLIGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPAQLQR LTGWNIVNGG VSGDTSQAL SRLPALLARK PKLVIVGIGG

```


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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEY GIPFPGGAWA EILGDNLLKS DQIHANGKGY RKFAEDLNQF
 201 LRRQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

	10	20	30	40	50	60
m996.pep	MNRR	TFLGAGALLTACGRKSARTHAKI	PEGSTVLALGDSLTF	FGYGANPGESYP	PAQLQK	
g996	MNRR	TFLGAGALLTACGRKSARTHAKI	PEGSTVLALGDSLTF	FGYGANPGESYP	PAQLQK	
	10	20	30	40	50	60
	70	80	90	100	110	120
m996.pep	LTGWNIVNGG	VSGDTSQAQALSRLPALLARKPKLVIVGIGG	NDFLRKVPKEQTRANI	AKII		
g996	LTGWNIVNGG	VSGDTSQAQALSRLPALLARKPKLVIVGIGG	NDFLRKVPKEQTRANI	AKII		
	70	80	90	100	110	120
	130	140	150	160	170	180
m996.pep	ETVQKENIPAVLVGVPHITL	GALFGHLSDHPLYEDLSEY	GIPFPGGAWAEILGDN	LLKS		
g996	ETVQKENIPAVLVGVPHITL	GALFGHLSDHPLYEDLSEY	GIPFPGGAWAEILGDN	LLKS		
	130	140	150	160	170	180
	190	200				
m996.pep	DQIHANGKGYRKFAEDLNQFL	RKQGFR				
g996	DQIHANGKGYRKFAEDLNQFL	RKQGFR				
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCC	GAACCCACGC	CAAAATTC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGCGGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCCGCGCA	ACTGCAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCGC	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCAGCAAA	CCCAAGCTTG	TGATTGTCGG	CATAGGCGGC
301	AACGACTTTC	TGCGCAAGT	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAATCATC	GAAACCGTGC	AGAAGGAAA	CATCCCCGCC	GTCCTCGTCG
401	GCGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATT	GAGCGATCAT
451	CCGCTGTATG	AGGATTGTG	CGAGGAATAC	GGCATTCCCG	TGTTCCGCGG
501	CGCGTGGGCG	GAAATTTTG	GCGATAATA	TCTGAAATCC	GACCAATCC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTG	CCGAAGATT	GAATCAATT
601	TTGAGAAAAC	AGGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRR	TFLGA	GALLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYP	PAQLQK	LTGWNIVNGG	VSGDTSQAQAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANIAKII	ETVQKENIPA	VLVGVPHITL	GALFGHLSDH	
151	PLYEDLSEY	GIPFPGGAWA	EILGDNLLKS	DQIHANGKGY	RKFAEDLNQF	
201	LRRQGFR*					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

	10	20	30	40	50	60
a996.pep	MNRR	TFLGAGALLTACGRKSARTHAKI	PEGSTVLALGDSLTF	FGYGANPGESYP	PAQLQK	

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```

|||||
m996      MNRRFTLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFYGANPGESYPALQK
          10      20      30      40      50      60

          70      80      90      100     110     120
a996.pep  LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          |||||
m996      LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          70      80      90      100     110     120

          130     140     150     160     170     180
a996.pep  ETVQKENIPAVLVGVPHITLGFHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
          |||||
m996      ETVQKENIPAVLVGVPHITLGFHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
          130     140     150     160     170     180

          190     200
a996.pep  DQIHANGKGYRKAEDLNQFLRKQGFRR
          |||||
m996      DQIHANGKGYRKAEDLNQFLRKQGFRR
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCCGGC TTGTCGCGCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGCGCGC CACACTGGCC
151 GGAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TGCGCCTGAT GAAAACCATC GGTTCCAGAC
251 CCCGTGCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTCTTGG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGC CAGCCCTTGG TCTGGGGCGC GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCCTGG CCGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCAGCGCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGcc CGCCCGCTG ACcGGCATTg CCGAcggaAC
951 ggcaCaatgG CTGCTTTgcc cgGGGCAGGc tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAatagc GTTCCGAcc GCGtcggygC GtttgcAAac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MNNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVLRIMRTI GSDPRAAFIR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPFH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCCAGGA CTGTCCGCGC CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGCGCGC CACACTGGCC
151 GGAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TGCGCCTGAT GAAAACCATC GGTTCCGATC
251 CCCGTGCCGC CTTTGTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CTGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAAGTCTTGG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
501 GCAGTTTGGC CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAA

```


1417

```

551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCGCCTTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCCTGCC CGCCCGCTG ACCGCGCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGAGGCT CGGACTGCCT GAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAAACCGG
1051 GCGTGGCGCG ACAAAGCCCA CGCCGACCTC AACGCGATCC TTCCGCATT
1101 TGAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
1151 CAGCCGATGC CCGCGCCGCG GACTTGTCTG GGTTCACCG GCACCGCATC
1201 TTCCCCGCGG GCGACTACCT CCACCCGGAC TACCCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```

m997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVLRMLMTI GSDPRAEFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKSQSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVW LLCRGRLGLP ENEVSAVISV SDRVGAFAFR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPD DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
g997.pep	NGQHILLGAYRGVLRMLMTIGSDPRAEFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVLRMLMTIGSDPRAEFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
g997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
g997.pep	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
	190	200	210	220	230	240
g997.pep	RLNTLPDGKVLVNGEAFDAAILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
	250	260	270	280	290	300
g997.pep	AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFANR					
m997	AEPVRLPAPLTGLADGTQWLLCRGLGLPENEVSAVISVSDRVGAFANRAWADKAHAD					
	310	320	330	340	350	

1418

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCCGGC TTGTCCGCGG CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGCGCCG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAATATACG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCAGACC
251 CCCATGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCG GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACGTGCTT
401 CCGATATGTC CGATTGCGAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCCGCTTGG CCGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG CGGAACCTTT CGATGCCGCC GTCCCGCCA CCGCGCCCTA
801 CCAGCGCGCC GCGCTCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCGGAACCCG TCGCTTGCC TGCCCGCTG ACCCGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTGCC GGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCGCGCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAGTTCA CGCGACCTC AAACGCATCC TTCCGCATT
1101 GGGCGAACC GAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCCGCG GATTGTGCT GGTGACCGG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCCAGAC TACCCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAACCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILGAY RGVRLMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDDA VPATAPYHAA ALLEPGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVW LLCRGRGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILGAYRGVRLMKTI GSDPHAAFLRVPLHWHMHGG LQFRALPLPAPLHILGGVLL					
m997	NGQHILGAYRGVRLMKTI GSDPHAAFLRVPLHWHMHGG LQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	NGQHILGAYRGVRLMKTI GSDPHAAFLRVPLHWHMHGG LQFRALPLPAPLHILGGVLL					
m997	NGQHILGAYRGVRLMKTI GSDPHAAFLRVPLHWHMHGG LQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPFAFKA KLLADMSDLQKSARLGQPD TTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRVPFAFKA KLLADMSDLQKSARLGQPD TTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	ARRVPFAFKA KLLADMSDLQKSARLGQPD TTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRVPFAFKA KLLADMSDLQKSARLGQPD TTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVL CNVLSGVLTKKSQSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC					
m997	PLETASLRVL CNVLSGVLTKKSQSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVL CNVLSGVLTKKSQSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC					
m997	PLETASLRVL CNVLSGVLTKKSQSDYLLPKQDLGAIVAE PALAELQRLGADIRLETRIC					

1419

```

m997      PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           |||||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
           |||||
m997      AEPVRLPAPLTGLADGTQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRRHRIFFAGDYLHPDYPATLEAAVQ
           |||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRRHRIFFAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TGTGTTTATC
51  AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAAGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACTTTTTC CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGTAAAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QSKTAQAE PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKDCGY DLTLMDFGA IALKLDEQQK
101 IRAISVGYIL KTDGERGQNL VNNAINGLHS IQAVLSLTTT DKLGESEAGK
151 QLFALTTEVV KESNOTGATA QKDVPADGIL YSVVFEKETN TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

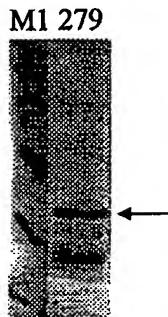
17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

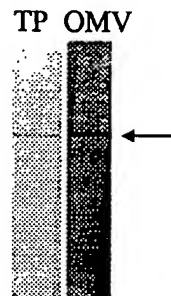
279 (10.5 kDa)

Fig. 2

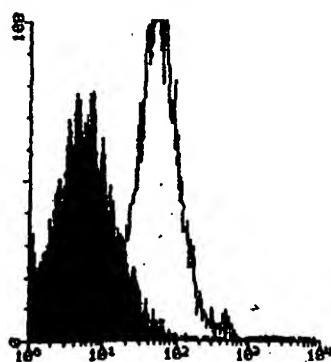
A) PURIFICATION



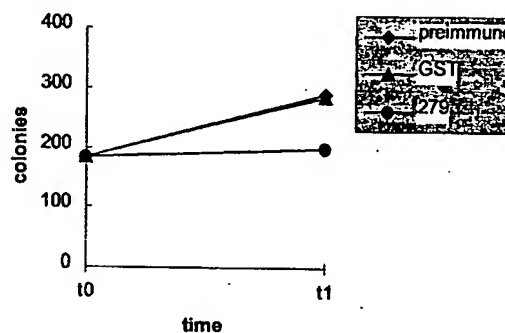
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

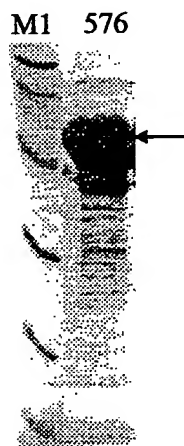
279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

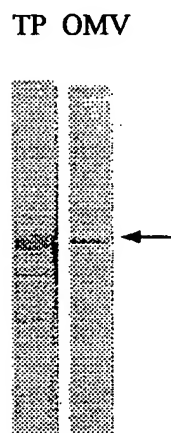
Fig. 3

576 (27.8 kDa)

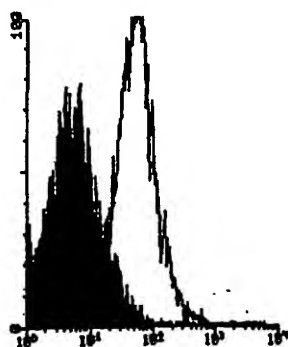
A) PURIFICATION



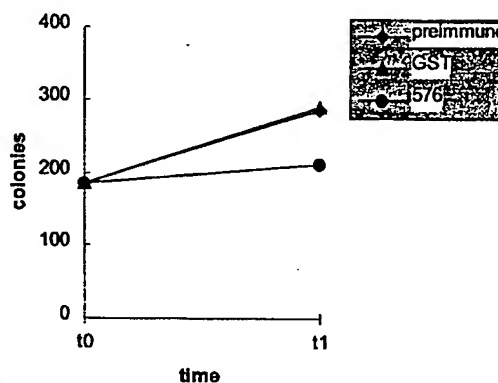
B) WESTERN BLOT



C) FACS

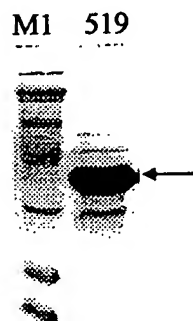
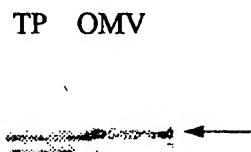
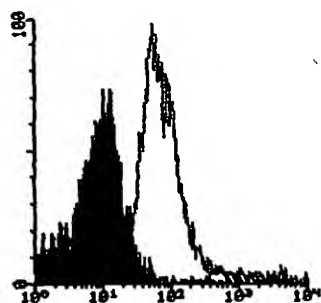
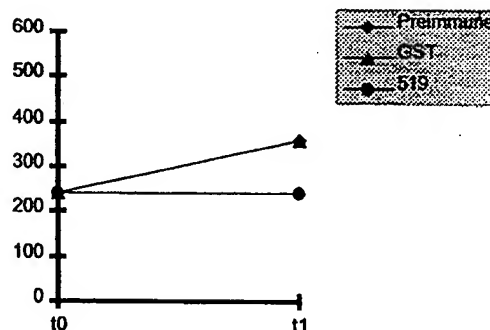


D) BACTERICIDAL ASSAY

E) ELISA assay: positive

576

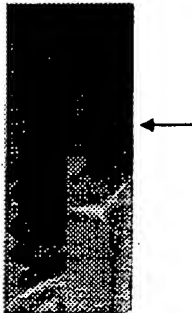
The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

519 (33 kDa)**Fig. 4****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****519**

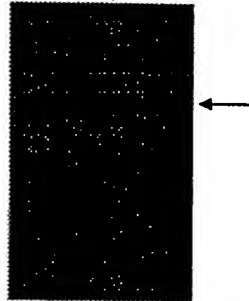
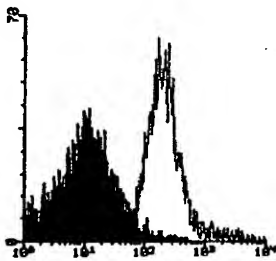
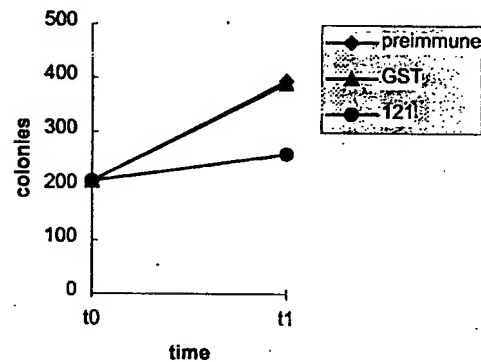
The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION**

M1 121

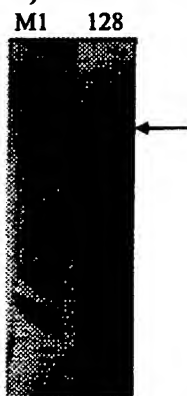
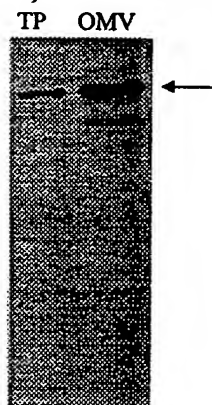
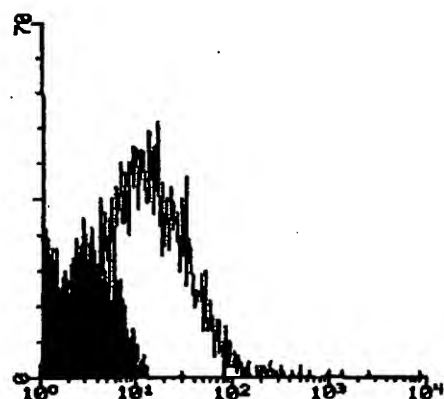
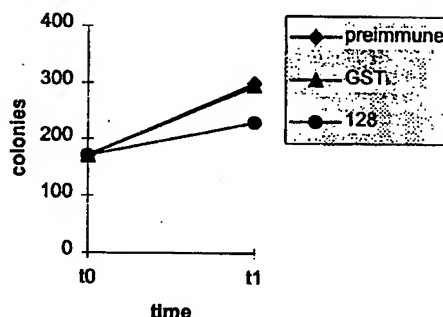
**B) WESTERN BLOT**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

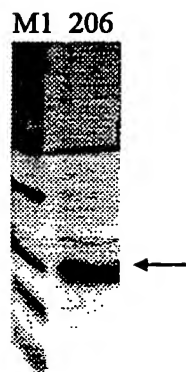
Fig. 5

128 (101 kDa)**Fig. 6****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****128**

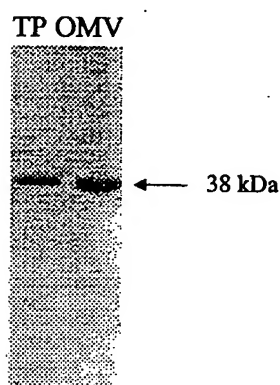
The predicted gene 128 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

A) PURIFICATION



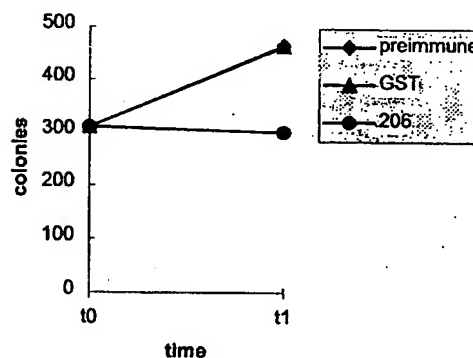
B) WESTERN BLOT



C) FACS



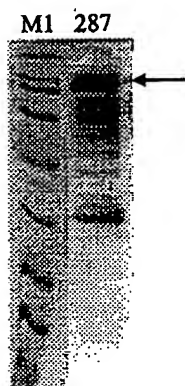
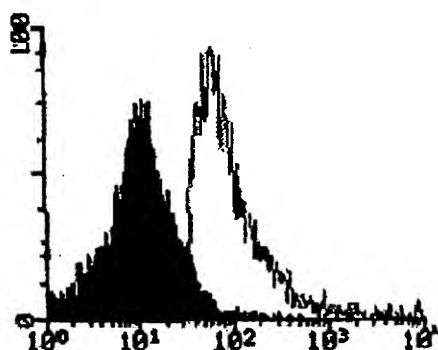
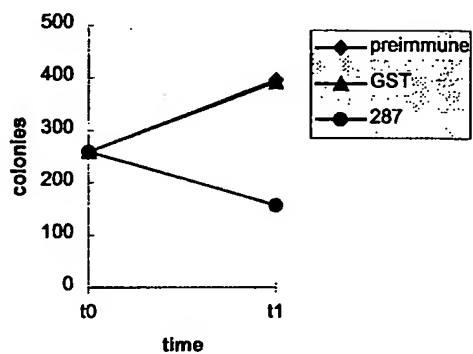
D) BACTERICIDAL ASSAY



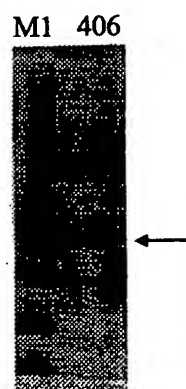
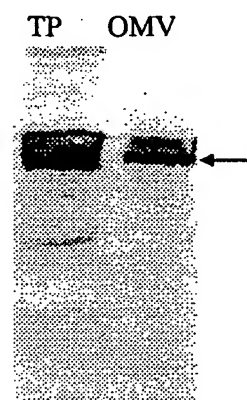
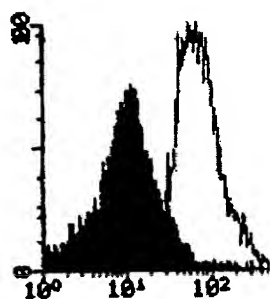
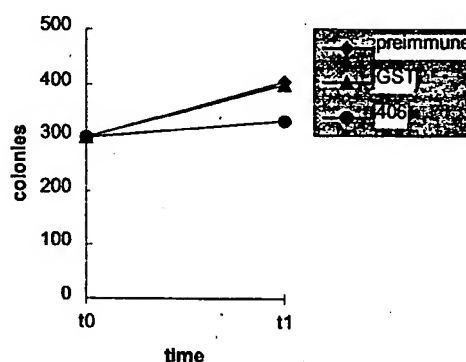
E) ELISA assay: positive

206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

287 (78 kDa)**Fig. 8****A) PURIFICATION****B) FACS****C) BACTERICIDAL ASSAY****D) ELISA assay : positive****287**

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

406 (33 kDa)**Fig. 9****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay : positive****406**

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

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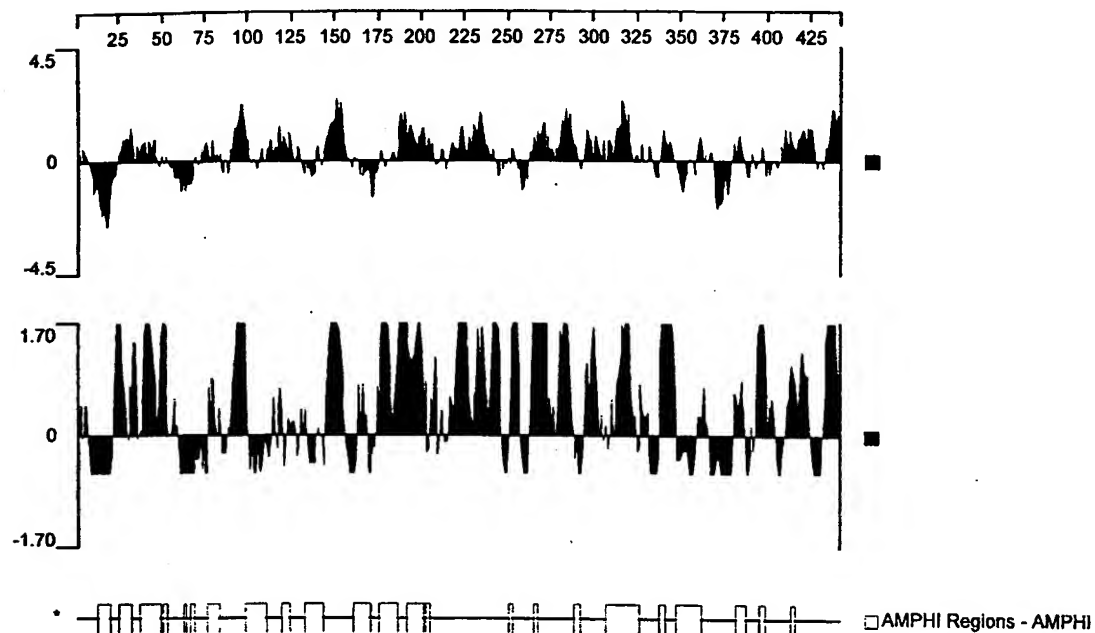
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

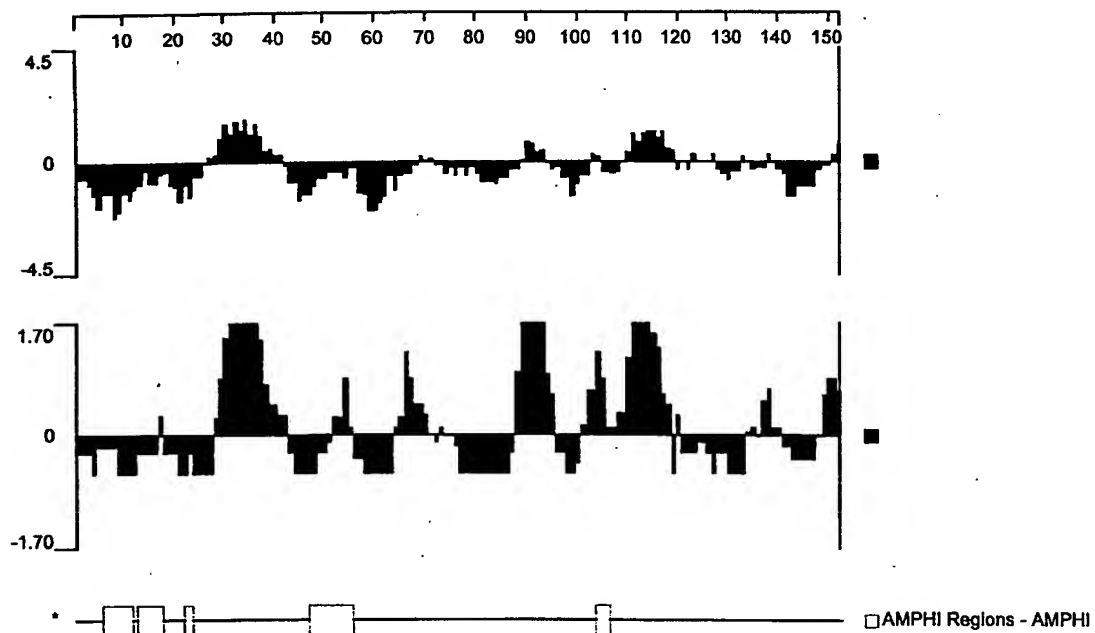
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

11/30

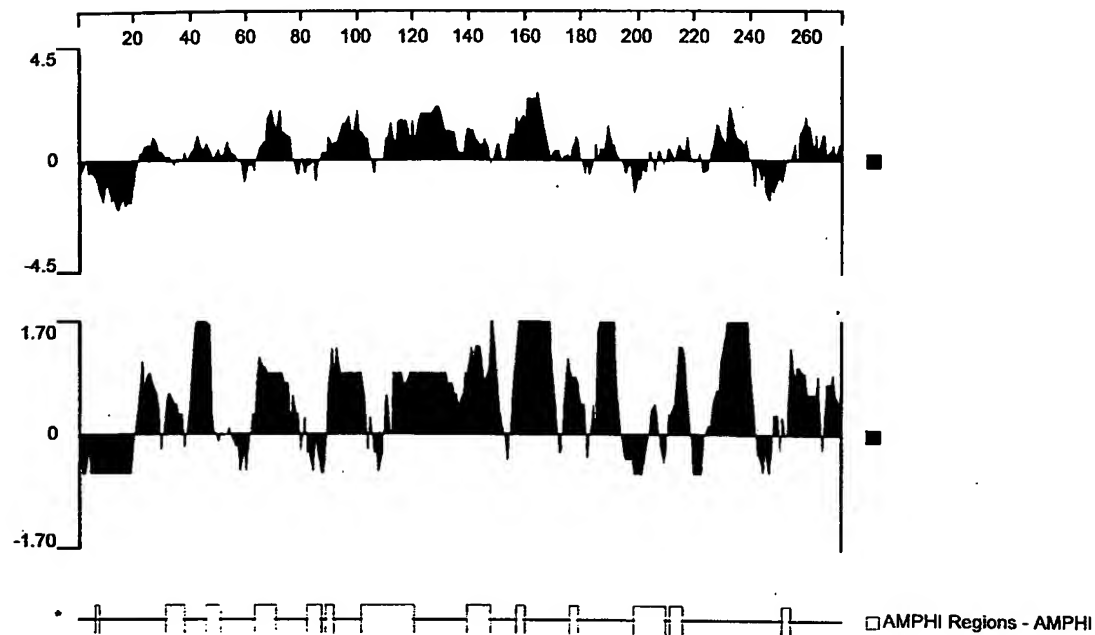
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

12/30

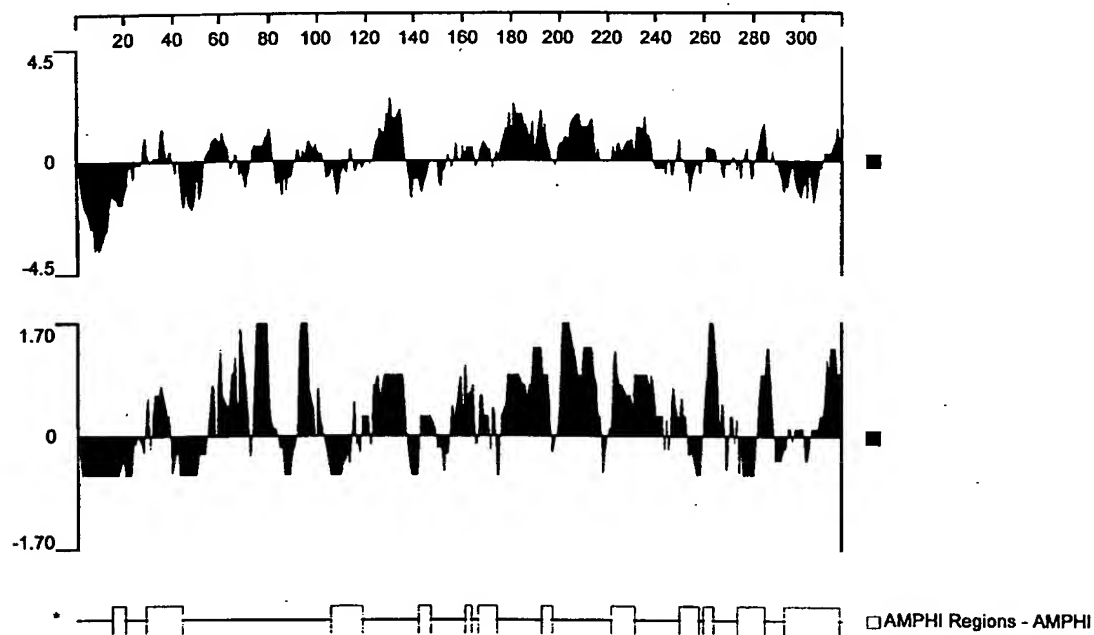
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

13/30

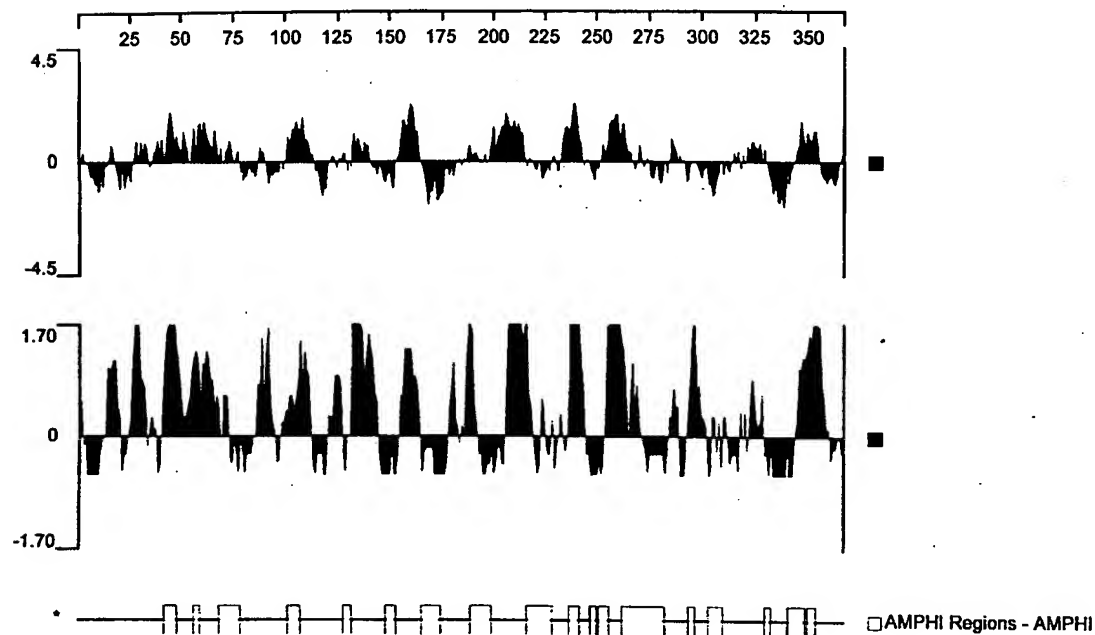
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

14/30

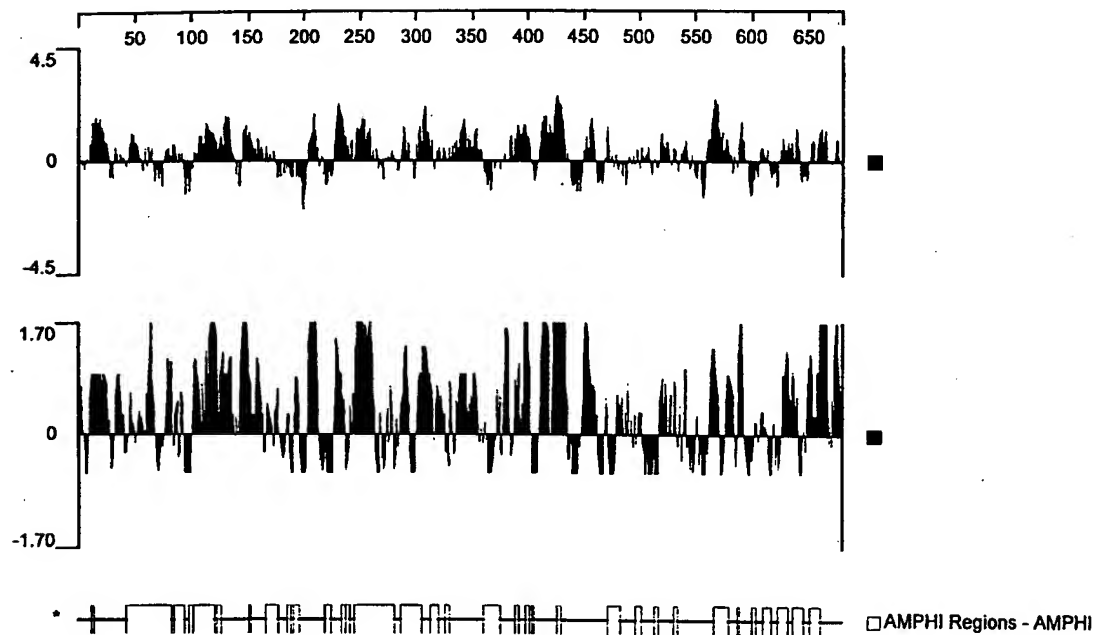
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

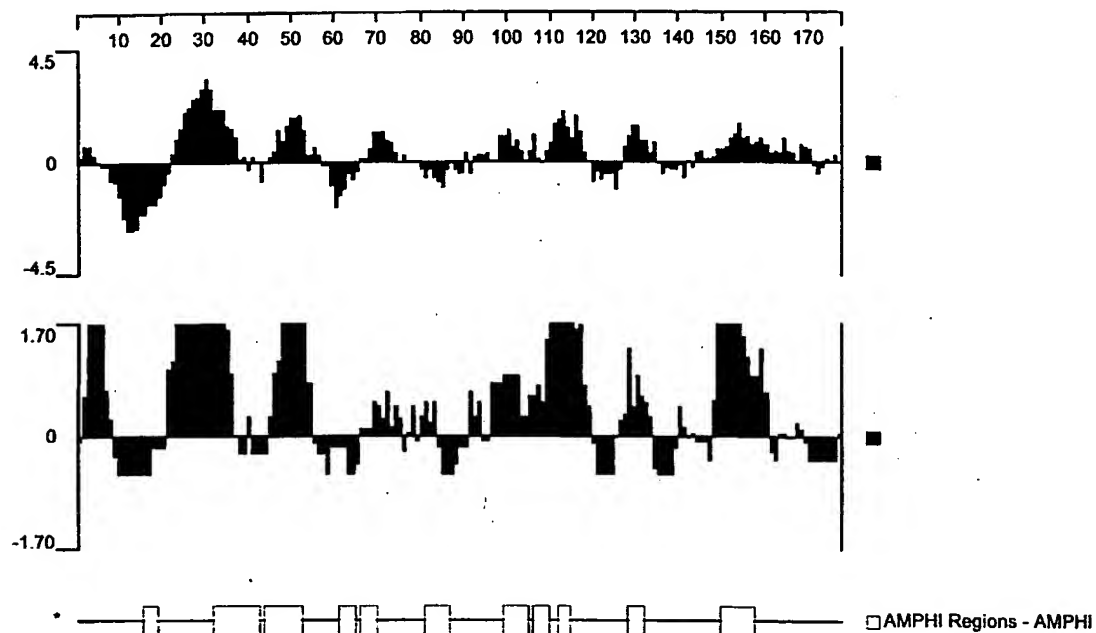
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

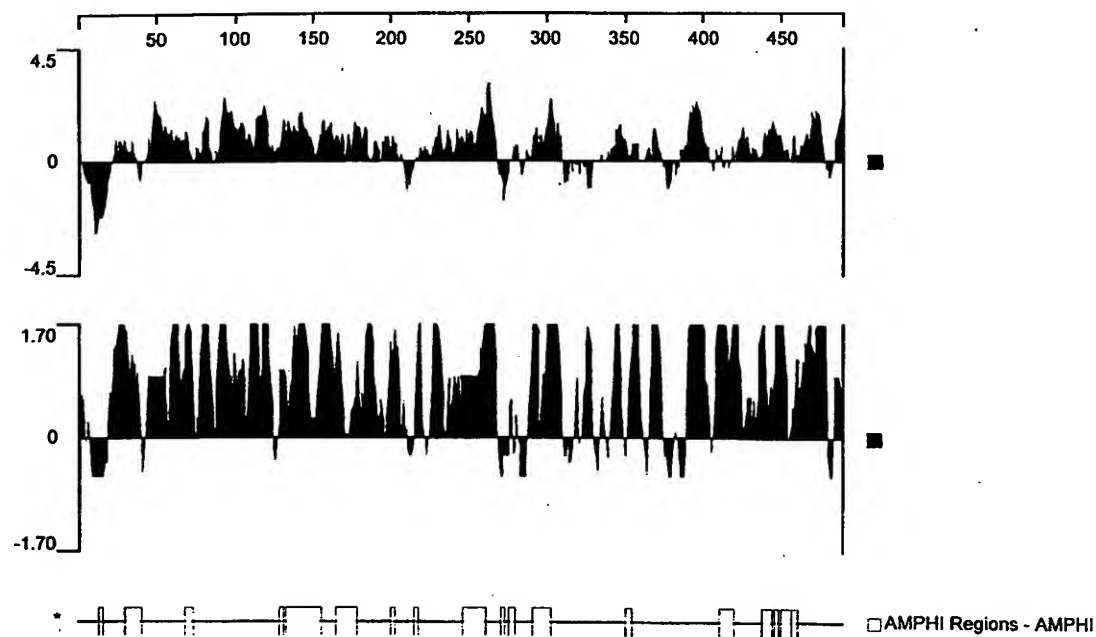
287Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

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406

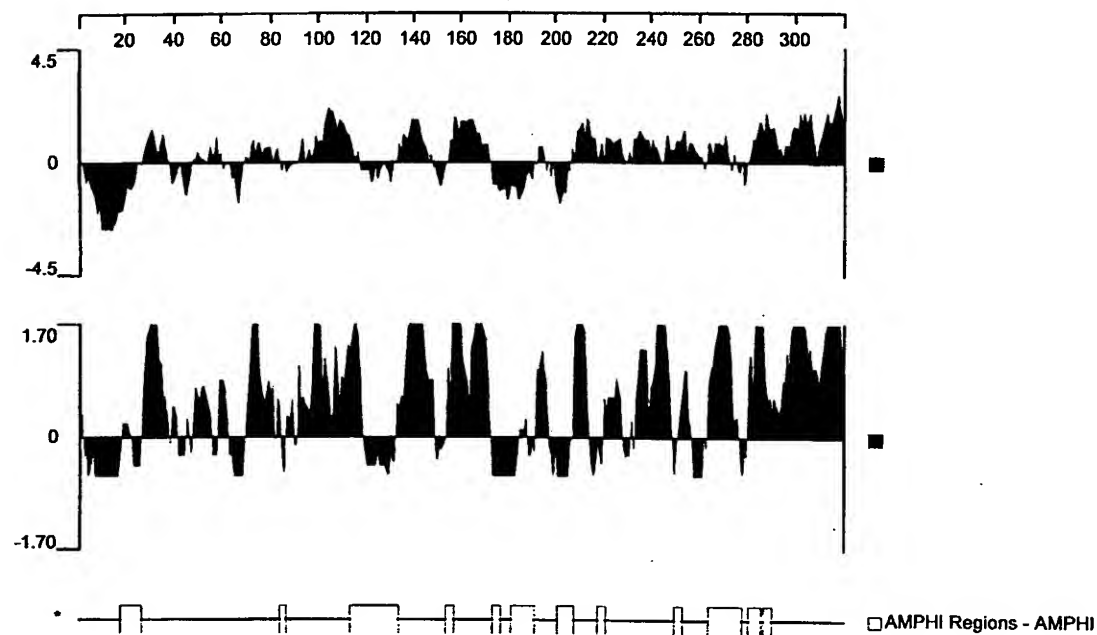
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

Fig. 19B

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

Fig. 20A


```

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fal090 121 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
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gnmq29 181 DRGYQVSKTAAYNLLSPYSHNGILKGRFVVEEQPK
x2491 181 DRGYQVSKTAAYNLLSPYSHNGILKGRFVVEEQPK
gnmq14 181 DRGYQVSKTAAYNLLSPYSHNGILKGRFVVEEQPK
gnmq18 181 DRGYQVSKTAAYNLLSPYSHNGILKGRFVVEEQPK
gnmq26 181 DRGYQVSKTAAYNLLSPYSHNGILKGRFVVEEQPK

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Fig. 20B


```

287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVVE.....KETEAK
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVVE.....KETEAK
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVVE.....KETEAK
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVVE.....KETEAK
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVVE.....KETEAK
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVVE.....KETEAK

287_14 50 KEDAPQAGSGQGQAPSKQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
287_2 50 KEDAPQAGSGQGQAPSKQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
287_21 50 KEDAPQAGSGQGQAPSKQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNDMPQNAADT
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287_9 61 VSGAPQADT...QDATAGCGQDMAAVSAENTGNGGAATDMPKNEDEGAQNDMPQNAAGT
fa1090 61 AGGAPQADT...QDATAGCGQDMAAVSAENTGNGGAATDMPKNEDEGAQNDMPQNAAGT

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287_21 110 DSLTPNHHTPASNMPAGNMENQAPDAGESQOPANQPDMANADGMQGGDDPSAGGQENAGNTA
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287_9 178 DQETNQAENNQTAGSQMPASSSTNPSTNSGGDFGRTHNSVVIDGPSQNTLTHCKGDS
fa1090 117 .ESANQTAGNQTAGSQMPASSSTNPSTNSGGDFGRTHNSVVIDGPSQNTLTHCKGDS

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287_2 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNKGKNEFVGLVADSVQMKGINQYII
287_21 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNKGKNEFVGLVADSVQMKGINQYII
z2491 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNKGKNEFVGLVADSVQMKGINQYII
287_9 238 CDRD.FLDEEAPPKSEFEKLSDAKISNYKKDGKNKGKNEFVGLVADSVQMKGINQYII
fa1090 176 CNGDNFLDEEAPPKSEFEKLSDAKISNYKKDGKNKGKNEFVGLVADSVQMKGINQYII

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287_21 286 FYKPKP...STARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
z2491 286 FYKPKP...STARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_9 293 IVKDKSAS...STARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
fa1090 232 FYTDKPT.....RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPGRFAA
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287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFHTENGRPSPGRFAA
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287_21 404 KVDFGSKSVGDIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
z2491 404 KVDFGSKSVGDIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_9 413 KVDFGSKSVGDIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
fa1090 345 KVDFGSKSVGDIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA

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FIG. 21A

287_14	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKEQD*

FIG. 21B

z2491_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv26_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv22_519ass	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
fa1090_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv32_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv11_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv28_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv96_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv02_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv03_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv04_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv05_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv01_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv07_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv12_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv18_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv19_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv21_519ass	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv27_519	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv20_519ass	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv06_519ass	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE
zv29_519ass	121	RMELDKTFFERDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQ	EILRSMQAQITAERE

FIG. 22A


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z2491_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR

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z2491_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass 241 LVAEANAEAIROIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

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z2491_519 301 ISAGMKIIDSSKTA*
zv26_519 301 ISAGMKIIDSSKTA*
zv22_519ass 301 ISAGMKIIDSSKTA*
fa1090_519 301 ISAGMKIIDSSKTA*
zv32_519 301 ISAGMKIIDSSKTA*
zv11_519 301 ISAGMKIIDSSKTA*
zv28_519 301 ISAGMKIIDSSKTA*
zv96_519 301 ISAGMKIIDSSKTA*
zv02_519 301 ISAGMKIIDSSKTA*
zv03_519 301 ISAGMKIIDSSKTA*
zv04_519 301 ISAGMKIIDSSKTA*
zv05_519 301 ISAGMKIIDSSKTA*
zv01_519 301 ISAGMKIIDSSKTA*
zv07_519 301 ISAGMKIIDSSKTA*
zv12_519 301 ISAGMKIIDSSKTA*
zv18_519 301 ISAGMKIIDSSKTA*
zv19_519 301 ISAGMKIIDSSKTA*
zv21_519ass 301 ISAGMKIIDSSKTA*
zv27_519 301 ISAGMKIIDSSKTA*
zv20_519ass 301 ISAGMKIIDSSKTA*
zv06_519ass 301 ISAGMKIIDSSKTA*
zv29_519ass 301 ISAGMKIIDSSKTA*

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Fig. 22B

Fig. 23A

Fig. 23B

Fig. 23C

fa1090	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMKPEYRP*
zm33asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm32asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm23asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm27bc	421	QKTTGYVWQLLPNGMKPEYRP*
zm09	421	QKTTGYVWQLLPNGMKPEYRP*
zm10	421	QKTTGYVWQLLPNGMKPEYRP*
zm24	421	QKTTGYVWQLLPNGMKPEYRP*
zm25	421	QKTTGYVWQLLPNGMKPEYRP*
zm14	421	QKTTGYVWQLLPNGMKPEYRP*
zm04	421	QKTTGYVWQLLPNGMKPEYRP*
zm11asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm08n	421	QKTTGYVWQLLPNGMKPEYRP*
zm96	421	QKTTGYVWQLLPNGMKPEYRP*
zm01	421	QKTTGYVWQLLPNGMKPEYRP*
zm02	421	QKTTGYVWQLLPNGMKPEYRP*
zm03	421	QKTTGYVWQLLPNGMKPEYRP*
zm07	421	QKTTGYVWQLLPNGMKPEYRP*
zm12	421	QKTTGYVWQLLPNGMKPEYRP*
zm18	421	QKTTGYVWQLLPNGMKPEYRP*
zm19	421	QKTTGYVWQLLPNGMKPEYRP*
zm20	421	QKTTGYVWQLLPNGMKPEYRP*
zm21	421	QKTTGYVWQLLPNGMKPEYRP*
zm06	421	QKTTGYVWQLLPNGMKPEYRP*
zm17	421	QKTTGYVWQLLPNGMKPEYRP*
zm13	421	QKTTGYVWQLLPNGMKPEYRP*
zm05	421	QKTTGYVWQLLPNGMKPEYRP*
z2491	421	QKTTGYVWQLLPNGMKPEYRP*
zm22	421	QKTTGYVWQLLPNGMKPEYRP*
zm26	421	QKTTGYVWQLLPNGMKPEYRP*
zm28	421	QKTTGYVWQLLPNGMKPEYRP*
zm29asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm16	421	QKTTGYVWQLLPNGMKPEYRP*
zm15	421	QKTTGYVWQLLPNGMKPEYRP*
zm31asbc	421	QKTTGYVWQLLPNGMKPEYRP*

Fig. 23D